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Supplementary Information for

Root-specific camalexin biosynthesis controls the plant growth promoting effects of multiple bacterial strains

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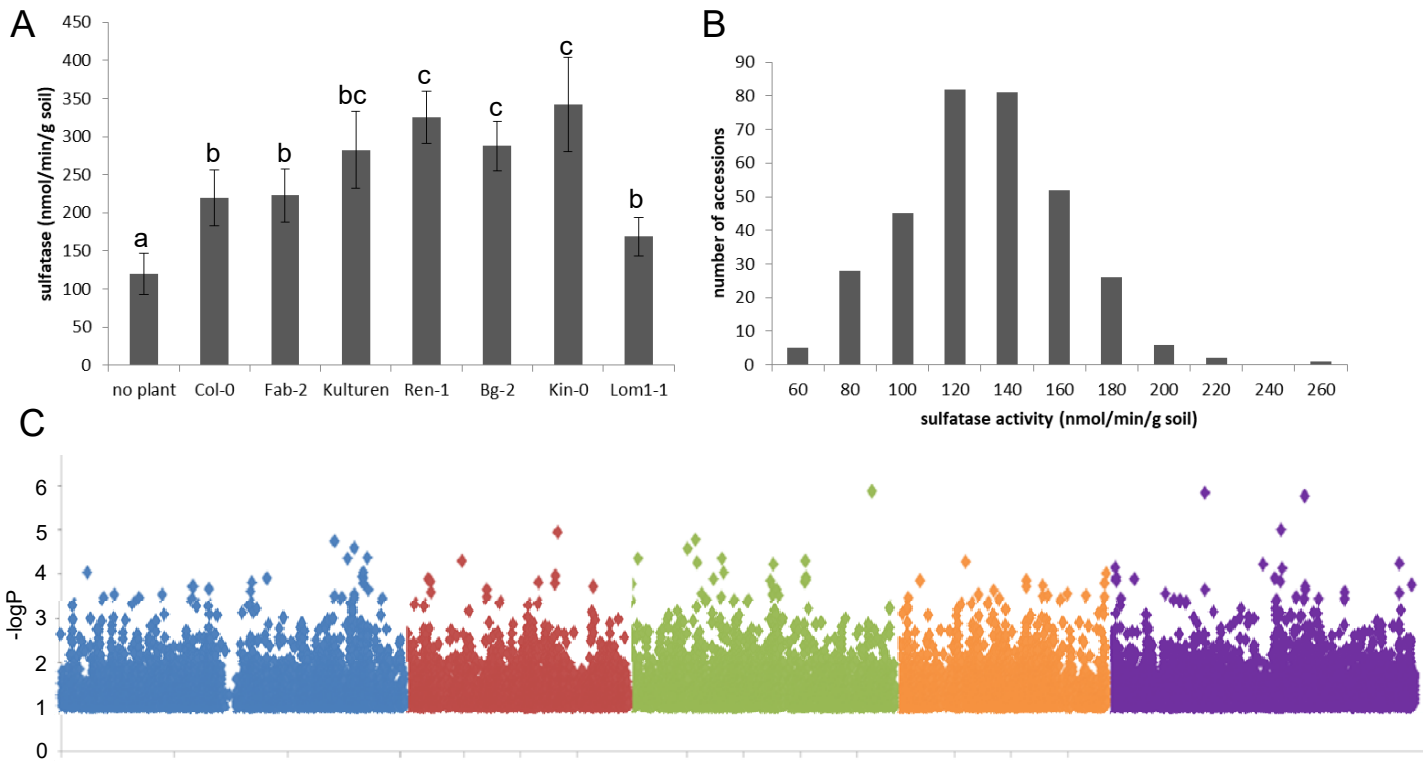


Fig. S1. Natural variation in sulfatase activity

A Sulfatase activity in a typical tray. Plants were grown for 2 weeks in soil (10%)/sand mixture, afterwards 2 soil samples were taken per plant and sulfatase activity was measured. Data are presented as means and S.E. from 10 samples derived from 5 independent plants. Different letters mark statistically different values (one way ANOVA).

B Distribution of the sulfatase activity among Arabidopsis accessions. Sulfatase activity was determined in soil from 173 Arabidopsis accessions varieties. Shown is the frequency of the activity among the 173 accessions.

C Manhattan plot of GWAS results obtained by GWAPP. Plotted are scores as $-\log_{10}p$ for each marker on the 5 Arabidopsis chromosomes.

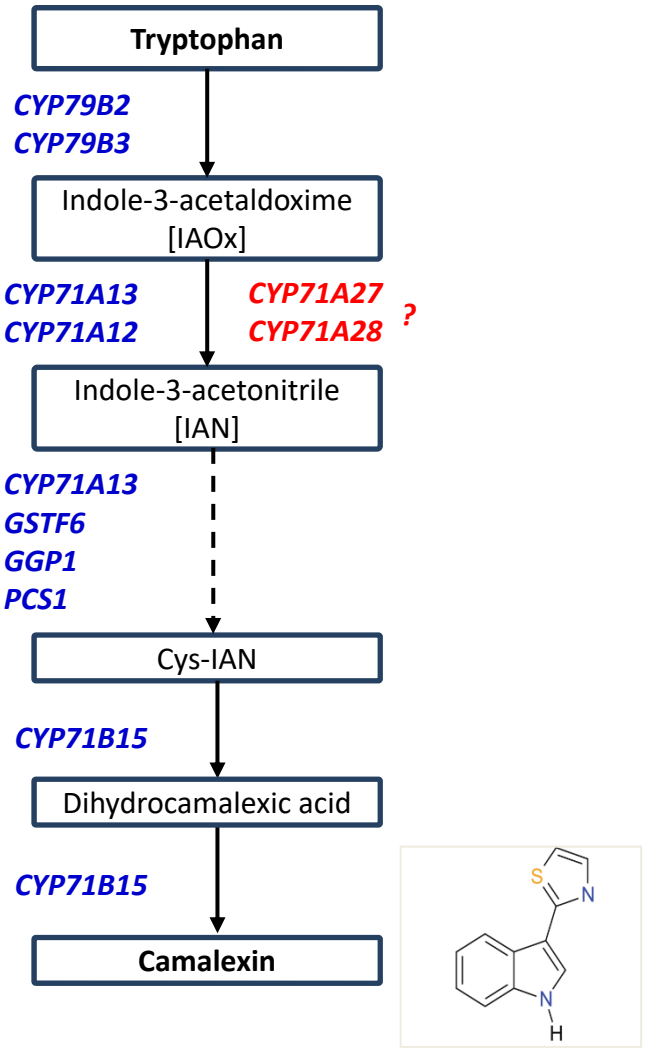


Fig. S2. Scheme of camalexin biosynthesis pathway.
Scheme adapted from Su et al. (2011). The possible position of the newly characterised CYP71A27 and CYP71A28 is indicated in red with a question mark.

	cyp71A27	*cyp71A28*	*cyp71A12*	*cyp71A13*
CYP71A12	9.9	5.02	0	5.33
CYP71A13	6.38	3.94	10	0
CYP71A27	0	0.7	1.05	0.49
CYP71A28	1.71	0	1.29	0.86
GST6	3.32	1.45	3.79	3.04
GGP	0.79	0.64	0.77	0.6
CYP71B15	0.94	0.56	1.03	0.83
MAM	1.26	1.17	1.4	1.24
TSB	1	1	1	1.06
CYP79F1	0.28	0.39	1.44	0.05
CYP79B2	0.56	0.56	0.65	0.32
MYB28	0.83	0.91	0.93	0.87
MYB51	1.43	0.89	1.2	0.94
SUR1	0.93	0.53	0.58	0.57
SOT16	1	0.61	0.64	0.63
SOT17	1	0.66	0.86	0.52

Fig. S3. Expression analysis of mutants in P-450 71A genes potentially involved in camalexin synthesis

RNA was isolated from roots of the 5 genotypes and accumulation of transcripts for genes of camalexin (black) and glucosinolate (red) synthesis was compared by qPCR. Data are shown relative to expression in Col-0, red boxes mark transcripts accumulating to a greater extent in the mutants and blue boxes indicate those that are repressed. The analysis was performed with three independent RNAs measured in duplicates.

