

SUPPLEMENTAL MATERIAL for Djami-Tchatchou, et. al

Supplemental Table 1. RNA-seq Data (Excel file).

Supplemental Table 2. COG assignments for differentially expressed genes (Excel File)

Supplemental Table 3. Primers used in this study

Gene	Forward primer (5'-3')	Reverse primer (5'-3')	Reference
PSPTO_0371 (<i>iaaL</i>)	GTCTGGGCATCATTCAAC	ACGGTCACCAGTTCTTT	This study
PSPTO_0537 (<i>rpoD</i>)	GAAGTTGACGAAAGCTGGACCG	CGACGGTTGATGTCCTTGATCTC	Djami-Tchatchou et al., 2020
PSPTO_0905 (<i>hopAH1</i>)	GGGTTATAAAGGCGACATC	ATTGAGCGGCGTATTTG	This study
PSPTO_1336	GTGTGTGTCACATATTCAGG	TACGTCCACTTGCCAAT	This study
PSPTO_1389 (<i>hrcC</i>)	CAGCCTTCAAGTGATTCC	GTCATTGATCGTCGACAC	This study
PSPTO_1404 (<i>hrpL</i>)	TCAGGAAAGCTGGGAAGACGAA GT	ATGTTTCGACGGCAGGCAATCAATG	Anderson et al., 2014
PSPTO_1483	GAAGCACTGTTGAGGTTG	CGAACTCGGTGGGTATT	This study
PSPTO_1767 (<i>ohr</i>)	GATTCTCGACGTCAAAGCTG	TTCAAAGCGCCGATAAAG	This study
PSPTO_1824	AGCTTTATTAGTGGCATTGG	GTTGAGCAGCCACTTTG	This study
PSPTO_1873 (<i>gntR</i>)	CCGGGACGAACAGATTTA	GCAAGACCTTGCGAATG	This study
PSPTO_2683	ATGACCAAGGTACACATCAT	GCTCGCCATCCTGAATC	This study
PSPTO_3100 (<i>mexF</i>)	GTTGTTACCAGCTACAC	GCAGGGTGTGCAAGATA	This study
PSPTO_3549 (<i>aefR</i>)	GCCTCACCGATCAGAAA	GTCCATGCTGGTGATCT	This study
PSPTO_3617	GGTCACCTACGGGATTT	GCCACTTTGACCTGATG	This study
PSPTO_3749	GTCGTCAGGTACGTCTG	GCACTTTGGTGAGAATCC	This study
PSPTO_4001 (<i>avrPto</i>)	ATGACGGGAGCGTCAGGAATCA AT	ATCCGTTCCGGTTCATAGTCGCAA	Anderson et al., 2014
PSPTO_4033 (<i>recA</i>)	TAGAACTTCAGCGCGTTACC	GCCAACTGCCTGGTTATCT	Smith et al., 2018
PSPTO_4233	TGTCCATACCGAAGAAGAG	GGATGCTGCTGAGTATGA	This study
PSPTO_4297	CTTTCTCTGTTCTGGCTTC	GGGAGGCTTTGGACATA	This study
PSPTO_4530 (<i>katG</i>)	CACGCGAACGAAGAAAG	CTTCCGGGTTACATAGA	This study
PSPTO_4851	GCATCTCCATCGAGTACA	GGTAATACCGGCTGAGAA	This study

