

Supplementary Materials

Metabolic Rewiring in tea plants in Response to Gray Blight Disease Unveiled by Multi-Omics Analysis

Shiqin Zheng ^{1,2,3}, Zhenghua Du ², Xiaxia Wang ², Chao Zheng ²,
Zonghua Wang ^{3,4,*} and Xiaomin Yu^{2,*}

¹Tea Research Institute, Fujian Academy of Agricultural Sciences,
Fuzhou 350013, China

²Center for Plant Metabolomics, Haixia Institute of Science and Technology,
Fujian Agriculture and Forestry University, Fuzhou 350002, China

³State Key Laboratory of Ecological Pest Control for Fujian and Taiwan
Crops, College of Plant Protection, Fujian Agriculture and Forestry
University, Fuzhou 350002, China

⁴Fuzhou Institute of Oceanography, Minjiang University,
Fuzhou 350108, China

* **Correspondence:** wangzh@fafu.edu.cn (Z.W.); xmyu0616@fafu.edu.cn (X.Y.)

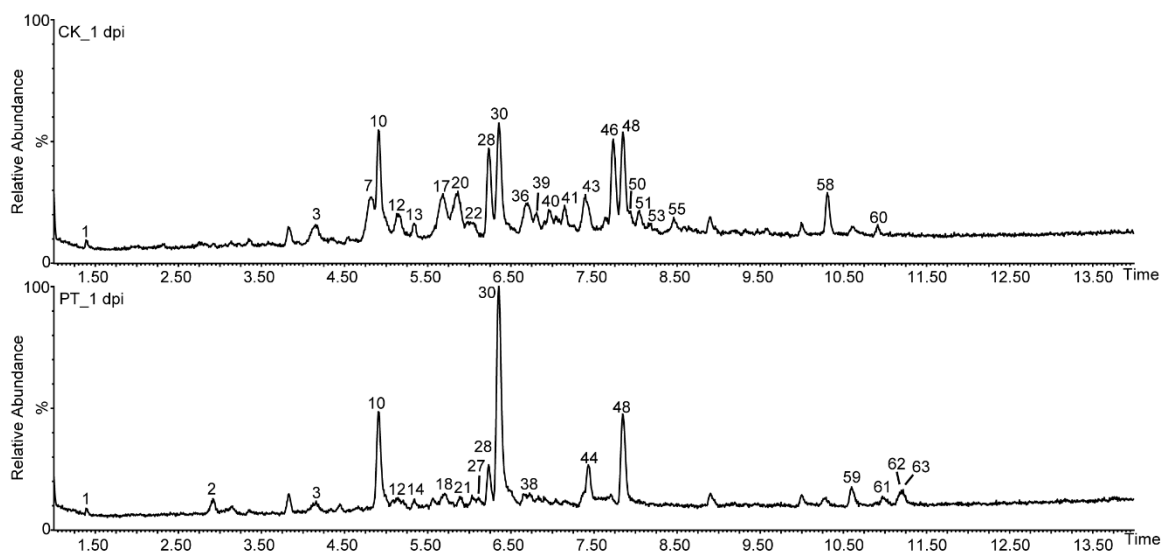


Figure S1. Representative total ion chromatograms of mock-inoculated and fungal-inoculated tea leaves at 1 dpi in the negative ionization mode. PT, tea leaves inoculated with *P. theae*. CK, tea leaves inoculated with the mock control. Peak numbering is the same as Table 1.