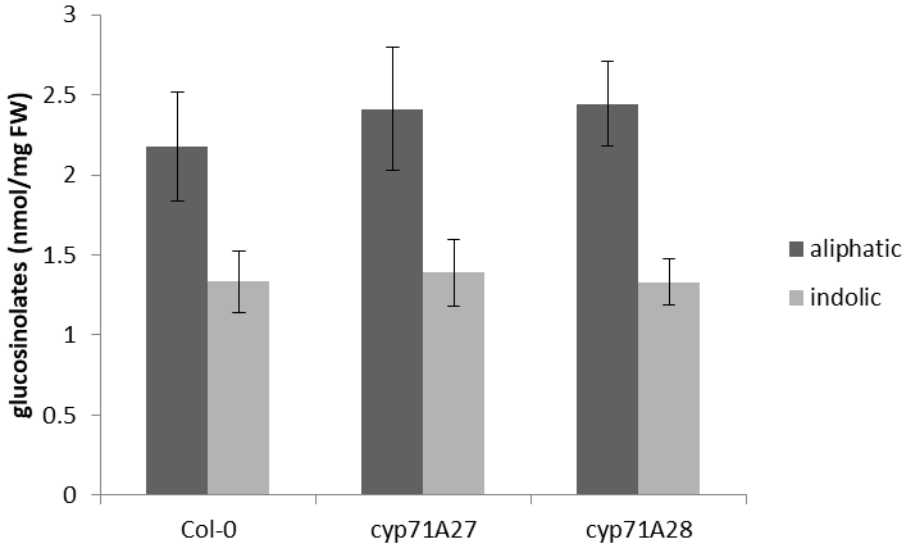


Fig. S4. Glucosinolate accumulation is not affected by loss of *CYP71A27* and *CYP71A28*
Col-0, *cyp71A27*, and *cyp71A28* plants were grown for 2.5 weeks on vertical agarose plates. Glucosinolate accumulation was determined in leaves by HPLC. Data are presented as means and S.D. from 4 biological replicates consisting of 2 shoots.

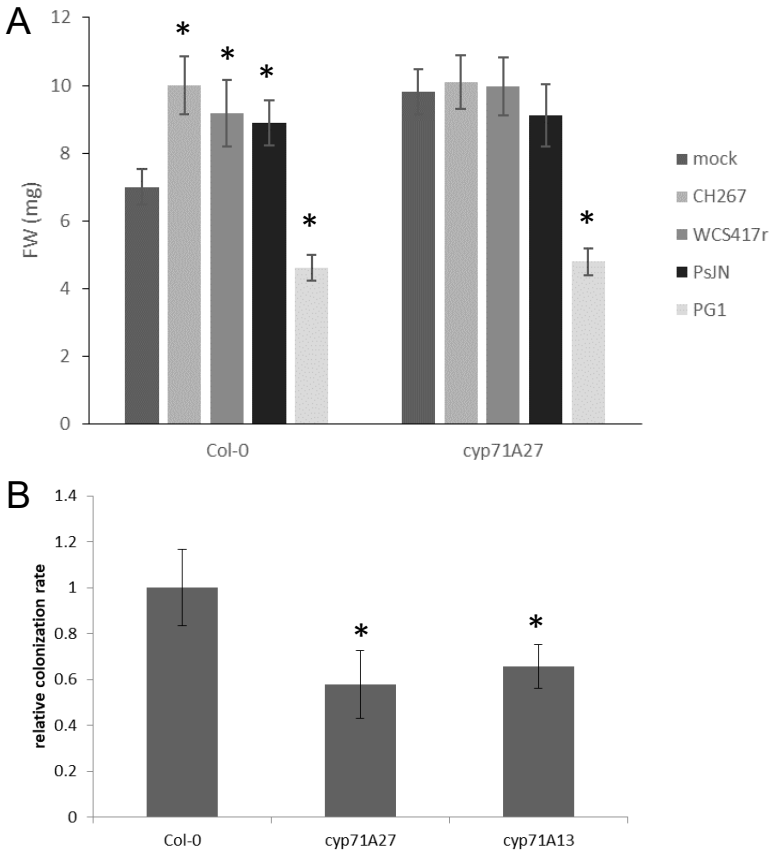


Fig. S5. CYP71A27 and CYP71A13 are important for plant microbe interaction.
A Col-0 and *cyp71A27* were grown for 2 weeks in presence of *Pseudomonas* sp. CH267, *P. simiae* WCS417r, *Paraburkholderia phytofirmans* PsJN, *Burkholderia glumae* PG1 or 10 µM $MgCl_2$ as mock, and the fresh weight of the whole plants was measured. Data are presented as means and S.E. from at least 20 plants grown on 4 independent plates. Asterisks indicate significant differences between mock and bacterial treatment at $p<0.05$ (Student´s T-test).
B Col-0, *cyp71A27*, and *cyp71A13* were grown for 2 weeks in presence of *Serendipita indica*, and the colonization rate was determined by quantification of fungal DNA in roots. Data are presented as relative abundance of fungal *SiTEF* transcripts compared to Arabidopsis *UBQ5* transcripts and as means and S.D. from 4 independent biological repetitions. The value in Col-0 was set to 1, asterisks indicate significant differences to Col-0 at $p<0.05$ (Student´s T-test).