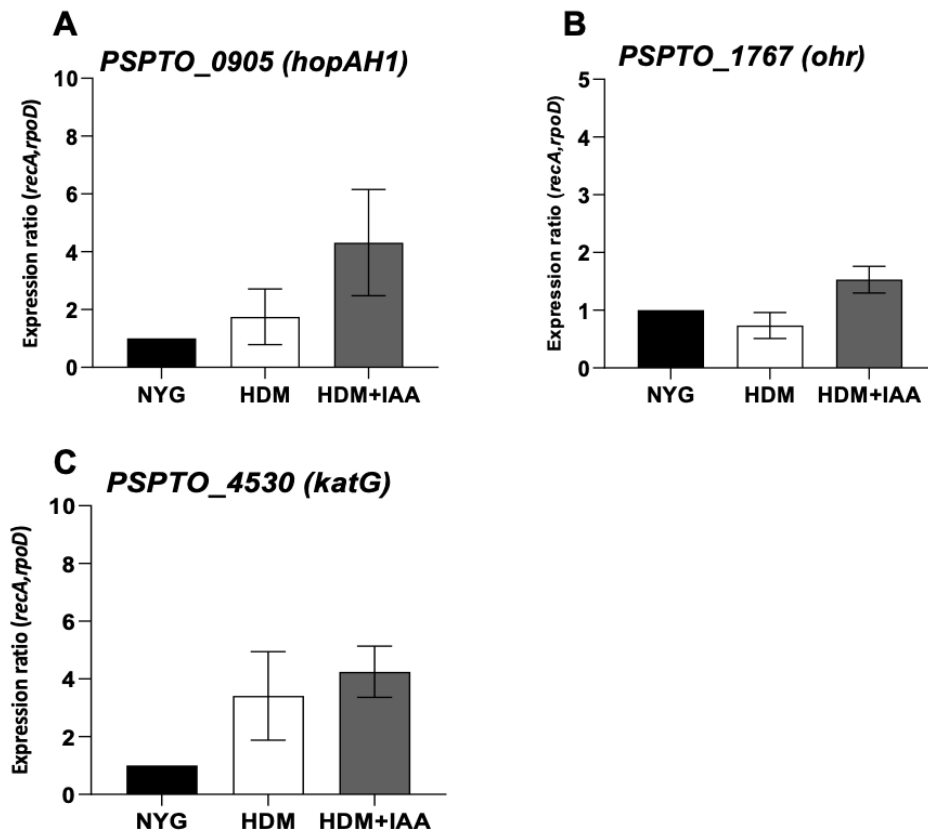
REFERENCES

Anderson JC, Wan Y, Kim YM, Pasa-Tolic L, Metz TO, Peck SC. 2014. Decreased abundance of type III secretion system-inducing signals in *Arabidopsis mkp1* enhances resistance against *Pseudomonas syringae*. *Proc Natl Acad Sci U S A* 111:6846-51.

Djami-Tchatchou AT, Harrison GA, Harper CP, Wang R, Prigge MJ, Estelle M, Kunkel BN. 2020. Dual role of auxin in regulating plant defense and bacterial virulence gene expression during *Pseudomonas syringae* PtoDC3000 pathogenesis. *Mol Plant Microbe Interact* 33:1059-1071.