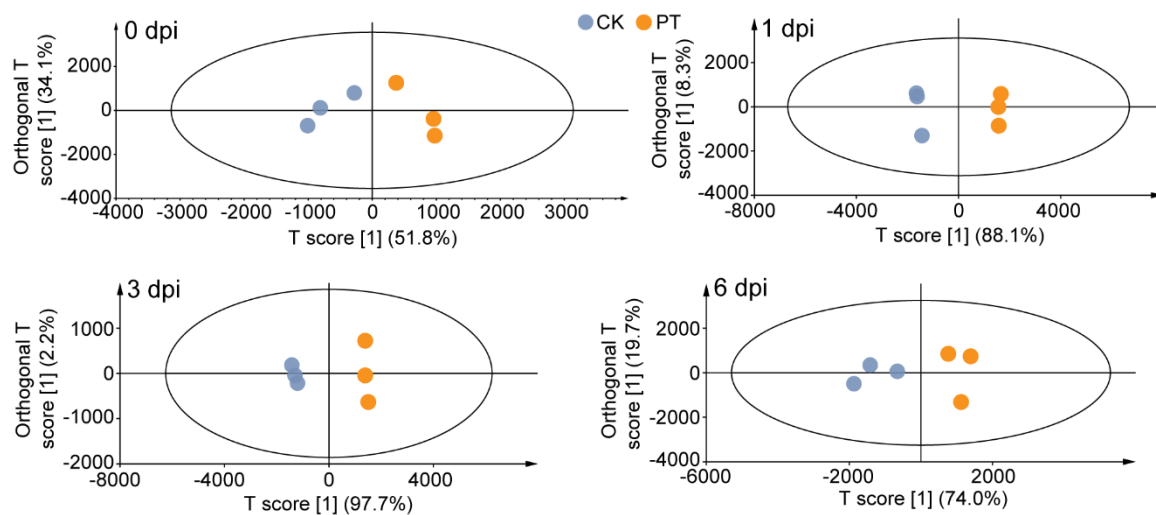


Figure S2. OPLS-DA analysis of the metabolomics datasets. PT, tea leaves inoculated with *P. theae*. CK, tea leaves