The Protein Elicitor PevD1 Enhances Resistance to Pathogens and Promotes Growth in *Arabidopsis*

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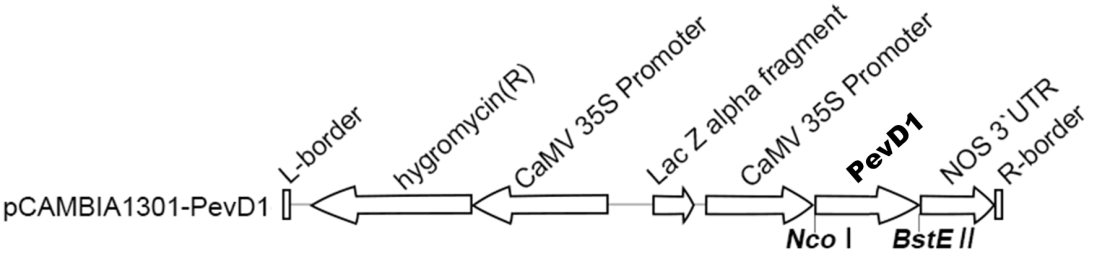

Figure S1. Structural diagram of the recombinant vectors used to transfer the *pevd1* gene. The sequence between the L-border and R-border, containing the gene coding for the PevD1 protein and the hygromycin resistance gene, both under the CaMV35s promoter, was inserted into the *Arabidopsis* genome

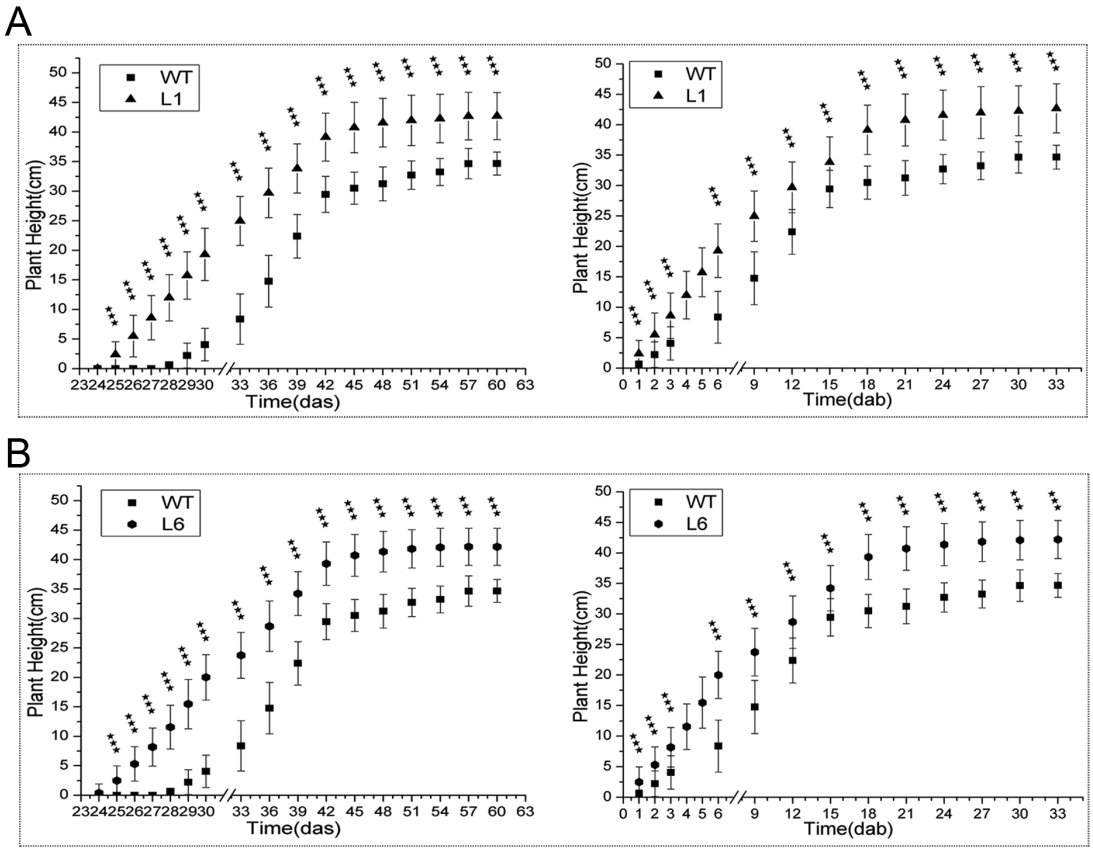

Figure S2. Plant height of WT and transgenic *Arabidopsis* L1 (A) and L6 (B) at the indicated times shown in days after sowing (das) and days after bolting (dab). All experiments were repeated three times, and the data presented are shown as the means ± SD of three independent experiments. The bars represent the standard deviation (n = 3). The asterisks indicate a significant difference between transgenic and WT Arabidopsis (Student's t-test: ⋆⋆⋆, $P < 0.01$).