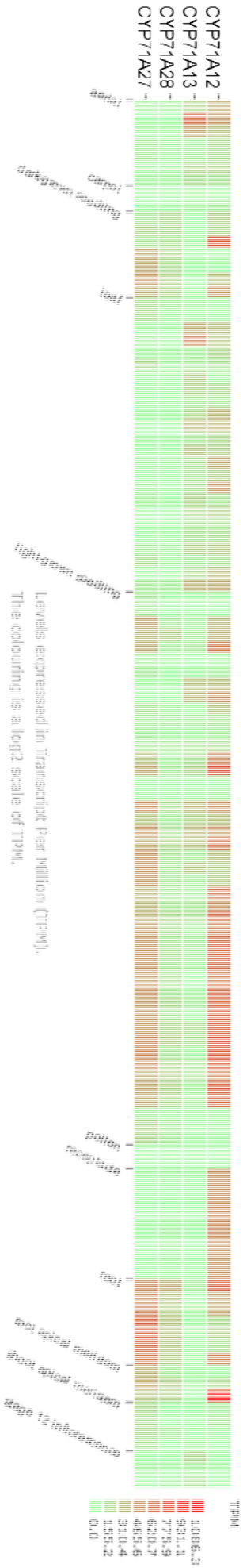
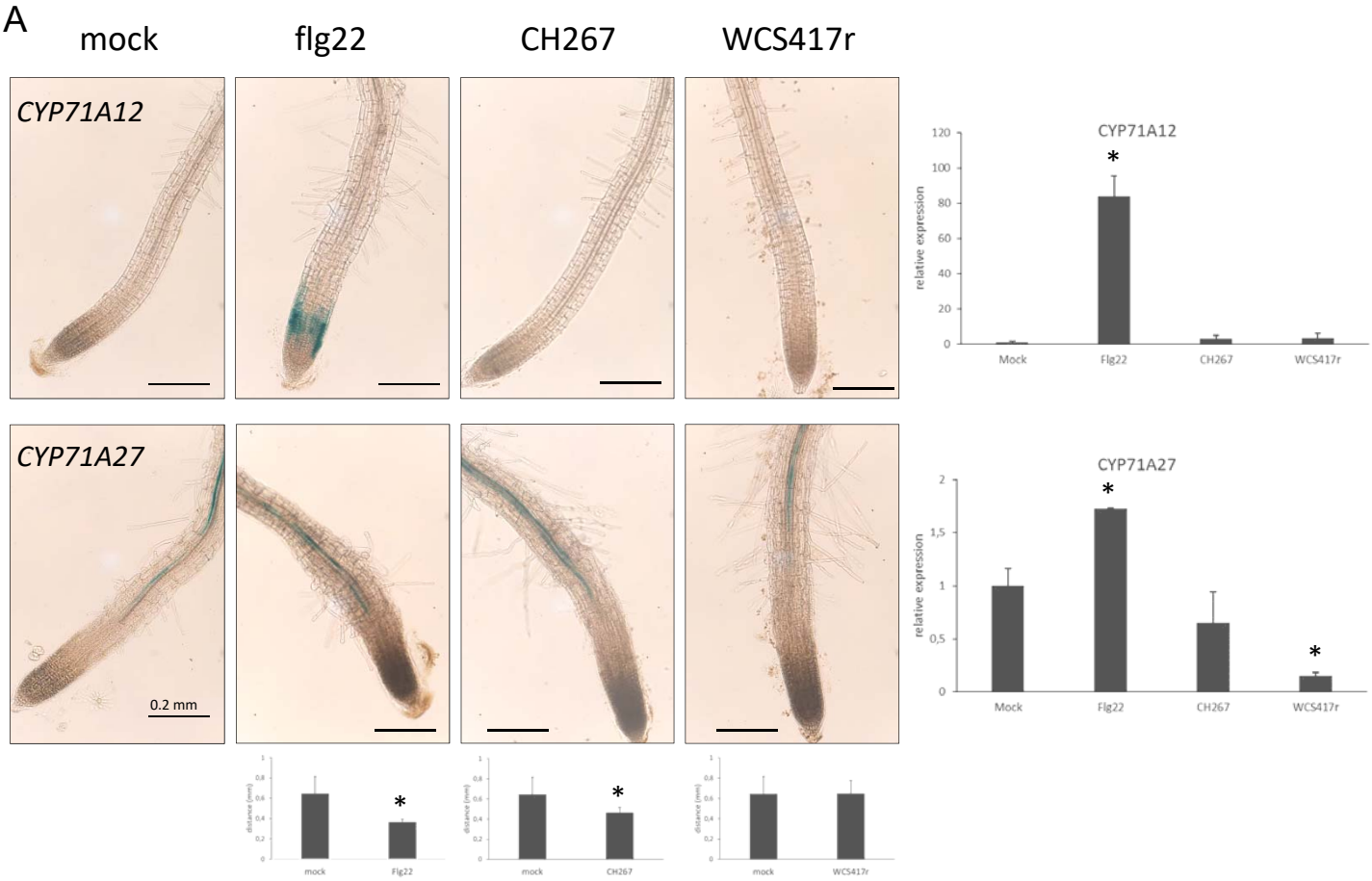


Fig. S6. Expression of *CYP71A27* and related CYP71 genes in different tissues.
The data was obtained from the Araport portal and show gene expression profiles in *Arabidopsis thaliana* developmental stages, organs and parts based on RNA-seq analysis. The transcript levels are shown in transcripts per million (TPM) and coloured according to $\log_2$TPM.

A


mock
flg22
CH267
WCS417r
CYP71A12
CYP71A27
0.2 mm
CYP71A12
relative expression
Mock
Flg22
CH267
WCS417r
CYP71A27
relative expression
Mock
Flg22
CH267
WCS417r

