

Molecular cloning and characterization of *PtrLAR3*, a gene encoding leucoanthocyanidin reductase from *Populus trichocarpa* and its constitutive expression enhances fungal resistance in transgenic plants

Authors:

¹Li Yuan, ¹Lijun Wang, ²Zujing Han, ¹Yuanzhong Jiang, ²Lili Zhao, ¹Hong Liu, ¹Li Yang, ¹Keming Luo*

¹Key Laboratory of Eco-environments of Three Gorges Reservoir Region, Ministry of Education, Institute of Resources Botany, School of Life Sciences, Southwest University, Chongqing 400715, China

²Beijing Genomics Institute-Shenzhen, Shenzhen 518083, China

Supplementary Material

Supplementary Table S1: Comparison of changes in expression levels of PA biosynthetic genes leading to PA accumulation following *Marssonina brunnea* f.sp. *multigermtubi* infection using digital gene expression (DGE) analysis.

| Gene ID | Gene_length | Read count (WT) | Read count (<i>M.brunnea</i> infection) | WT4-RPKM | <i>M.brunnea</i> infection-RPKM | Log2 Ratio (<i>M.brunnea</i> infection/WT) | Up-/down-regulation (<i>M.brunnea</i> infection/WT) | P-value |
|------------------|-------------|-----------------|--|-------------|---------------------------------|---|--|-------------|
| POPTR_0006s12870 | 2145 | 5328 | 4264 | 669.5861187 | 589.910896 | -0.182772563 | Down | 6.54E-10 |
| POPTR_0008s03810 | 2136 | 306 | 439 | 38.61799306 | 60.99016248 | 0.659303369 | Up | 5.95E-10 |
| POPTR_0006s12870 | 2145 | 2526 | 1262 | 356.5261046 | 589.910896 | -0.182772563 | Down | 6.54E-10 |
| POPTR_0016s09230 | 2148 | 756 | 838 | 94.87614725 | 115.7727262 | 0.287178091 | Up | 7.13E-05 |
| POPTR_0010s23100 | 2136 | 14 | 22 | 1.766836284 | 3.056454612 | 0.790690778 | Up | 0.10728 |
| POPTR_0019s15110 | 1518 | 583 | 321 | 103.5300217 | 62.75231894 | -0.722308504 | Down | 2.17E-13 |
| POPTR_0013s15380 | 1518 | 735 | 541 | 130.5224116 | 105.7601388 | -0.303501574 | Down | 0.000194042 |
| POPTR_0014s14200 | 1191 | 201 | 170 | 45.49396801 | 42.35782759 | -0.103046673 | Down | 0.495438 |
| POPTR_0001s14320 | 1176 | 1 | 47 | 0.229225116 | 11.8600646 | 5.693202933 | Up | 0.000567202 |
| POPTR_0001s14310 | 1173 | 0 | 72 | 0.001 | 18.21507663 | 14.15284544 | Up | 0 |
| POPTR_0003s17530 | 1176 | 5 | 64 | 1.146125578 | 16.1498752 | 3.816685987 | Up | 3.48E-05 |
| POPTR_0002s03500 | 1041 | 29 | 272 | 7.50959975 | 77.53801754 | 3.368095928 | Up | 3.81E-11 |
| POPTR_0006s08750 | 987 | 13 | 143 | 3.550550725 | 42.99474755 | 3.5980457 | Up | 4.76E-07 |
| POPTR_0004s03030 | 1008 | 32 | 232 | 8.557737646 | 68.30051388 | 2.996595077 | Up | 6.67E-12 |
| POPTR_0003s11900 | 1086 | 0 | 20 | 0.001 | 5.465082078 | 12.41602745 | Up | 3.39E-07 |
| POPTR_0001s08410 | 1083 | 5 | 177 | 1.244546334 | 48.49995417 | 5.284291537 | Up | 3.48E-05 |
| POPTR_0008s11540 | 1059 | 25 | 118 | 6.363756748 | 33.06606885 | 2.377400941 | Up | 4.11E-10 |
| POPTR_0015s03360 | 1050 | 0 | 13 | 0.001 | 3.674096609 | 11.84317385 | Up | 6.13E-05 |
| POPTR_0013s07050 | 1566 | 95 | 368 | 16.35314809 | 69.73528488 | 2.092320429 | Up | 0 |
| POPTR_0010s21980 | 672 | 95 | 109 | 38.10867545 | 48.13419836 | 0.336942798 | Up | 0.095666 |

^aThe gene expression level is calculated by using RPKM method (Reads Per kb per Million reads) (Mortazavi et al., 2008), and the formula is shown as follows: $RPKM = 10^6 C/NL/10^3$. Given RPKM(A) to be the expression of gene A, C to be number of reads that uniquely aligned to gene A, N to be total number of reads that uniquely aligned to all genes, and L to be number of bases on gene A.

