Supplemental Informations

PRR2, a pseudo-response regulator, promotes salicylic acid and camalexin accumulation during plant immunity

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Legends of Supplemental Informations

Supplemental Information 1

Molecular characterization of *prr2* mutant lines. *The prr2* mutants were identified in the *Arabidopsis* T-DNA insertion lines collections from plant resource centers. (**A**) Schematic illustration of the T-DNA insertions into the genomic region of *PRR2* gene. The *prr2-1* (Col) and *prr2-2* (WS) mutants contain a T-DNA insertion in the first intron, 629bp and 425bp downstream of the transcription start site of *PRR2* gene respectively. (**B**) Semi-quantitative analysis of *PRR2* transcripts accumulation was carried out on homozygous lines using primers *F1* and *R1* (see panel A for primers positions). Actin 2 was used as a control. Data indicate that *PRR2* transcripts can be detected in both insertional mutants, but they accumulate at a lower level than that observed in wild-types, indicating a down-regulation of *PRR2* expression in the mutants. (**C**) Quantitative RT-$_{Q}$PCR was performed to measure the relative *PRR2* gene expression level in mutants compared to WT. As shown, *PRR2* expression is respectively decreased by about 3 and 7 fold in *prr2-1* and *prr2-2* compared to Col and WS.

Supplemental Information 2

Molecular characterization of Over-Expressing *PRR2* transgenic lines. (**A**) Relative expression of *PRR2-3HA* transcript in *p35S::*$_{CDS}$*PRR2.1* (*OE-PRR2.1*) and *p35S::*$_{CDS}$*PRR2.2* (*OE-PRR2.2*) lines compared to WT (Col) by quantitative RT-PCR. (**B**) Western blot of total protein from WT (Col), *OE-PRR2.1* and *OE-PRR2.2*. Total proteins were extracted and separated in SDS-PAGE before blotting and

immunodetection using antibodies raised against the 3HA epitope. Presence and length of the 3HA-tagged PRR2 protein is indicated by the arrow.

Supplemental Information 3

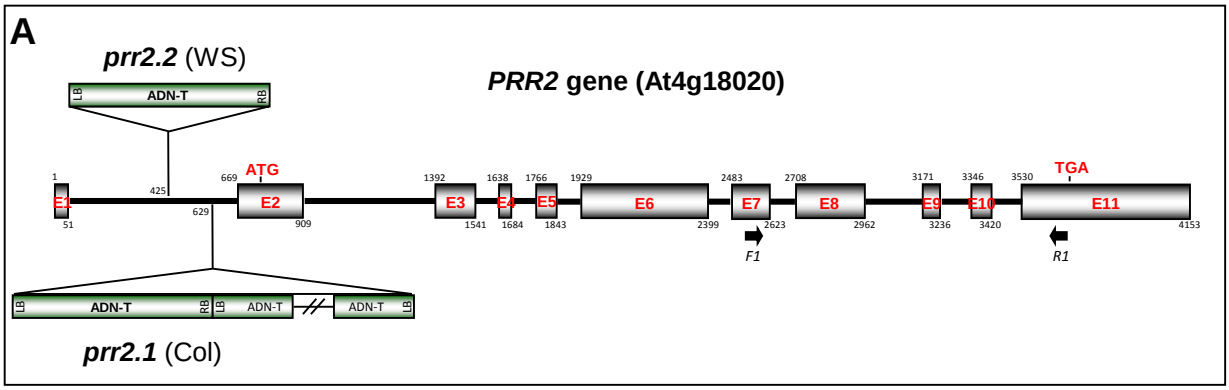
(**A**) Phenotype of 6-day-old WT (Col), *OE-PRR2.1*, *OE-PRR2.2, prr2.1* and WT (*WS) and prr2.2* plants grown in standard conditions. All plants were photographed from the same distance. (**B**) Phenotype of 4-week-old WT (Col0), *prr2.1*, *OE-PRR2.1*, *OE-PRR2.2* and WT (WS*) and prr2.2* plants grown in standard conditions. All plants were photographed from the same distance.