B

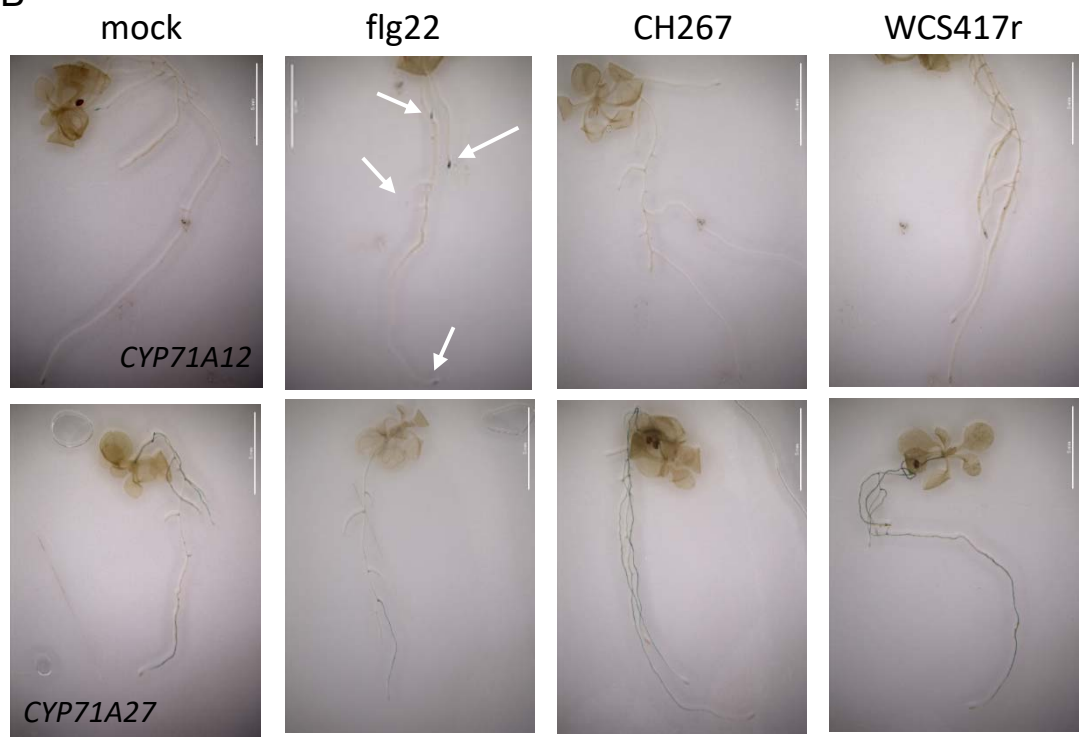

mock
flg22
CH267
WCS417r
CYP71A12
CYP71A27

Fig. S7. *CYP71A27* has a different expression pattern from *CYP71A12*
GUS stainings of transgenic plants expressing *CYP71A12pro::GUS* (21) (upper panel) and *CYP71A27pro::GUS* (bottom panel).
A Seven days old seedlings were transferred to liquid nutrient solution and treated with *Pseudomonas* sp. CH267 and *P. simiae* WCS417r (final OD_{600}=0.002), 1 µM flg22, or 10 µM $MgCl_2$ as mock for 24 hours before GUS staining. Scale bars, 0.2 mm. Photos representative of at least 7 plants.
Bottom row: The distance between root tip to the beginning of GUS staining was measured in *CYP71A27pro::GUS* plants after the different treatments and compared to mock. Data are shown as means and S.D. from at least 7 plants.
Right column: Expression analysis of *CYP71A12* and *CYP71A27*. RNA was isolated from roots of the treated seedlings and accumulation of transcripts for *CYP71A12* and *CYP71A27* was compared by qPCR. The analysis was performed with three independent RNAs measured in duplicates, data are shown as means and S.D. expression in mock is set to 1.
Asterisks indicate significant differences to mock at $p<0.05$ (one way ANOVA).
B Five days old seedlings were transferred on plates containing *Pseudomonas* sp. *CH267* and *P. simiae WCS417r* (final $OD_{600}=3.2 \times 10^{-6}$) or 10 µM $MgCl_2$ and cultivated for 7 days. For flagellin treatment 2 week old plants were treated with 1 µM flg22 for 5 h. The plants were stained for GUS activity and photos were made with a Leica MZ 16 F stereomicroscope. Scale bars, 5 mm. Photos representative of at least 6 plants. Arrows point to flg22-induced expression of *CYP71A12* in root tips.

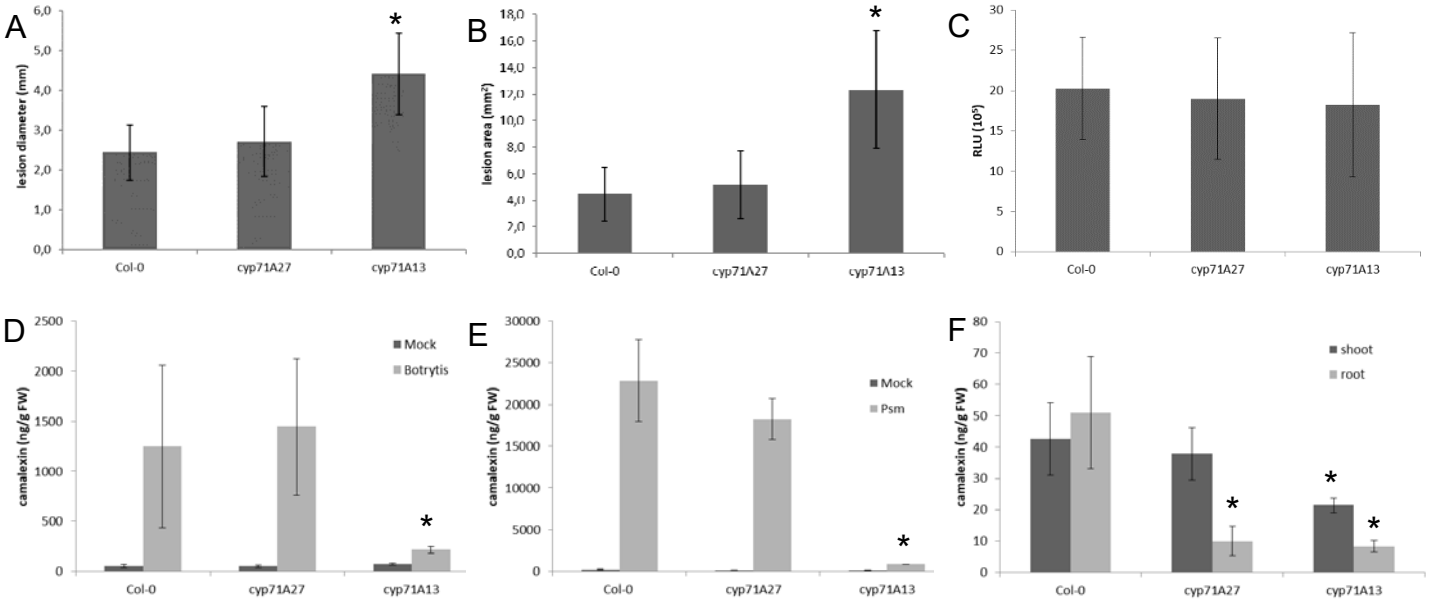


Fig. S8. CYP71A27 is not involved in pathogen defense in the leaves
Col-0, *cyp71A27*, and *cyp71A13* plants were grown for 4 weeks at short days and inoculated with pathogens.
Three leaves per each of 6 plants were inoculated with four 5 µl droplets containing *Botrytis cinerea* B05.10 spores (5 x 10^4/ml). After 3 days the lesion diameter (**A**) and area (**B**) were determined. Shown are means and S.E. from 72 lesion mesasurements.
C Leaves were inoculated with *Pseudomonas syringae pv maculicola* ES4326 (Psm) carrying the LUX operon from *P. luminescens.* The luminescence per area of leaf disks (RLU) was determined.
Camelexin was determined in leaves inoculated with *Botrytis* (**D**) or Psm (**E**) by HPLC. Data are presented as means and S.D. from 3 independent pools of 6 leaves (3 per plant).
F Col-0, *cyp71A27*, and *cyp71A13* plants were treated with $AgNO_3$ and camalexin was determined in the shoots and roots by HPLC. Data are shown as means and S.D. from three independent pools of at least 10 plants.
Asterisks indicate significant differences to Col-0 at $p<0.05$ (one way ANOVA).

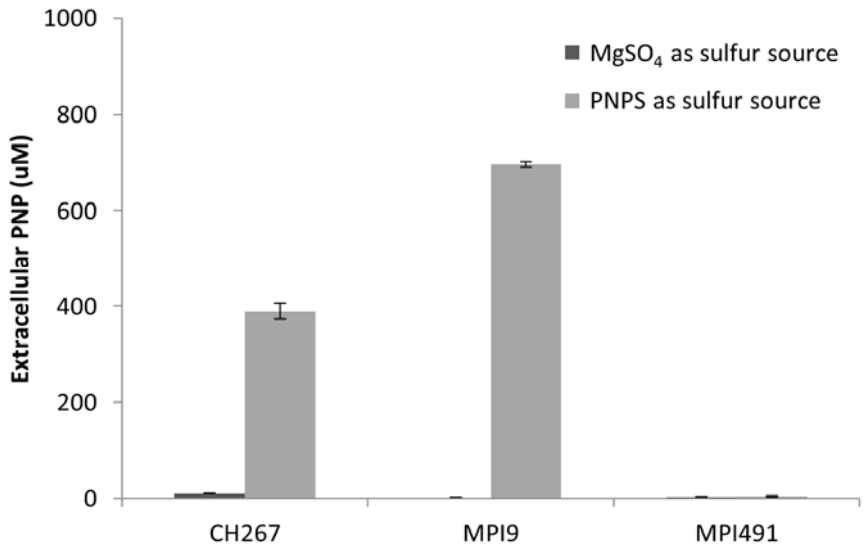


Fig. S9. Sulfatase activity of CH267, MPI9 and MPI491 bacterial strains. Bacterial strains were cultivated on an M9 minimal medium using either $MgSO_4$ or p-nitrophenyl sulfate (PNPS) as the sole sulfur source. After 48 hours growth, bacterial sulfatase activity was quantified by spectrophotometric measurement of p-nitrophenyl (PNP) concentration in the culture supernatant at 400 nm. Shown are means and S.D. from four replicates.