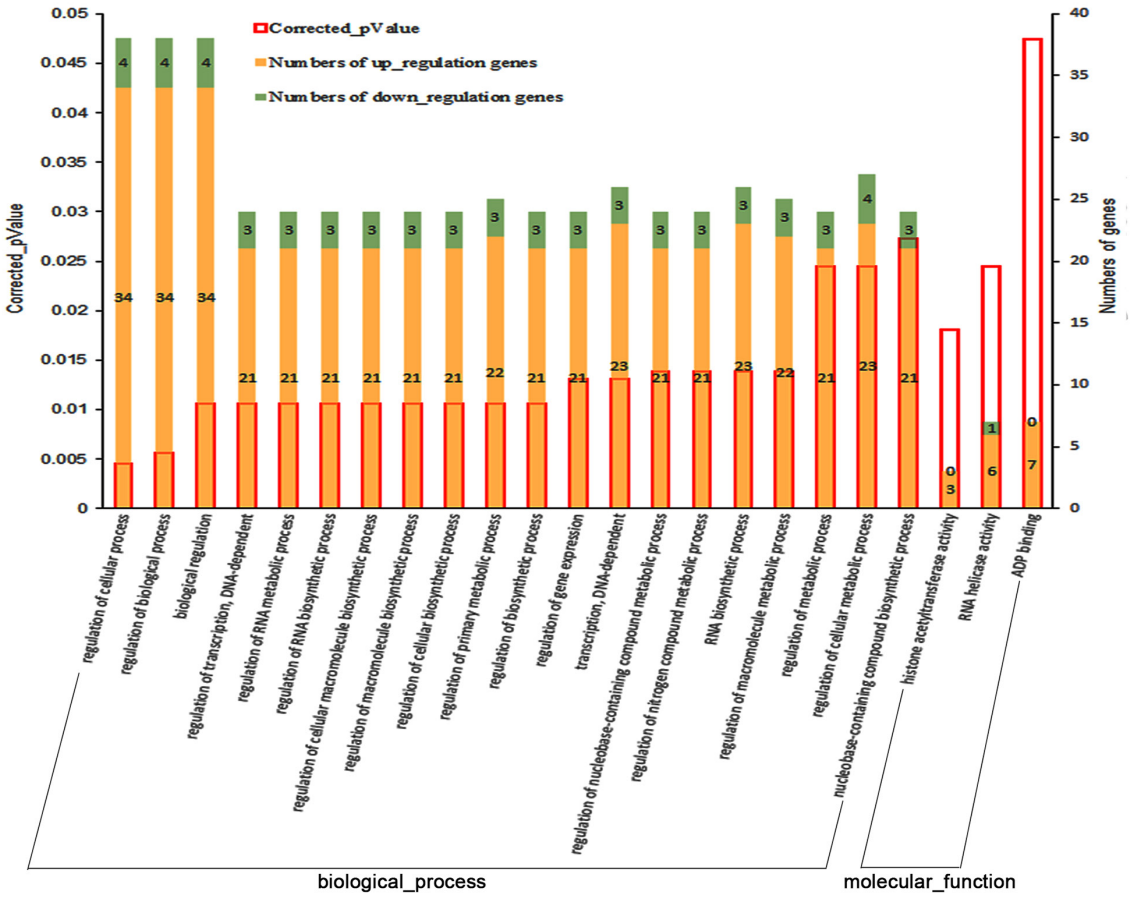

Figure S3. The 23 most enriched ($p_{corrected} < 0.05$) Gene Ontology (GO) terms in transgenic and WT Arabidopsis (AtRNA_T vs AtRNA_W). Twenty GO terms belong to biological processes and another 3 GO terms belong to molecular functions. The values shown on the columns indicate the number of up-regulated or down-regulated genes involved in the corresponding GO terms. GO terms were sorted based on corrected p-values. x-axis: GO terms; left y-axis: corrected p-values; right y-axis: number of genes.

