Supplementary Material

Title:

Arbuscular mycorrhizal fungus alters root system architecture in *Camellia sinensis* L. as revealed by RNA-Seq analysis

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## Supplementary Tables and Figures

Supplementary Table 1 Primers of each gene in real-time quantitative RT-PCR

|  |  |  |
| --- | --- | --- |
| **Gene ID** | **Gene Description** | **Sequence of primer (5’-3’)** |
| 114278857 | auxin-responsive protein SAUR32-like | F: ACCCGAAGGTTGCTTCTCAGR: GCCACAGCGACCCATAGAAA |
| 114308158 | auxin response factor 10 | F: ACACACCGGAGATGAACCCTR: GAAGCAGGTTTCTCCCACAAC |
| 114277140 | auxin-repressed protein | F: GGACGATGTGTTAGCCGGACR: CGACGACGAAGACGAACTTG |
| 114282010 | serine carboxypeptidase-like 40 | F: CCACACGGTGAATCAACCAAR: AAGAAGGAAGGCTAGGATCGG |
| 114301937 | 1-deoxyxylulose 5-phosphate synthase | F: CACACCTGACAACATCCCCAR: GGTGTGGGTTGCTTTTCTCC |
| 114263278 | NADPH-dependent 1-acyldihydroxyacetone phosphate reductase | F: GGCTAAGGCTGGTCCAACAAR: ACTAGCGCCACGTTAATCCC |
| 114288835 | terpenoid synthase, partial | F: GGTTTCGACTCGCTTTCGTCR: AAGACGTGTCAACCACCCATT |
| 114273524 | lactate dehydrogenase | F: AATAGCCAAGGTTGAGAGAAGAGTR: CCTAGTCCATTAGGGTTGCTTTTC |
| 114305402 | gibberellin-regulated family protein | F: ATTGCGTGGAAGCTCTCTGGR: CAGGAAGCTCAAGACTGGGA |
| 114260196 | ethylene response factor | F: CCATCCCGACTCTGTCTTCTCR: GGGCTCTCTGCTCCACTCAT |
| 114323882 | ethylene-responsive transcription factor ERF110 | F: TCCCTCTCCACCCAATACCCR: CCGAACCCCTCTGTAGGACT |
| 114263353 | sugar transport protein 1-like | F: CAAGTTCAGAGGCAACAAGGCR: TCTGTGCTCATCCTCTGCAAC |
| 114278857 | auxin-responsive protein SAUR32-like | F: CTTCGTCATCTTCTTCGTGCCR: TCCATTCTTCATCTCGATTTCCTT |
| AB120309.1 | Camellia sinensis 18S Ribosomal RNA | F: CGCGCAAATTACCCAATCCTR: ACCAGACTTGCCCTCCAATG |