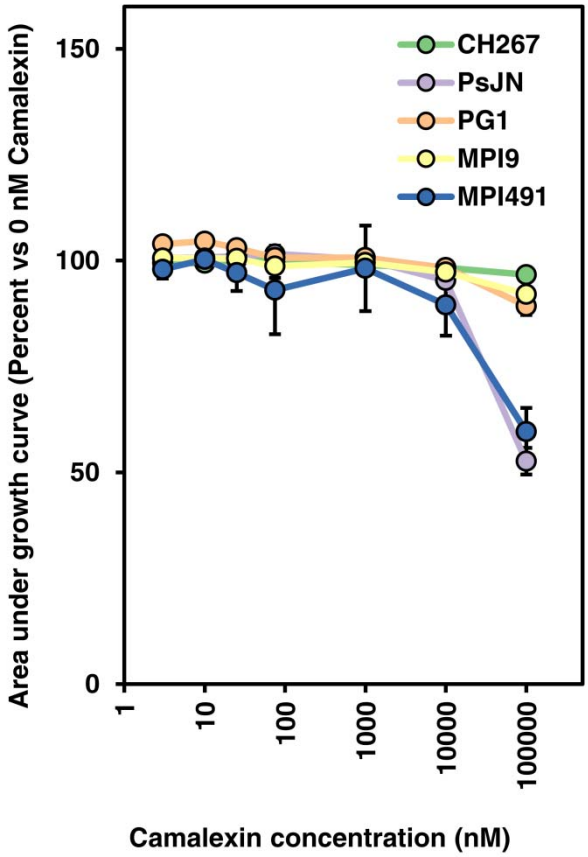


Fig. S10. Effect of camalexin on bacterial growth.
Growth of five bacterial strains was measured in the presence of different camalexin concentrations: 0, 3 nM, 10 nM, 25 nM, 75 nM, 1 µM, 10 µM, and 100 µM. Bacteria were cultivated on ½ TSB medium in 48-well plates in a plate reader at 28°C for 24 h with shaking. For each well, OD600 was measured every 10 min without correcting for path length. Resulting growth curves were quantified by integrating the Area Under Curve (AUC), and AUC values for different camalexin concentrations are normalised versus the 0 camalexin control for that strain. Shown are means and S.D. from three replicates.

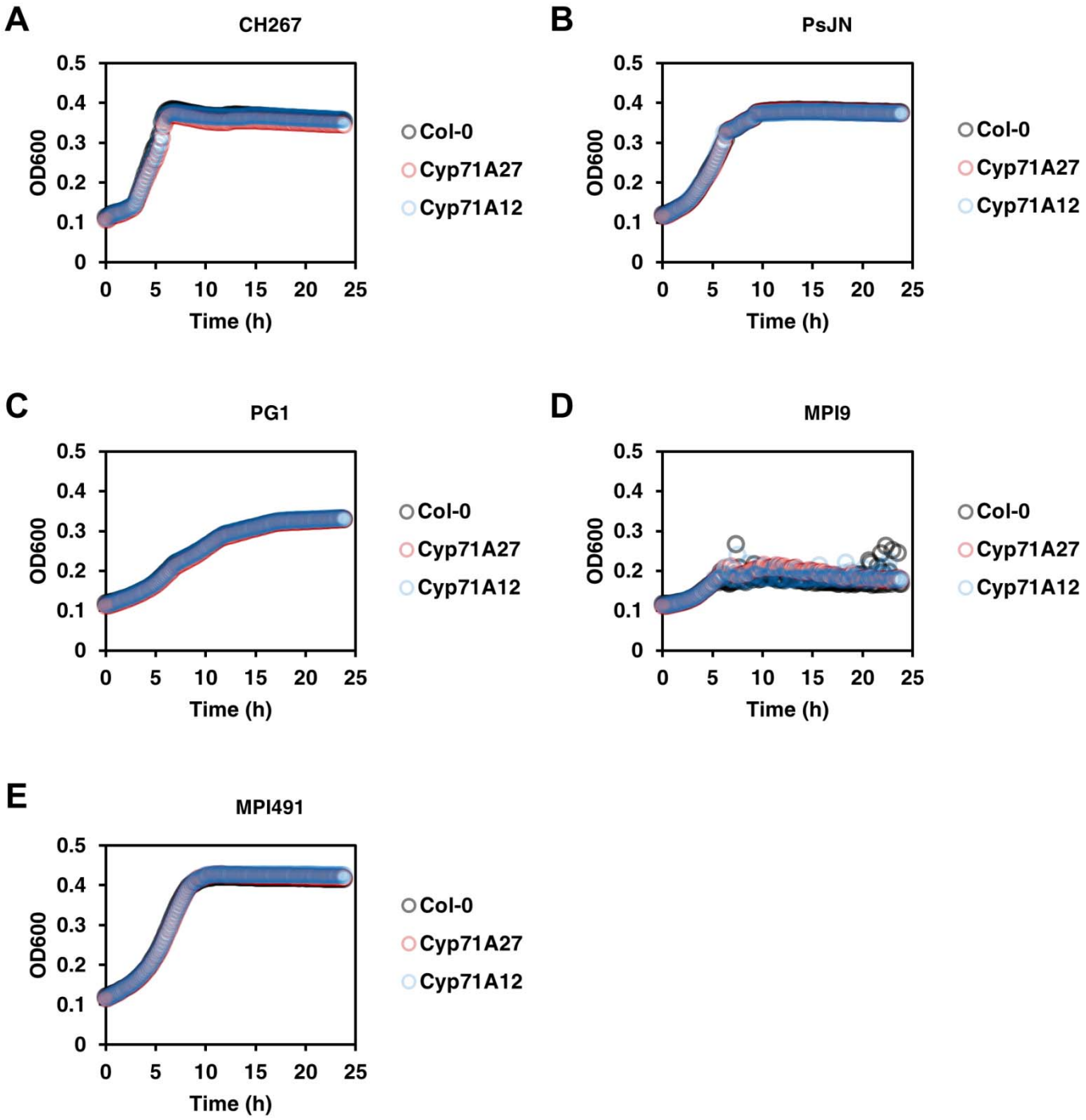


Fig. S11. Growth of bacteria on root extracts.
Growth of five bacterial strains was measured in media where the sole carbon source was root extract harvested from different Arabidopsis genotypes. M9 minimal media were formulated to contain root extract as the sole carbon source, with a carbon concentration of 720 mg C/l. In a 48-well plate, washed bacterial cells were inoculated into growth media at an OD600 of 0.05, and cultivated in a plate reader at 28°C for 24 h with shaking. For each well, OD600 was measured every 10 min without correcting for path length.