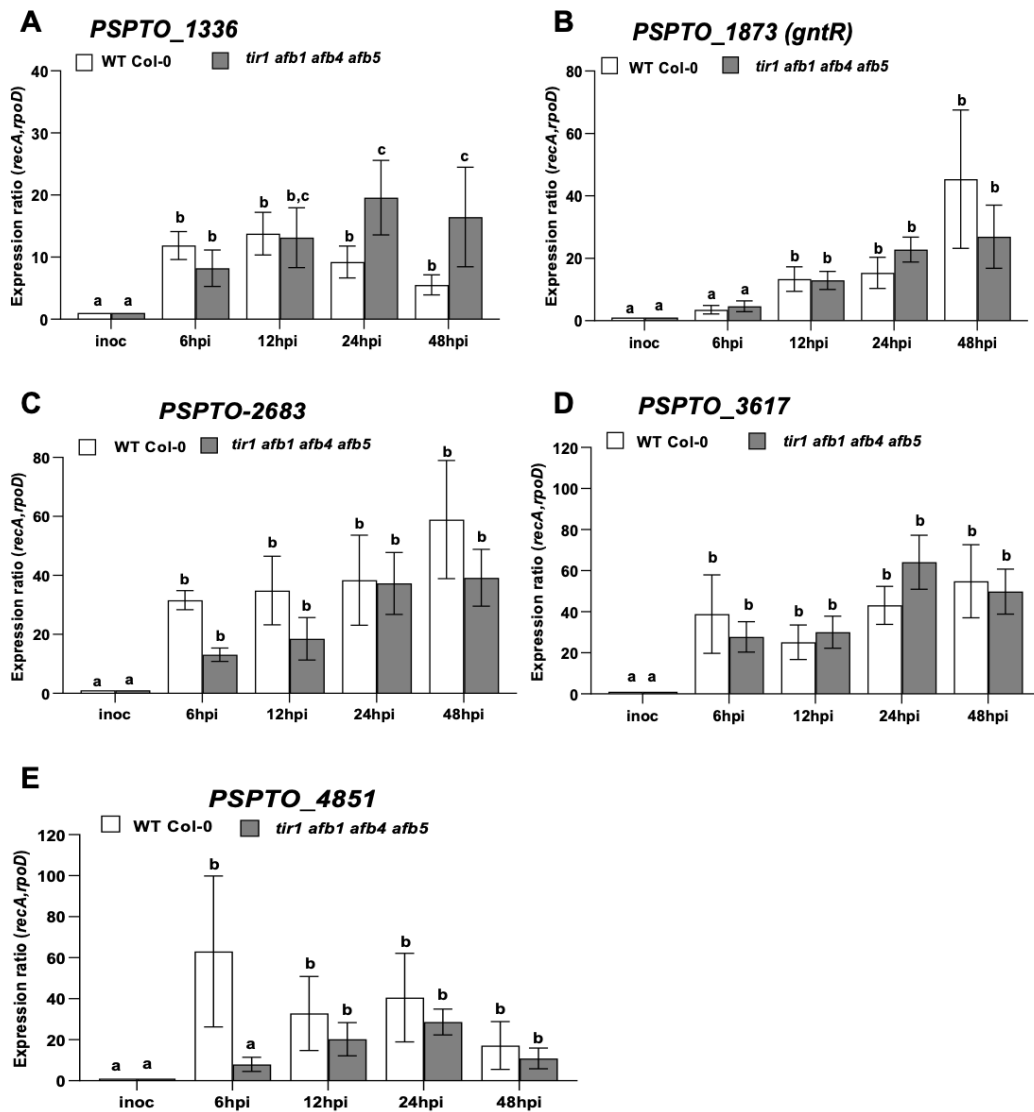
Smith A, Lovelace AH, Kvitko BH. 2018. Validation of RT-qPCR approaches to monitor *Pseudomonas syringae* gene expression during infection and exposure to pattern-triggered immunity. *Mol Plant Microbe Interact* 31: 410-19.

SUPPLEMENTAL FIGURES and FIGURE LEGENDS



Supplemental Fig. 1 Expression of selected genes not confirmed to be up-regulated by IAA in culture.

Expression of genes **(A)** *PSPTO_0905 (hopAH1)* **(B)** *PSPTO_1767 (ohr)*, and **(C)** *PSPTO_4530 (katG)*; 30 min after being transferred from NYG to HDM or HDM containing 100 μ M IAA (HDM+IAA). Expression levels in cells growing in NYG was used as the calibrator for relative expression. The relative expression was calculated using the reference genes *rpoD* and *recA*. Each data point represents the average of 3 biological replicates, and error bars representing the SEM between biological replicates. Results were analyzed using ANOVA, followed by a Tukey's post test.



Supplemental Fig. 2. Expression in *planta* of additional genes up-regulated by IAA in culture. Expression of bacterial genes (A) *PSPTO_1336*, (B) *PSPTO_1873 (gntR)* (C) *PSPTO_2683*, (D) *PSPTO_3617* and (E) *PSPTO_4851* in *PtoDC3000* growing in *A. thaliana* WT Col-0 or *tir1afb1afb4afb5* mutant plants. Infected leaves were harvested 6, 12, 24 and 48 hours after inoculation, and total RNA isolated and used for qRT-PCR to quantify bacterial gene expression. RNA prepared from the *PtoDC3000* cell suspension used for the inoculum was used as the calibrator for relative expression. The data shown were compiled from 2 (A) or 3 (B-E) independent experiments, carried out on different days. The relative expression was calculated using the reference genes *recA* and *rpoD*.

Each data point is the average of 6 or 9 biological replicates, and error bars represent the SEM between biological replicates. Results were analyzed using ANOVA, followed by a Tukey's post test. Different letters indicate significant difference between samples with $p < 0.05$.