

**Title**

RNA-seq analysis fluorescence imaging of melon powdery mildew disease reveal an orchestrate reprogramming of host physiology

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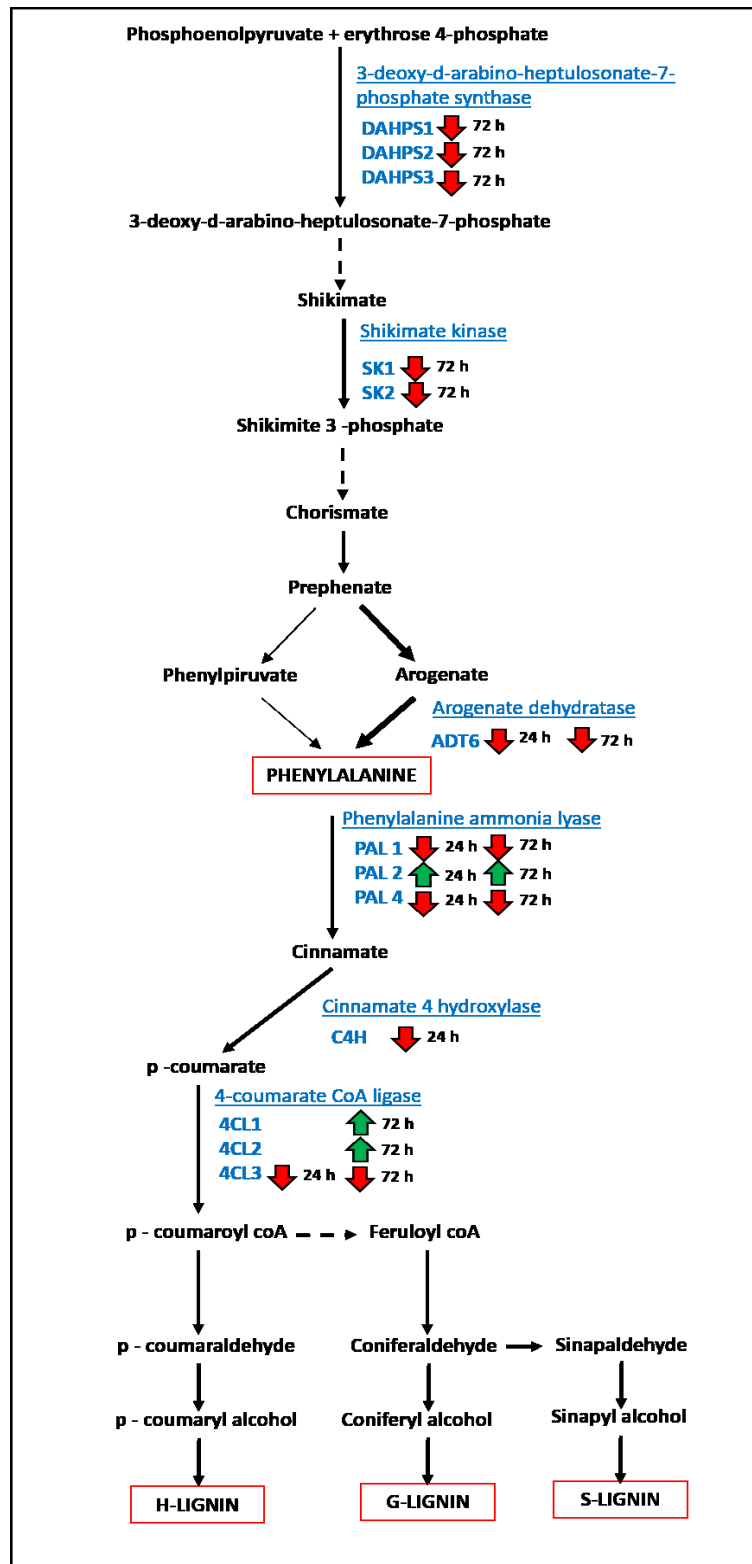
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**Table S1** Summary of statistics of RNA-Seq analysis of melon-*P. xanthii* interaction