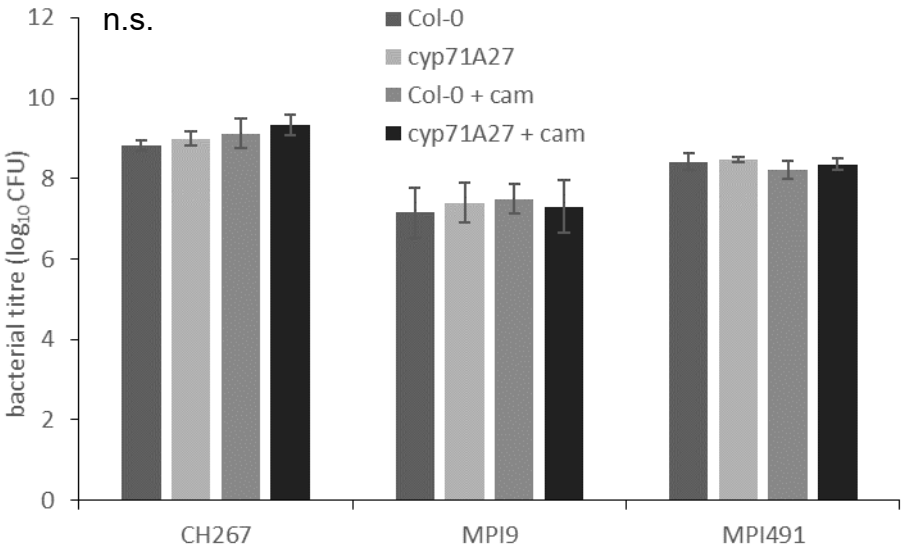


Fig. S12. Quantification of bacteria in roots.
Col-0 and *cyp71A27* were grown for 2 weeks in presence Pseudomonas sp. CH267, MPI9, and MPI491, with or without addition of 10 µM camalexin (cam). The bacterial titre was determined by colony counting. Data are presented as means and S.D. from 8 plates per genotype and treatment and the experiments was independently repeated. n.s. No significant differences for the individual strains were detected.

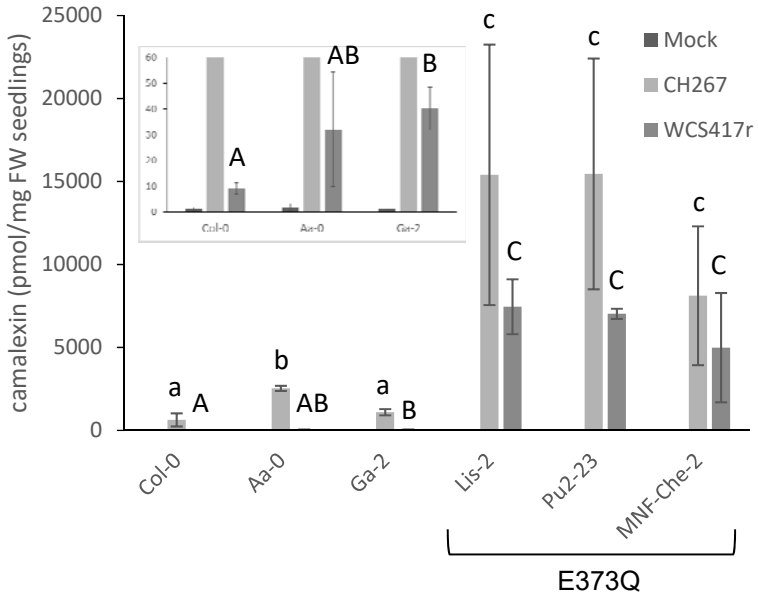


Fig. S13. Camalexin exudation

Three representative accessions of the two *CYP71A27* haplotypes were grown for 7 days on sterile 100 µm nylon mesh (six seedlings per sample) in 12 well plates placed on 1 ml of ½ MS medium with 0.5 % sucrose. Seven µl of *Pseudomonas* sp. CH267, *P. simiae* WCS417r cultures diluted to OD_{600}= 0.0001, or 10 µM $MgCl_2$ as mock were inoculated into each well. The plates were further incubated under the same conditions for 6 days with occasional shaking. Camalexin was determined in the nutrient solution after purification on 1 ml solid phase extraction tubes (Discovery-DSC18) by HPLC.

Data are shown as means and S.D. from four exudate samples from 6 plants, normalized per FW of the whole seedlings. Two way ANOVA confirmed that the camalexin amount depends on haplotype ($P = 1.7 \times 10^{-5}$), treatment ($P = 8.2 \times 10^{-5}$) and haplotype:treatment (P = 00059). Different letters indicate significantly different values at $p<0.05$.

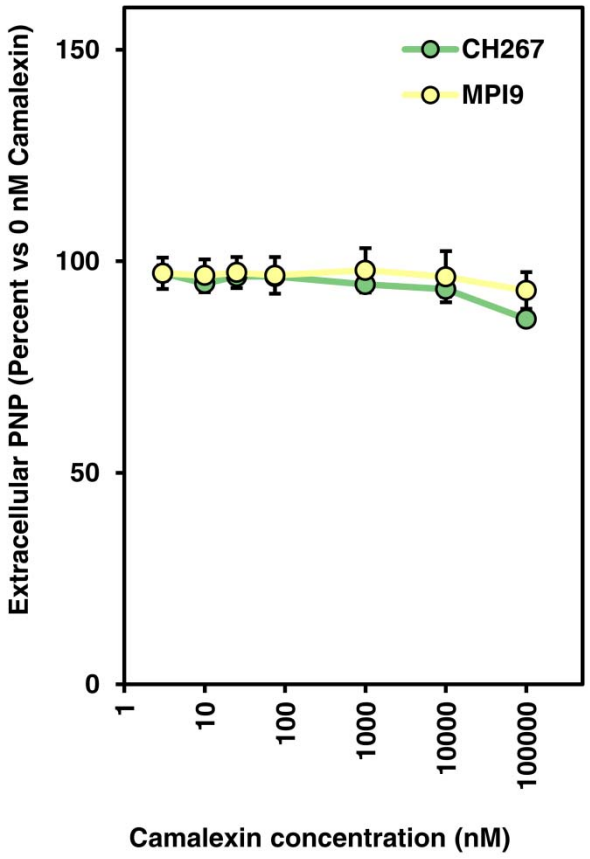


Fig. S14. Effect of camalexin on bacterial sulfatase activity.
Bacterial strains were cultivated in a 48-well plate on an M9 minimal medium using p-nitrophenyl sulfate (PNPS) as the sole sulfur source, in the presence of different camalexin concentrations: 0, 3 nM, 10 nM, 25 nM, 75 nM, 1 µM, 10 µM, and 100 µM. (A) Extracellular PNP: After 48 hours growth, bacterial sulfatase activity was quantified by spectrophotometric measurement of p-nitrophenyl (PNP) concentration in the culture supernatant at 400 nm. Shown are means and S.D. from three replicates. (B) Growth rate: For each well, OD600 was measured every 10 min without correcting for path length. Resulting growth curves were fitted against the logistic growth equation, and shown here are the maximum growth rate (r) values across different camalexin concentrations. Values are normalised versus the 0 camalexin control for that strain. Shown are means and S.D. from three replicates.