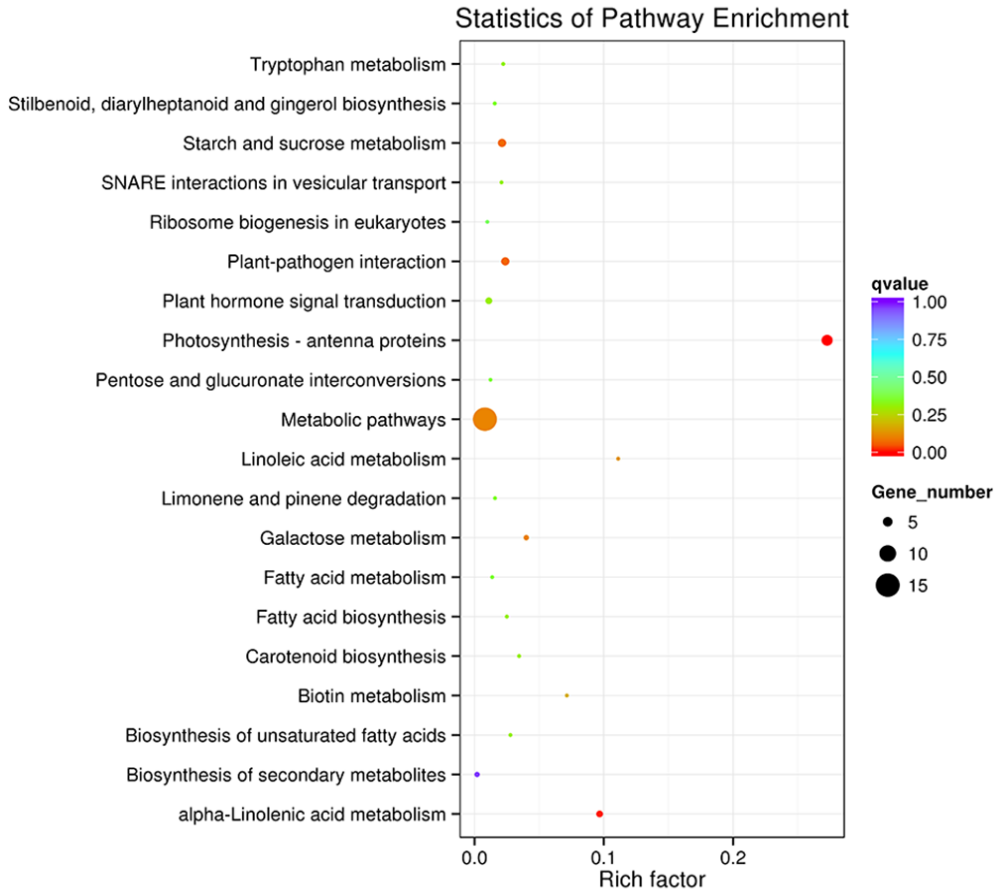

Figure S4. Scattered Plot of KEGG pathway terms of differentially expressed genes. Dot size represents the number of different genes and the color indicates the value of $p_{corrected}$.

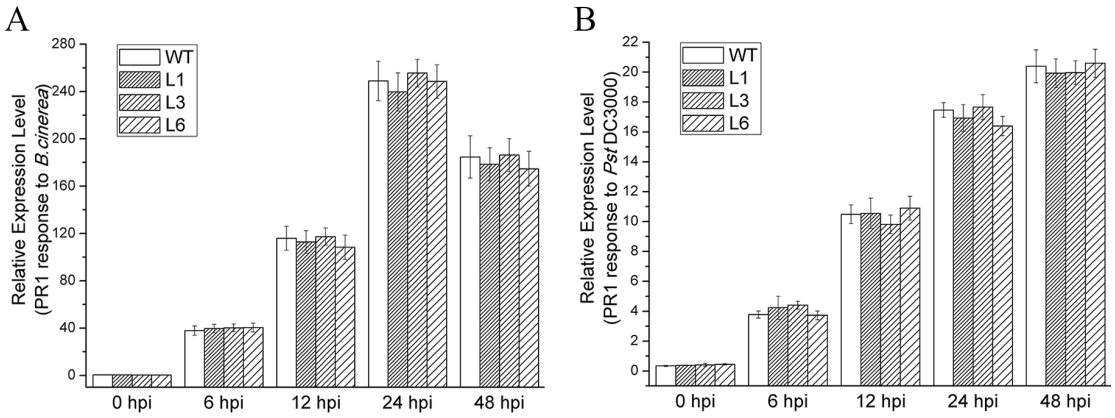

Figure S5. The relative expression level of PR1 induced by *B. cinerea* (A) and *Pst* DC3000 (B) infection in WT and transgenic *Arabidopsis*. The Actin2 gene was used as an internal control to normalize the expression data. The bars represent the standard deviation (n = 3).