A Student's *t*-test (two-sample, unpaired, one-sided) was performed to test significance (*P*) of up- or downregulation of each transcript between infected and control leaves.

Supplementary Figure S1: Photographs of *PtrLAR3* overexpressing *Populus tomentosa* Carr. after four weeks of growth. No phenotypic or growth differences were observed between *PtrLAR3* overexpressing and control plants under the same growth conditions.

Supplementary Figure S2: PCR analysis of transgenic poplar plants. Genomic DNAs were isolated from hygromycin-resistant plants transformed with the *35S:PtrLAR3* vector. PCR amplification using primers specific for the production of a 562-bp *PtrLAR3* fragment. M, D2000 DNA Ladder; WT, non-transgenic plants; P, corresponding plasmid DNA (positive control); Lanes 1–10, independent transgenic lines. Numbers on the left indicate DNA marker sizes in base pairs.

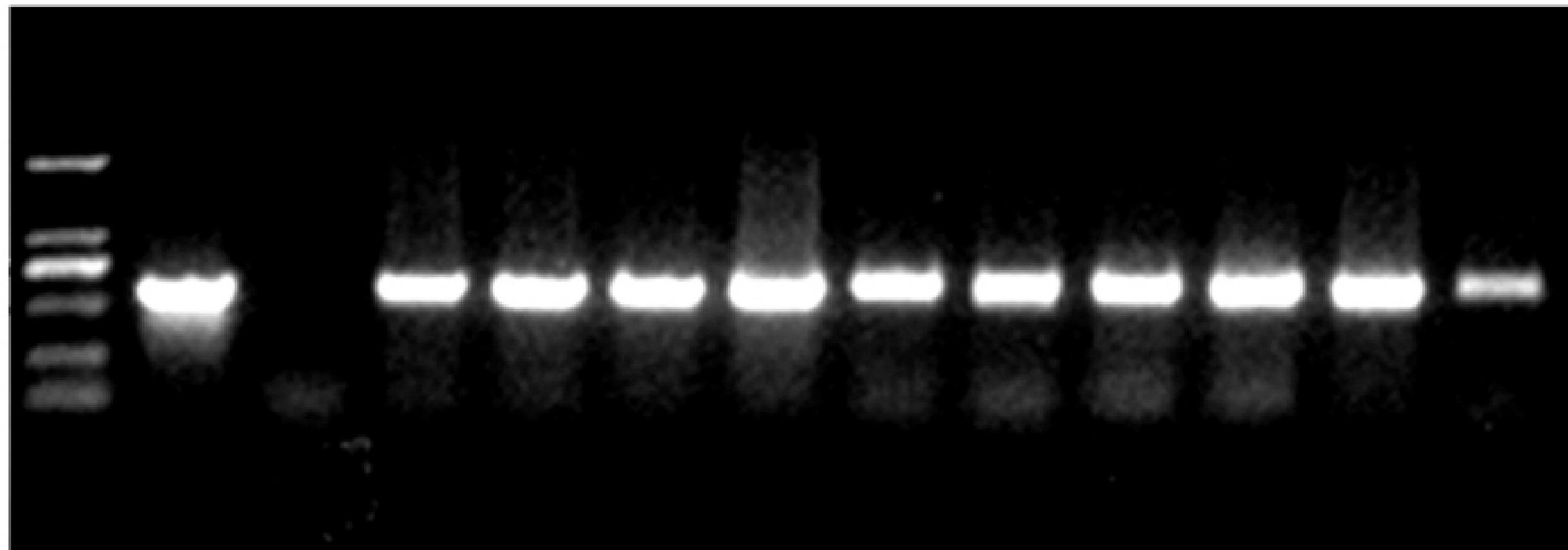
Reference

Mortazavi A, Williams BA, McCue K, Schaeffer L, Wold B. 2008 Mapping and quantifying mammalian transcriptomes by RNA-Seq. *Nature Methods* 5, 621-628.



M P WT 1 2 3 4 5 6 7 8 9 10

750 bp
500 bp



562 bp