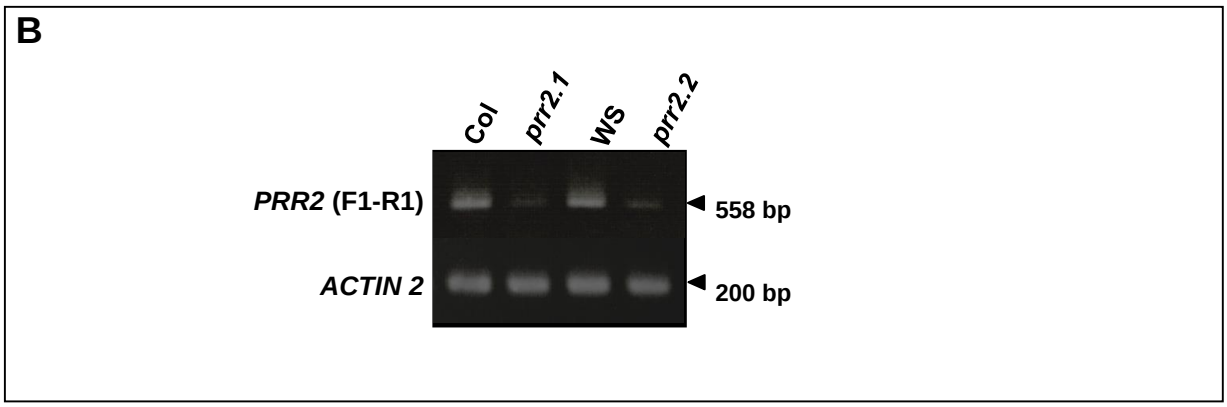
Supplemental Information 4

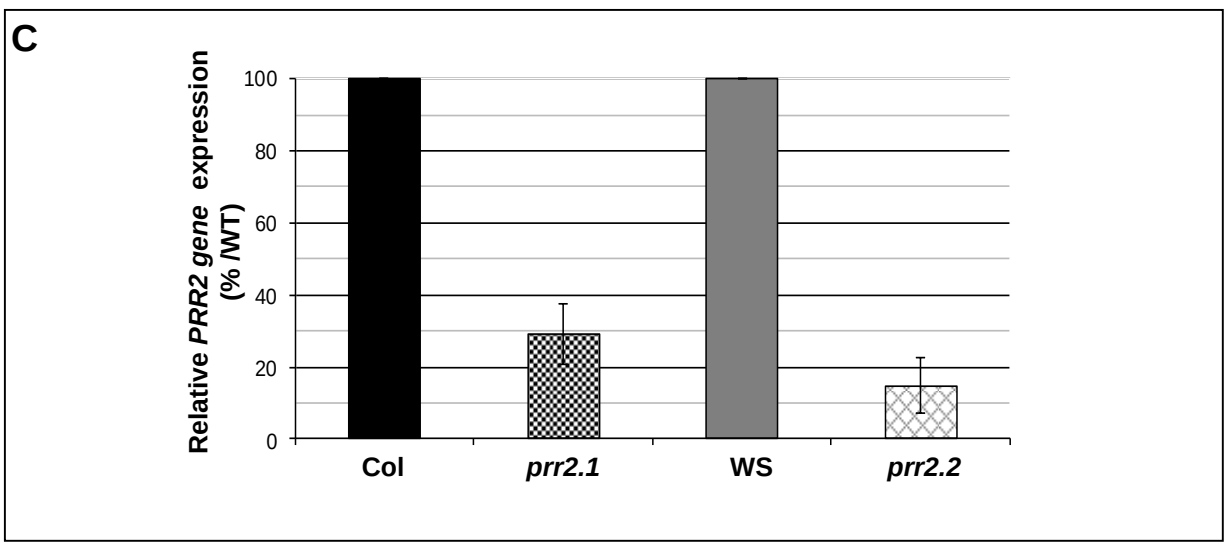
Quantifications of *in planta* bacterial growth in WT (WS) and *prr2.2* mutant line. Bacterial growth quantifications were performed at 0 and 1 dpi with *Pst* DC3000 **(A)** or *Pseudomonas syringae pv maculicola* **(B)***.* Data are representative of 5 replicates of three independent experiments. P values were calculated using the two-tailed Mann-Whitney U-test to indicate significant differences between the genotypes. Asterisks illustrate $p<0.05$. Error bars represent SEM.