Table S1. Primer sequences used in this study

Gene	Sequence	Description
PevD1	CATGCCATGGCCCCCGCGTCTCCCGGC GGGTGACCTTAAGCCTCGGCGGGAGCG	pCAMBIA1301
	GCCCCCGCGTCTCCCGGC TTAAGCCTCGGCGGGAGCG	genomic DNA PCR
	ACGGCACCATCAAGTACGTC TGATGACGTTGGAAGGCAGG	qRT-PCR
PDF1.2 (AT5G44420)	CATCACCCTTATCTTCGC CTTCTCGCACAACTTCTG	qRT-PCR
LOX4 (AT1G72520)	CTTTCTTGAGAGCATCACC GGCAAGTAAGGCTGATTAG	qRT-PCR
AOC1 (AT3G25760)	TCTCATCTAACGGTCCAG TGAACTTTGCTTGGTCTG	qRT-PCR
OPR3 (AT2G06050)	TCAGATGAACAAGTAGAAGC TTGATACACTGCATGAGAAG	qRT-PCR
WRKY40 (AT1G80840)	GTAGCTCAACGGATCAAG CTTTCACAACGAGGGTAG	qRT-PCR
HAI2 (AT1G07430)	TCTACAGATCATAAGCCTGA CTAAAACGCCTAAGACTCTT	qRT-PCR
PP2CA (AT3G11410)	GTCTAGAGCAATTGGTGAT CAACATCCCATAGTCCATC	qRT-PCR
CML38 (AT1G76650)	CTGCTGTTAGATTGTCTGAT GCTCCATCTTCTTCTCTTC	qRT-PCR
WRKY22 (AT4G01250)	CATATCCAAGAGGATACTACAG GAGAGAATTACGGTGTGTC	qRT-PCR
WRKY33 (AT2G38470)	CTGATTCTGTTGGTGACG CCCTTTCCATCTCTTTGC	qRT-PCR
ACTIN2 (AT3G18780)	TCAGCCGTTTTGAATCTCCGGC TGCATCCTTCTGGTTCATCCCAACC	genomic DNA PCR
	CACCACCTGAAAGGAAGTAC GATCCACATCTGCTGGAATG	qRT-PCR

Table S2. The quality of sequencing data

Sample name	Raw reads	Clean reads	Clean bases	Error rate(%)	Q20(%)	Q30(%)	GC content(%)
AtW1	11021108	10982778	0.55G	0.01	98.19	94.72	46.15
AtW2	11606251	11561726	0.58G	0.01	98.17	94.67	46.21
AtT1	11837410	11808969	0.59G	0.01	98.14	94.57	46.4
AtT2	10828192	10777098	0.54G	0.01	98.23	94.78	46.22

1) Sample name: the names of samples
2) Raw Reads: the original sequencing reads counts
3) Clean Reads: number of reads after filtering
4) Clean Bases: clean reads number multiply read length, saved in G unit
5) Error Rate: average sequencing error rate, which is calculated by Qphred = -10log10(e)
6) Q20: percentages of bases whose correct base recognition rates are greater than 99% in total bases
7) Q30: percentages of bases whose correct base recognition rates are greater than 99.9% in total bases
8) GC content: percentages of G and C in total bases.

Table S3 Overview of mapping status

Sample name	AtW1	AtW2	AtT1	AtT2
Total reads	10982778	11561726	11808969	10777098
Total mapped	10676023 (97.21%)	11216480 (97.01%)	11114777 (94.12%)	10331234 (95.86%)
Multiple mapped	355810 (3.24%)	381406 (3.3%)	342045 (2.9%)	316584 (2.94%)
Uniquely mapped	10320213 (93.97%)	10835074 (93.72%)	10772732 (91.23%)	10014650 (92.93%)
Reads map to “+”	5163428 (47.01%)	5423100 (46.91%)	5387209 (45.62%)	5009168 (46.48%)
Reads map to “-“	5156785 (46.95%)	5411974 (46.81%)	5385523 (45.61%)	5005482 (46.45%)
Non-splice reads	8699543 (79.21%)	9154202 (79.18%)	9087823 (76.96%)	8424474 (78.17%)
Splice reads	1620670 (14.76%)	1680872 (14.54%)	1684909 (14.27%)	1590176 (14.76%)

1) Total number of filtered reads (Clean data).
2) Total number of reads that can be mapped to the reference genome. In general, this number should be larger than 70% when there is no contamination and the correct reference genome is chosen.
3) Number of reads that can be mapped to multiple sites in the reference genome. This number is usually less than 10% of the total.
4) Number of reads that can be uniquely mapped to the reference genome.
5) Number of reads that map to the positive strand (+) or the minus strand (-).
6) Splice reads can be segmented and mapped to two exons (also named junction reads), whereas non-splice reads can be mapped entirely to a single exon. The ratio of splice reads depends on the insert size used in the RNA-seq experiments.

Table S4 The number of genes with different expression levels

RPKM interval	AtW1	AtW2	AtT1	AtT2
0~1	16476(49.03%)	16439(48.92%)	16155(48.08%)	16336(48.62%)
1~3	2705(8.05%)	2782(8.28%)	2737(8.15%)	2762(8.22%)
3~15	7599(22.61%)	7593(22.60%)	7626(22.70%)	7511(22.35%)
15~60	5009(14.91%)	4964(14.77%)	5176(15.40%)	5107(15.20%)
>60	1813(5.40%)	1824(5.43%)	1908(5.68%)	1886(5.61%)