| Samples           | Input reads | Output reads | Rejected reads<br>(%) | Reads aligned to<br>reference (%) |
|-------------------|-------------|--------------|-----------------------|-----------------------------------|
| Uninfected24hpi_1 | 87,809,876  | 75,500,680   | 10.41                 | 85.69                             |
| Uninfected24hpi_2 | 76,542,470  | 68,370,412   | 7.76                  | 84.78                             |
| Uninfected24hpi_3 | 106,356,748 | 94,607,324   | 7.82                  | 83.35                             |
| Uninfected48hpi_1 | 118,995,292 | 102,632,628  | 10.44                 | 85.27                             |
| Uninfected48hpi_2 | 77,108,192  | 68,918,670   | 7.77                  | 88.15                             |
| Uninfected48hpi_3 | 115,508,352 | 102,702,870  | 7.65                  | 85.83                             |
| Uninfected72hpi_1 | 93,416,186  | 82,948,230   | 8.00                  | 87.68                             |
| Uninfected72hpi_2 | 69,539,512  | 58,948,720   | 11.34                 | 85.00                             |
| Uninfected72hpi_3 | 110,202,904 | 85,023,518   | 19.62                 | 84.25                             |
| Infected24hpi_1   | 109,377,644 | 97,468,648   | 7.38                  | 83.61                             |
| Infected24hpi_2   | 93,731,880  | 85,484,974   | 5.80                  | 84.10                             |
| Infected24hpi_3   | 76,648,932  | 67,916,294   | 8.26                  | 84.90                             |
| Infected48hpi_1   | 87,981,974  | 74,466,522   | 11.31                 | 84.00                             |
| Infected48hpi_2   | 89,057,812  | 76,561,898   | 9.84                  | 83.87                             |
| Infected48hpi_3   | 85,438,210  | 73,423,600   | 10.31                 | 83.64                             |
| Infected72hpi_1   | 88,500,998  | 74,541,194   | 11.80                 | 85.10                             |
| Infected72hpi_2   | 76,639,666  | 66,055,082   | 9.75                  | 84.89                             |
| Infected72hpi_3   | 98,931,690  | 80,396,216   | 14.68                 | 83.80                             |



**Fig. S1** Schematic representation of phenylpropanoids pathway of *P. xanthii*-infected melon leaves showing all DEGs at 24 and 72 hpi. The colour key represents dysregulation of melon genes from infected plants compared to uninfected controls. Green arrows represent up-regulated genes and red arrows represent down-regulated genes. Discontinuous black arrows show incomplete pathway

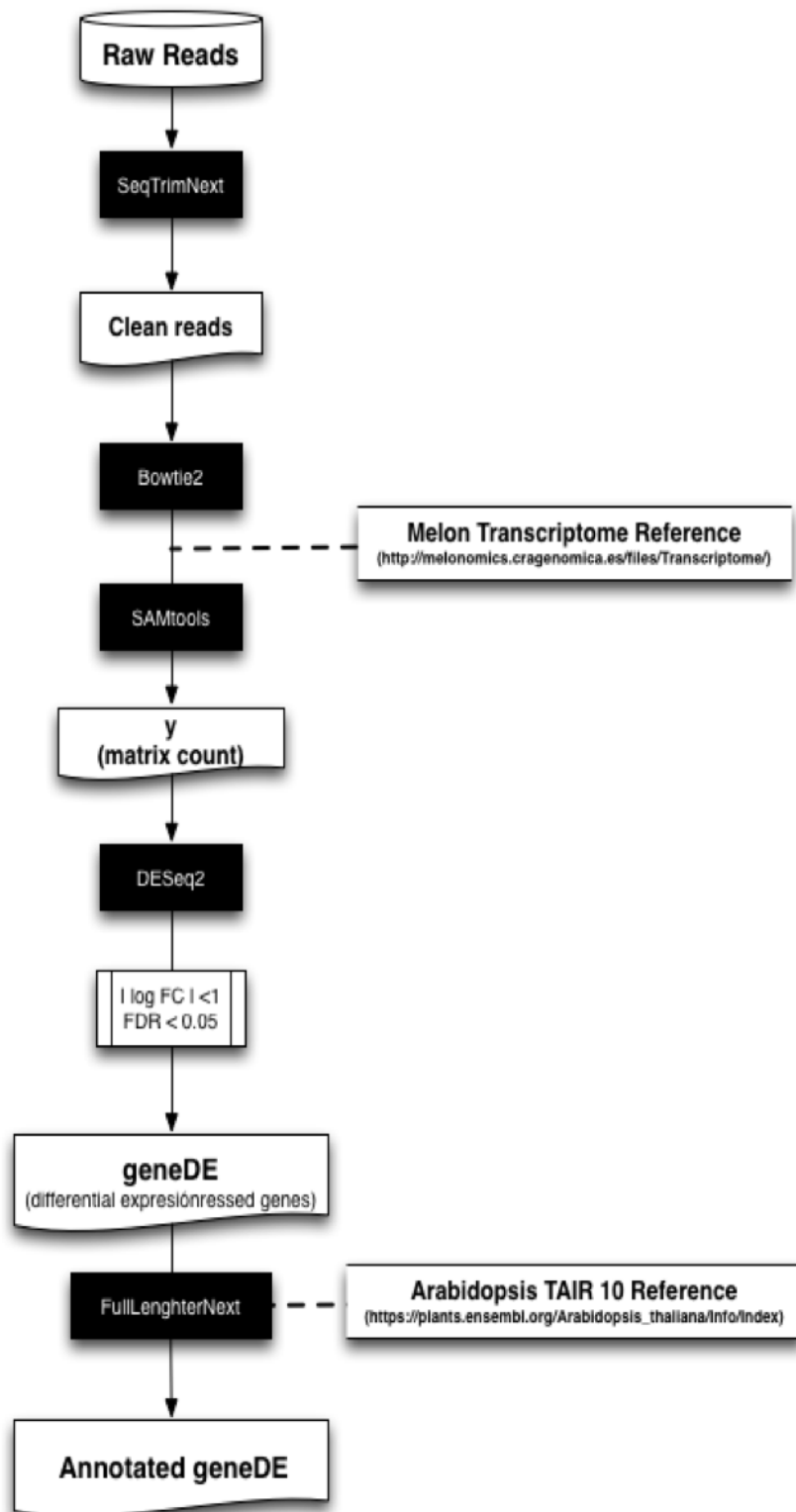
**Table S4** Impact of *P. xanthii* infection on pigment content of melon leaves