Table S1: List of primers used for quantitative PCR and molecular characterization of the *prr2* genotypes**.**

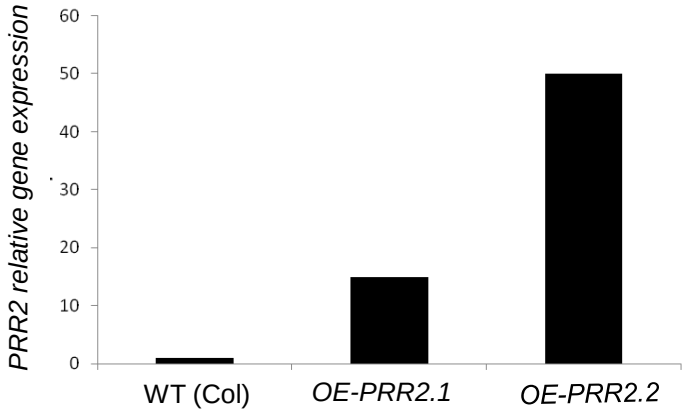
Name	Sequence	
ACTIN8	5’-CACCCGAGAGGAAGTACAGTG-3’	Forward
	5’-CATACTCTGCCTTAGAGATCCACA-3’	Reverse
PRR2	5’- GAGCGATTCCACCTTTGTT-3’	Forward
	5’- CAACCCCATGCATTACCG -3'	Reverse
WRKY6	5'- GCAACAGCAACAACAGAACAA -3'	Forward
	5'- TGCCTTGGTACTATCGTCTCC-3'	Reverse
MYB51	5'- GGCCAATTATCTTAGACCTGACA -3'	Forward
	5'- CCACGAGCTATAGCAGACCATT -3'	Reverse
CYP71B15 / PAD3	5'- CACCACTGATCATCTCAAAGGA -3'	Forward
	5'- CGGTCATTCCCCATAGTGTT -3'	Reverse
CBP60G	5'- ATCGCAGCACATCGACTTT -3'	Forward
	5'- GTGGACCGTTGAGCTTGAA -3'	Reverse
PromPRR2	5'- CATACGGTTTTTATAAGTAATGAAGC -3'	Forward
	5'- CATAGCTGGTTTTGCATCGTTTTTG -3'	Reverse


A
prr2.2 (WS)
ADN-T
LB
RB
PRR2 gene (At4g18020)
ATG
TGA
E1
E2
E3
E4
E5
E6
E7
E8
E9
E10
E11
F1
R1
prr2.1 (Col)