inoculated with the mock control.

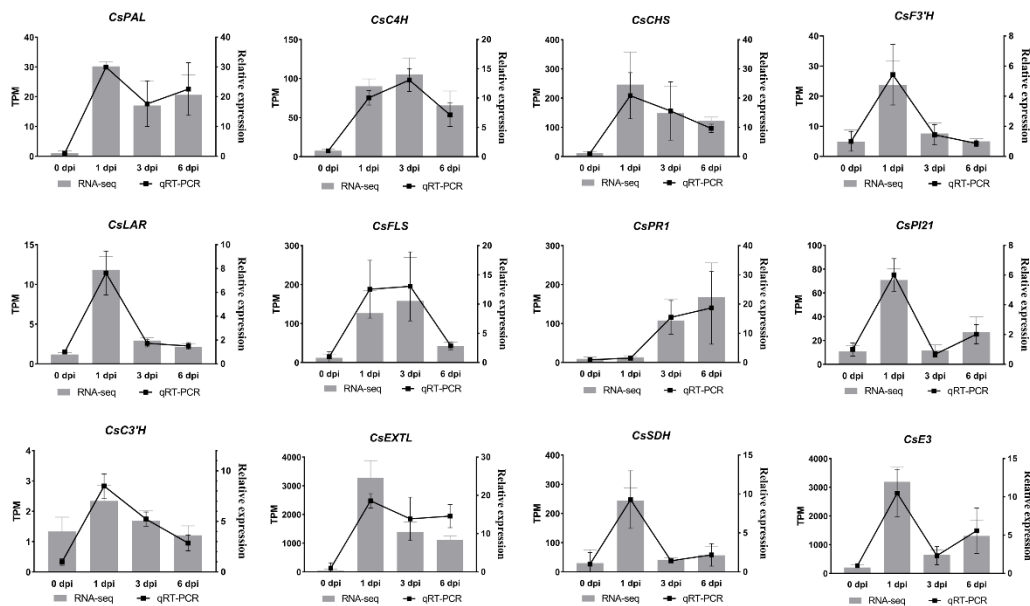
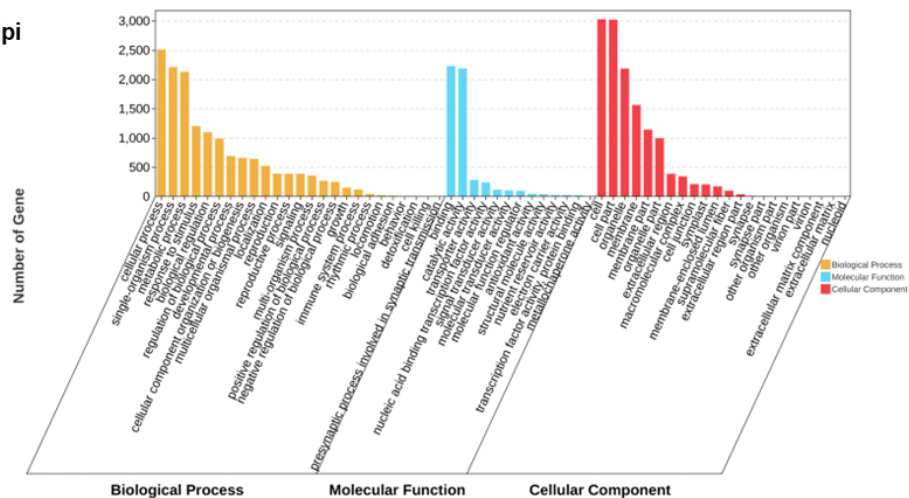
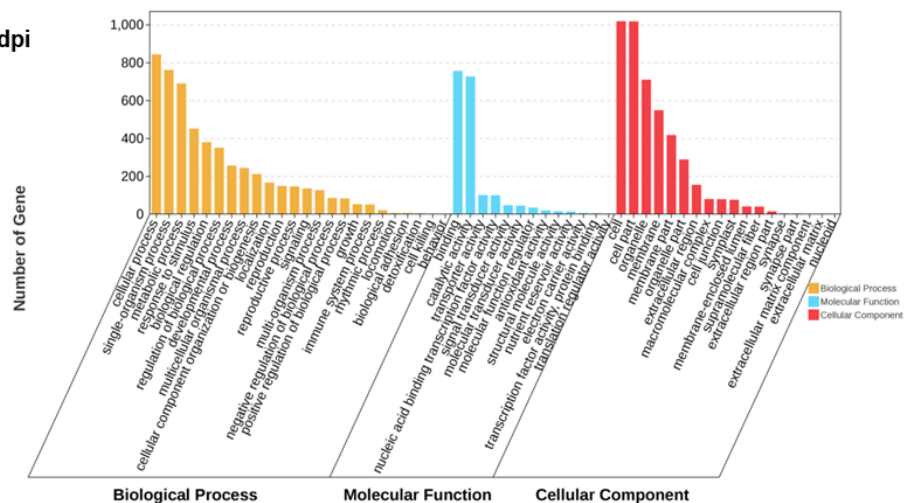