| Pigments <sup>a</sup> | 24 hpi                   |           | 72 hpi     |           |
|-----------------------|--------------------------|-----------|------------|-----------|
|                       | Uninfected               | Infected  | Uninfected | Infected  |
| Chl <i>a</i>          | 0.84±0.12 <sup>b,c</sup> | 0.78±0.03 | 0.73±0.04  | 0.65±0.05 |
| Chl <i>b</i>          | 0.26±0.03                | 0.29±0.03 | 0.27±0.04  | 0.20±0.04 |
| Chl T                 | 1.10±0.12                | 1.08±0.06 | 1.00±0.09  | 0.85±0.09 |
| Xant + Car            | 0.21±0.02                | 0.20±0.01 | 0.18±0.01  | 0.19±0.01 |

<sup>a</sup>Abbreviations are: Chl *a*, chlorophyll *a*; Chl *b*, chlorophyll *b*; Chl T, total chlorophyll content; Xant + Car, xanthophylls and carotenoids.

<sup>b</sup>Values shown are average values (n=6) in  $\mu\text{g mg}^{-1}$  of fresh weight  $\pm$ SE.

<sup>c</sup>No statistically significant differences between uninfected and infected samples were obtained according to two-tailed Student's *t* test.



**Fig S2.** Schematic workflow used to perform the RNA-seq analysis of *P. xanthii*-melon compatible interaction

**Table S5** Oligonucleotides used in this study

| Gene         | Primer name | Sequence                    | Amplicon size |
|--------------|-------------|-----------------------------|---------------|
| <i>lhcb6</i> | lhcb6-F     | 5'-GAATCCCATGGTTCTGAAGCC-3' | 214 bp        |
|              | lhcb6-R     | 5'-GGATACCCTTGTCTCCGGT-3'   |               |
| <i>psbA</i>  | psbA-F      | 5'-TTCTGCAGCTATCGGTTTGC-3'  | 175 bp        |
|              | psbA-R      | 5'-AATCCAAGGACGCATACCCA-3'  |               |
| <i>psbS</i>  | Psbs-F      | 5'-GTTTCACCCCTCTTGCTGTG-3'  | 175 bp        |
|              | Psbs-R      | 5'-AATGATGCAGCAAAGCCGAT-3'  |               |
| <i>petE</i>  | petE2-F     | 5'-CATCCCCAAAGCTTAGCGTC-3'  | 201 bp        |
|              | petE2-R     | 5'-ATCCCGCGTTGTTCTTGAAC-3'  |               |
| <i>gr5</i>   | pgr5-F      | 5'-CCTCTTTCCTCCTCCTTCCA-3'  | 176 pb        |
|              | pgr5-R      | 5'-GCAAGAACAACAACAGGTGC-3'  |               |
| <i>rbcS</i>  | rbcS-2b-F   | 5'-GGGGAAGAGTTCAGTGCATG-3'  | 222 pb        |
|              | rbcS-2b-R   | 5'-ATGGTCCAGTAGCGTCCATC-3'  |               |
| <i>pal1</i>  | pal1-F      | 5'-CAAGATCGCTATGCCCTTCG-3'  | 164 pb        |
|              | pal1-R      | 5'-CCTTGGAAGTTGCCTCCATG-3'  |               |
| <i>pal2</i>  | pal2-F      | 5'-GCTGAGCAACACAACCAAGA-3'  | 231 pb        |
|              | pal2-R      | 5'-TGAAGGATCGAGTGCACCAT-3'  |               |
| <i>pal4</i>  | pal4-F      | 5'-ACCACAATGTACACCTTGC-3'   | 236 pb        |
|              | pal4-R      | 5'-TCCAACACCCGTCCCATTA-3'   |               |
| <i>rca</i>   | rca-F       | 5'-TGCTGGACTTCGACAATACG-3'  | 150 pb        |
|              | rca-R       | 5'-CCTCCCCAAATACCCAGAAT-3'  |               |
| <i>prk</i>   | prk-F       | 5'-AACCCATGGCTGATAACCTG-3'  | 152 pb        |
|              | prk-R       | 5'-TCTGGATTTCACCTCTTGG-3'   |               |
| <i>ohp</i>   | ohp-F       | 5'-GGGGAAGAGGGAAAGTTCTG-3'  | 176 pb        |
|              | ohp-R       | 5'-GGCAGAAGACCCAATTTGAA-3'  |               |
| <i>adt6</i>  | adt6-F      | 5'-ATCCATAACTCCACCGCTTG-3'  | 177 pb        |
|              | adt6-R      | 5'-GCCACTCACGATTACCGATT-3'  |               |