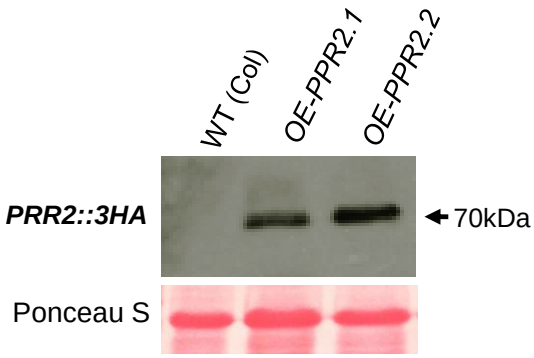

B
Col
prr2.1
WS
prr2.2
PRR2 (F1-R1)
ACTIN 2
558 bp
200 bp


C
Relative PRR2 gene expression (% WT)
100
80
60
40
20
0
Col
prr2.1
WS
prr2.2

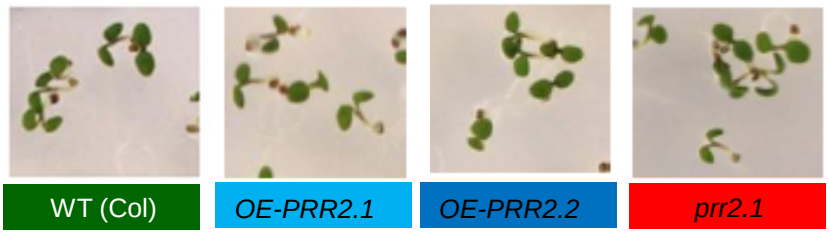
A

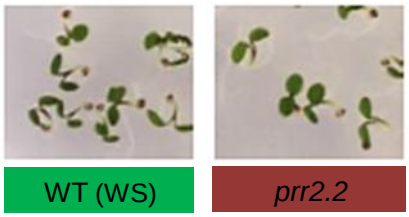

PRR2 relative gene expression
60
50
40
30
20
10
0
WT (Col)
OE-PRR2.1
OE-PRR2.2

B

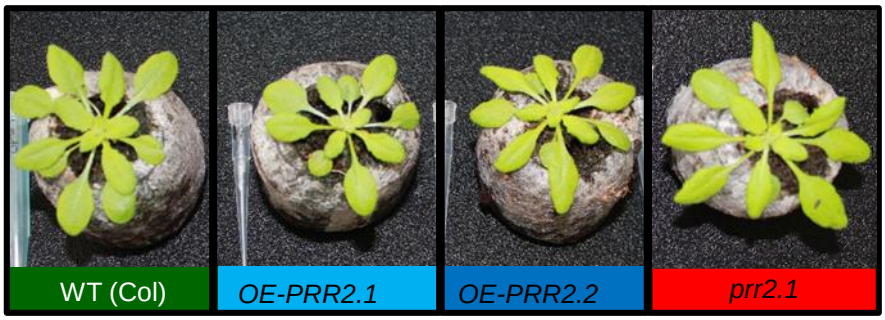

WT (Col)
OE-PRR2.1
OE-PRR2.2
PRR2::3HA
70kDa
Ponceau S

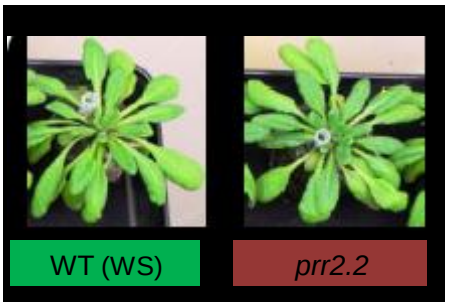
A

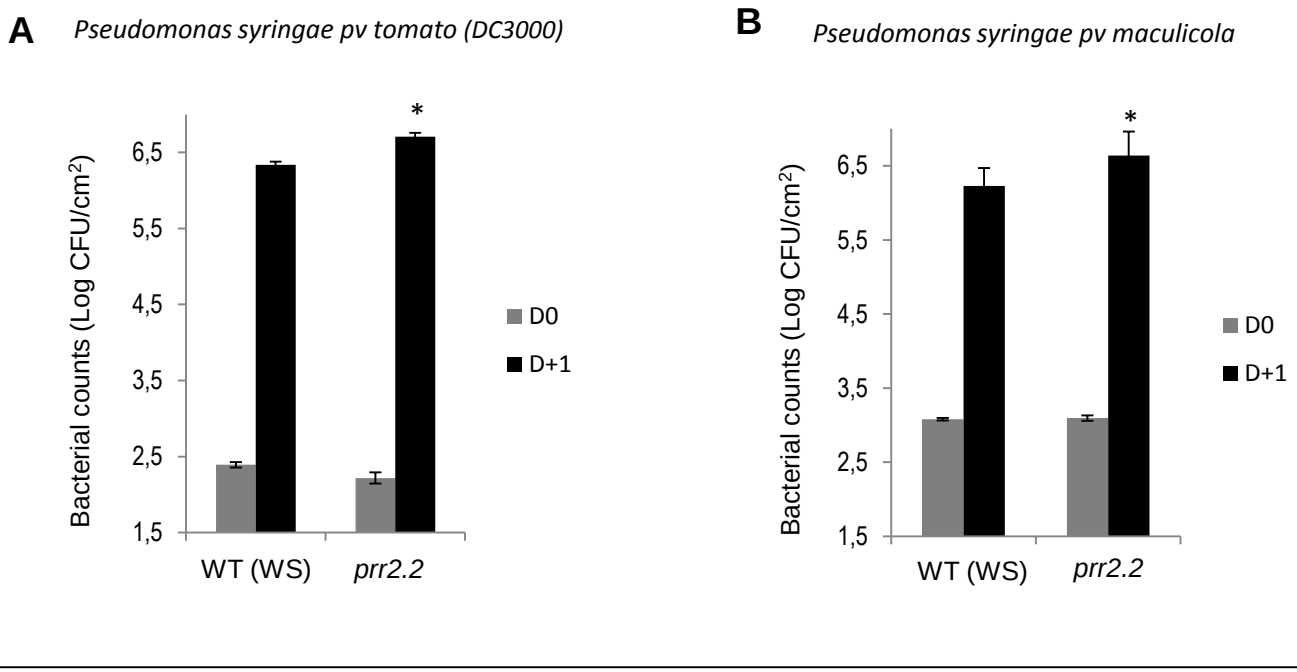

WT (Col)
OE-PRR2.1
OE-PRR2.2
prr2.1


WT (WS)
prr2.2

B


WT (Col)
OE-PRR2.1
OE-PRR2.2
prr2.1


WT (WS)
prr2.2


A
Pseudomonas syringae pv tomato (DC3000)
Bacterial counts (Log CFU/cm2)
6,5
5,5
4,5
3,5
2,5
1,5
*
D0
D+1
WT (WS)
prr2.2
B
Pseudomonas syringae pv maculicola
Bacterial counts (Log CFU/cm2)
6,5
5,5
4,5
3,5
2,5
1,5
*
D0
D+1
WT (WS)
prr2.2