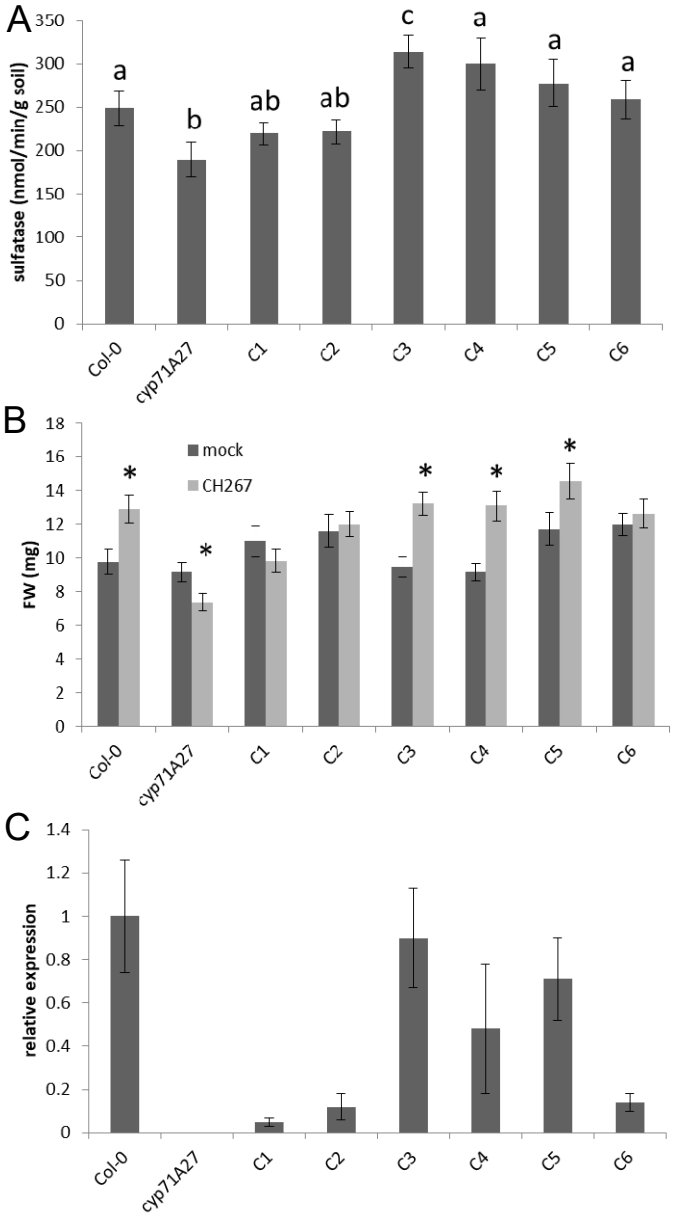


Fig. S15. Complementation of *cyp71A27* mutant.
A Col-0, *cyp71A27*, and 6 complemented lines were grown for 2 weeks in soil (10%)/sand mixture, afterwards 2 soil samples were taken per plant and sulfatase activity was measured. Data are presented as means and S.E. from 10 samples corresponding to 5 independent plants. Different letters indicate differences significant at $p<0.05$ (one way ANOVA).
B Col-0, *cyp71A27*, and 6 complemented lines were grown for 2 weeks in presence of *Pseudomonas* sp. CH267 or 10 µM $MgCl_2$ as mock, and the fresh weight of the whole plants was measured. Data are presented as means and S.E. from at least 20 plants grown on 4 independent plates. Asterisks indicate significant differences between mock and bacterial treatment at $p<0.05$ (Student´s T-test).
C RNA was isolated from roots of the 8 genotypes and *CYP71A27* transcript accumulation was compared by qPCR. The value in Col-0 was set to 1. Data are shown as means and S.D. from three independent plants measured in duplicates.

Supplementary Table S1. Sulfatase activity in soil from 172 *Arabidopsis thaliana* accessions Sulfatase activity (nmol/min/g soil); shown are means from 10 soil samples, corresponding to 5 independent plants and activity relative to Col-0.

accession	ID	mean activity	activity rel. to Col-0
Aa-0	7000	96,24	1,13
Alc-0	6988	129,47	1,52
ALL1-2	1	157,67	1,85
ALL1-3	2	56,96	0,67
Alst1	6989	269,32	3,16
Amel-1	6990	95,14	1,12
An-1	6898	126,97	1,49
Ang-0	6992	110,68	1,30
Ann-1	6994	61,79	0,73
App1-16	5832	144,02	1,69
Baa-1	7002	104,24	1,22
Be-1	7011	90,02	1,06
Belmonte-4-94	957	127,29	1,49
Benk-1	7008	69,79	0,82
Bg-2	6709	188,98	2,22
Bil-5	6900	65,99	0,77
Blh-1	8265	98,13	1,15
Boot-1	7026	109,87	1,29
Bor-1	5837	108,17	1,27
Brö1-6	8231	220,44	2,59
Bs-2	7004	67,25	0,79
Bsch-0	7031	134,97	1,58
Bu-0	8271	86,39	1,01
Bu-8	7056	129,50	1,52
Bur-0	6905	118,23	1,39
C24	6906	103,50	1,22
Ca-0	7062	119,10	1,40
Can-0	8274	164,92	1,94
Cha-0	7069	141,05	1,66
CIBC-2	6727	168,85	1,98
CIBC-4	6729	191,32	2,25
Cit-0	7075	151,41	1,78
CLE-6	78	222,04	2,61
Co-2	7078	46,09	0,54
Co-4	7080	118,56	1,39
Col-0	6909	85,17	1,00
Com-1	7092	97,97	1,15
Cvi-0	6911	91,29	1,07
Da-0	7094	60,35	0,71
Di-1	7098	48,55	0,57
Do-0	7102	49,40	0,58
Dr-0	7106	168,03	1,97
Dra-0	7103	131,31	1,54
Dra3-1	8283	108,31	1,27

DraIV.1.5	5887	126,94	1,49
Ede-1	7110	65,41	0,77
Eden-1	6009	81,76	0,96
Es-0	7126	38,25	0,45
Est-0	7128	124,67	1,46
Est-1	6916	89,20	1,05
Fäb-2	6917	113,59	1,33
Fei-0	8215	45,12	0,53
Fja1-1	8422	73,08	0,86
Fja1-5	6020	121,24	1,42
Fr-4	7135	171,26	2,01
Ga-2	7141	89,76	1,05
Ge-0	8297	132,54	1,56
Gel-1	7143	182,02	2,14
Gie-0	7147	81,07	0,95
Go-0	7151	123,34	1,45
Gr-1	8300	14,86	0,17
Gu-1	7150	111,53	1,31
Gul1-2	8234	149,34	1,75
Ha-0	7163	78,36	0,92
Hn-0	7165	157,45	1,85
Hod	8235	151,61	1,78
Hov-3-2	6036	112,61	1,32
Hovdala-2	6039	87,16	1,02
Hs-0	8310	18,95	0,22
HSm	8236	54,00	0,63
In-0	8311	70,53	0,83
JEA	91	69,68	0,82
Jm-1	7178	90,48	1,06
KBS-Mac-8	1716	86,58	1,02
Kin-0	6926	46,84	0,55
Kno-18	6928	130,41	1,53
Krot-0	7203	109,88	1,29
Krot-2	7205	127,00	1,49
Kulturen-1	8240	295,57	3,47
Kyoto	7207	60,68	0,71
LAC-3	94	91,98	1,08
LDV-25	116	161,90	1,90
Ler-1	6932	107,62	1,26
Li-7	7231	86,46	1,02
Lip-0	8325	326,20	3,83
LL-0	6933	217,31	2,55
Lm-2	8329	134,89	1,58
Lom1-1	6042	167,43	1,97
Lov-1	6043	133,17	1,56
Lov-5	6046	116,55	1,37
Mc-0	7252	98,82	1,16
Mh-0	7255	161,15	1,89
MIB-84	223	80,91	0,95