Figure S3. qRT-PCR validation of RNA-seq DEGs. PAL, phenylalanine ammonia-lyase; C4H, cinnamate-4-hydroxylase; CHS, chalcone synthase; F3'H, flavonoid 3'-hydroxylase; LAR, leucocyanidin reductase; FLS, flavonol synthase; PR1, pathogenesis-related protein 1; PI21, PYRICULARIA ORYZAE RESISTANCE 21 ; C3'H, 5-*O*-(4-coumaroyl)-D-quinic acid 3'-monooxygenase; EXTL, extension-like; SDH, shikimate dehydrogenase; E3, E3 ubiquitin ligase. The left Y-axis represents the expression data (gray bars) and the right Y-axis represents the relative expression values obtained through RT-qPCR analysis (black lines). *GADPH* gene (accession no. KA295375.1) was used as the internal control. The expression of genes in 0 dpi is set to 1.0. All values are mean \pm SD (n = 3).

1 dpi



3 dpi



6 dpi

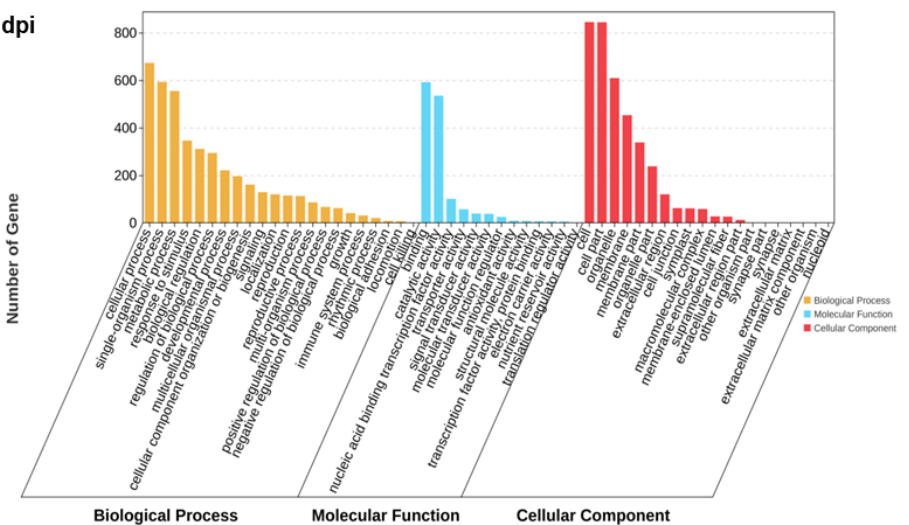


Figure S4. Gene ontology (GO) enrichment analysis of differentially expressed genes in gray blight-infected tea plants at 1, 3 and 6 dpi.

Table S1. List of primers for qRT-PCR.

Target Gene ^a	Forward primer (5'-3')	Reverse primer (5'-3')
<i>CsPAL</i>	TCCAATTCCTTGCCAATCCTGTAA	ATCAACTGCCTCGGCTGTCTTTCT
<i>CsC4H</i>	TGCAAAGCTCTCTGGCTATG	CCTGAACTCTTCTGGGTCTTC
<i>CsCHS</i>	GTGCTATCGATGGGCATCTT	AGGGTTGGAATGCCTCATTTA
<i>CsF3'H</i>	GTTCGACCAGAACGATTCTACC	ATAACTGGACCATACGCAACCCTA
<i>CsLAR</i>	AACTCCCTAGAGTAACCATCA	GATGAAGATGTCGTGGGTGAA
<i>CsFLS</i>	TGGAAAGACGGTAATTGGGTAG	ACTCCTGTGAAGAACTCTTG
<i>CsPR1</i>	TCCTATGCCCAAACTCACAACAAG	ACCCATCCTCGAACTAGCATACCT
<i>CsPI21</i>	CTACAGGAATCCAAAGAGTCCAA	CATAGCATTGCCCACAACATATC
<i>CsC3'H</i>	CGGCAACCTCTACGACATAAA	CAACTCTGAGCTCGAACTATCA
<i>CsEXTL</i>	TGTCTCTGAGCTTGCCATTAG	GAGGTGGTGGTGATTTGTAGT
<i>CsSDH</i>	GTATTGCTCCCATCTCCGCTCACTG	ATGACAACCCTCGCTCCTCTGCTT
<i>CsE3</i>	GATGCTGCTACTCGGTTCTT	GGCATGACGGTTACATCATTTTC

^aPAL, phenylalanine ammonia-lyase; C4H, cinnamate-4-hydroxylase; CHS, chalcone synthase; F3'H, flavonoid 3'-hydroxylase; LAR, leucocyanidin reductase; FLS, flavonol synthase; PR1, pathogenesis-related protein 1; PI21, PYRICULARIA ORYZAE RESISTANCE 21 ; C3'H, 5-*O*-(4-coumaroyl)-D-quinic acid 3'-monooxygenase; EXTL, extension-like; SDH, shikimate dehydrogenase; E3, E3 ubiquitin ligase.

Table S2. The quality of RNA-seq data.

Sample	Clean reads	Q30	GC%	Mapped rate (%)
PT1_0dpi	25805408	93.21	44	87.50
PT2_0dpi	26011094	92.30	45	88.18
PT3_0dpi	36586286	95.14	45	89.61
PT1_1dpi	25979638	89.29	43	86.66
PT2_1dpi	26575605	93.38	43	86.90
PT3_1dpi	26345386	91.98	43	86.09
PT1_3dpi	28349686	90.43	43	86.98
PT2_3dpi	26270282	92.31	43	86.00
PT3_3dpi	27623253	93.89	43	87.12
PT1_6dpi	28009516	91.86	43	86.84
PT2_6dpi	26367665	89.98	43	87.02
PT3_6dpi	26717807	91.03	44	87.32