Supplementary Table 2 Correlation analysis results between contents of sugar and phosphorus and indexes of root system architecture. Correlation coefficients filled with red and dark red indicated significance at *p* < 0.05 and *p* < 0.01, respectively. AR: adventitious root number; LR: lateral root number; TLR: total lateral root number; TRL: total root length; TPA: total root projected area; TSA: total root surface area; TV: total root volume; AD: average diameter of root; D1L: length of 0.000 mm ≤ AD < 0.500 mm; D2L: length of 0.500 mm ≤ AD < 2.000 mm; D3L: length of 2.000 mm ≤ AD < 3.000 mm; D4L: length of 3.000 mm ≤ AD < 5.000 mm.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| RSA indexes | Sucrose | Reducing sugar | Soluble sugar | Phosphorus |
| TRL | **-0.813\*** | -0.549 | -0.461 | 0.638 |
| TPA | -0.705 | -0.491 | -0.589 | 0.509 |
| TSA | -0.705 | -0.491 | -0.589 | 0.509 |
| TV | -0.65 | -0.566 | -0.639 | 0.439 |
| AD | -0.729 | -0.271 | -0.505 | 0.654 |
| D1L | **-0.833\*** | -0.491 | -0.217 | 0.714 |
| D2L | -0.252 | -0.276 | -0.623 | 0.082 |
| D3L | -0.197 | -0.627 | -0.186 | 0.195 |
| D4L | -0.513 | 0.301 | 0.283 | 0.537 |
| AR | 0.709 | 0.68 | 0.301 | -0.787 |
| 1st LR | -0.329 | -0.178 | -0.544 | 0.469 |
| 2nd LR | **-0.957\*\*** | -0.659 | -0.661 | **0.941\*\*** |
| 3rd LR | 0.541 | 0.66 | 0.383 | -0.656 |
| 4th LR | 0.800 | 0.683 | 0.715 | **-0.892\*** |
| TLR | **-0.818\*** | -0.488 | -0.658 | **0.820\*** |
| 1st LR / AR | -0.763 | -0.666 | -0.553 | **0.919\*\*** |
| 2nd LR / 1st LR | **-0.982\*\*** | -0.734 | -0.582 | **0.926\*\*** |
| 3rd LR / 2nd LR | 0.811 | 0.772 | 0.624 | **-0.919\*\*** |
| 4th LR / 3rd LR | **0.860\*** | 0.673 | 0.723 | **-0.876\*** |
| 1st LR / TRL | 0.423 | 0.294 | -0.045 | -0.207 |
| 2nd LR / TRL | **-0.877\*** | -0.609 | -0.635 | **0.961\*\*** |
| 3rd LR / TRL | **0.896\*** | 0.791 | 0.602 | **-0.942\*\*** |
| 4th LR / TRL | **0.845\*** | 0.705 | 0.709 | **-0.921\*\*** |
| TLR / TRL | -0.186 | -0.053 | -0.405 | 0.371 |

Supplementary Table 3 Model fit and quality indices

|  |  |  |
| --- | --- | --- |
| **Index** | **Value** | **Value Interpretation** |
| Average path coefficient (APC) | 0.967*p* < 0.001 | Significant if *p* <  0.05 |
| R-squared (AARS) | 0.844*p* < 0.001 | Significant if *p* <  0.05 |
| Average adjusted R-squared (AARS) | -0.797*p* < 0.001 | Significant if *p* <  0.05 |
| Average block VIF (AVIF) | Inf | acceptable if <= 5, ideally <= 3.3 |
| Average full collinearity VIF (AFVIF) | Inf | acceptable if <= 5, ideally <= 3.3 |
| Tenenhaus GoF (GoF) | 0.515 | small >= 0.1, medium >= 0.25, large >= 0.36 |
| Sympson’s paradox ratio (SPR) | 0.818 | acceptable if >= 0.7, ideally = 1 |
| Statistical suppression ratio (SSR) | 0.727 | acceptable if >= 0.7 |
| Nonlinear bivariate causality direction ratio (NLBCDR) | 0.727 | acceptable if >= 0.7 |

Supplementary Table 4 Total effects of different paths.

|  |  |  |
| --- | --- | --- |
| **Path** | **Path coefficient** | ***p* value** |
| AMF→P | 0.980 | <0.001 |
| AMF→Sugar | 0.311 | 0.166 |
| AMF→Lipid | 0.688 | 0.008 |
| AMF→Auxin | 0.704 | 0.007 |
| AMF→Ethylene | 0.706 | 0.006 |
| AMF→Root branching (indirect) | 1.234 | <0.001 |
| AMF→Root branching(direct) | 2.500 | <0.001 |
| AMF→Root branching | 3.734 | <0.001 |
| P→Root branching | 1.730 | <0.001 |
| Sugar→Root branching | 0.084 | 0.415 |
| Lipid→Root branching | -0.387 | 0.103 |
| Auxin→Root branching | 1.117 | <0.001 |
| Ethylene→Root branching | -1.429 | <0.001 |

Supplementary Figure 1 Validation of RNA-seq results by qRT-PCR. Data from qRT-PCR (Black-filled circle) and RNA-Seq (White column) of 12 selected genes were means of three replicates and bars represent Standard Error. C: non-mycorrhizal treatment, T: mycorrhizal treatment.



Supplementary Figure 2 Correlation analysis of fold change data between qRT-PCR and RNA-seq. Scatterplots were generated by the log2(Fold change) from RNA-seq (x-axis) and qRT-PCR (y-axis).



Supplementary Figure 3 Number of differentially expressed genes enriched in different GO terms



Supplementary Figure 4 The main results of KEGG pathway analysis