MNF-Che-2	1925	75,80	0,89
Mnz-0	7244	134,54	1,58
Mr-0	7522	76,79	0,90
Mrk-0	6937	113,89	1,34
Mv-0	7248	121,20	1,42
N13	7438	94,25	1,11
N7	7449	114,53	1,34
Nc-1	7430	101,44	1,19
NC-6	8246	85,26	1,00
No-0	7275	45,93	0,54
Nyl-13	9433	143,41	1,68
Nz-1	7263	126,05	1,48
Or-0	7282	99,34	1,17
Ors-2	7284	119,13	1,40
Oy-0	6946	245,67	2,88
PAR-4	259	60,64	0,71
Paw-3	2150	98,72	1,16
Pent-1	2187	14,36	0,17
Per-1	8354	84,32	0,99
PHW33	7504	57,34	0,67
PHW-34	7505	150,49	1,77
PHW35	7506	45,82	0,54
PHW36	7507	64,31	0,76
PHW37	7507	141,02	1,66
Pi-0	7298	45,34	0,53
Pla-0	7300	170,62	2,00
Pro-0	8213	40,69	0,48
Pt-0	7305	50,77	0,60
Pu2-23	6951	49,40	0,58
Rak-2	8365	127,45	1,50
Rd-0	8366	20,43	0,24
Ren-1	6959	231,48	2,72
Rev-2	6076	182,51	2,14
Rmx-A180	7525	95,25	1,12
Rou-0	7320	88,05	1,03
RRS-10	7515	147,84	1,74
Sav-0	7340	119,92	1,41
Sei-0	7333	76,65	0,90
Sg-1	7344	79,41	0,93
Shadahra	6962	48,96	0,57
St-0	8387	132,69	1,56
Ste-3	2290	54,27	0,64
T1040	6094	42,59	0,50
T1060	6096	91,25	1,07
T1110	6100	15,44	0,18
T540	6112	165,52	1,94
T620	6119	93,70	1,10
TDr-18	6203	118,30	1,39
Ting-1	7354	226,55	2,66

Tol-0	7356	181,41	2,13
Tomegap-2	6242	163,28	1,92
Tottarp-2	6243	101,35	1,19
TOU-A1-62	328	153,77	1,81
TOU-E-11	366	260,62	3,06
TOU-H-13	374	132,01	1,55
TOU-K-3	386	96,07	1,13
Ts-1	6970	49,43	0,58
Tscha-1	7372	72,66	0,85
Tsu-0	7373	39,95	0,47
Tul-0	7377	180,23	2,12
Uk-2	7379	125,52	1,47
UKNW06-436	5606	197,82	2,32
UKSE-278	5122	101,52	1,19
Ull2-3	6973	88,56	1,04
Ull2-5	6974	40,09	0,47
Ull3-4	6413	84,88	1,00
Utrecht	7382	54,82	0,64
Van-0	7383	48,90	0,57
Ven-1	7384	152,46	1,79
VOU-1	390	33,31	0,39
Wa-1	7394	60,68	0,71
Wc-2	7405	60,16	0,71
Wl-0	7411	35,68	0,42
Ws-0	6980	138,52	1,63
Ws-2	6981	60,15	0,71
X328PNA054	8692	133,55	1,57
Yo-0	6983	144,79	1,70
Zdr-6	6449	125,76	1,48
Zu-1	7418	85,45	1,00

Supplementary Table S2. Markers significantly associated with variation in sulfatase
Shown are positions of markers with score ($-\log_{10}P$) higher than 4.

chromosome	position	score
5	16093269	5,781
2	8948991	5,768
5	18619037	5,387
2	6300485	5,356
4	7369340	5,306
1	13052365	5,211
3	21352347	5,137
1	5484572	5,112
4	9865729	5,072
4	9874455	5,072
4	9885694	5,072
5	4734285	5,070
3	4559978	5,067
2	7332044	4,830
3	4574994	4,825
5	19728614	4,816
5	23670216	4,810
1	22744494	4,798
5	8427481	4,797
4	10930013	4,780
2	8588043	4,775
4	12026369	4,758
5	23765316	4,687
5	22814448	4,682
3	4555946	4,655
3	4556265	4,655
2	8672858	4,611
5	3912479	4,575
3	8300660	4,529
5	16463903	4,508
5	18036619	4,441
5	3373458	4,409
1	17866252	4,407
1	5062465	4,404
5	18552017	4,386
5	20299888	4,358
4	7283307	4,339
5	14734084	4,329
2	272607	4,326
1	2214123	4,322
2	272690	4,315
1	22744473	4,272
3	12912061	4,272
1	12073641	4,266
1	12111200	4,266

chromosome	position	score
2	8060333	4,266
4	7296652	4,266
1	898397	4,246
3	18002103	4,229
1	22960034	4,213
1	17864022	4,189
3	18002412	4,182
1	17600900	4,163
5	8429895	4,147
3	2366209	4,145
5	2685965	4,145
2	8612698	4,114
2	8583271	4,093
2	8586121	4,093
2	10501739	4,092
4	15210413	4,067
3	1145882	4,065
3	12599993	4,061
5	23700786	4,056
5	23705451	4,056
5	23715848	4,056
5	23777633	4,056
1	6895487	4,030
5	1557906	4,024
3	11052579	4,016

Supplementary Table S3. Candidate genes for analysis of T-DNA lines.
"gene" is the candidate gene selected within the linkage disequilibrium.
"p sulfatase" represents the p value of the comparison of sulfatase activity with Col-0. Red marks significant differences at p<0.05

rank	chrom.	position	score	gene		annotation	T-DNA line	p sulfatase	sulfatase activity relative to Col-0
2	2	8948991	5,768113	At2g20780	MRS	Major facilitator superfamily protein	SAIL_759_E05	0,35	0,9
3	5	18619037	5,386588	At5g45875		family of small, secreted, cysteine rich proteins	SALK_089063	0,14	0,72
4	2	6300485	5,356145	At2g14750	APK1	APS kinase 1	SALK_053427	0,41	1,06
7	3	21352347	5,13653	At3g57650	LPAT2	lysophospatidyl transferase			
8	1	5484572	5,112086	At1g15950	CCR1	cinnamoyl CoA reductase	GK-622C01	0,007	0,46
13	3	4559978	5,066509	At3g13870	RHD3	root hair defective			
18	1	22744494	4,797908	At1g61680	TPS14	terpene synthase			
20	4	10930013	4,77969	At4g20235	CYP71A28	cytochrome P-450	SALK_064792C	0,04	0,49
				At4g20240	CYP71A27	cytochrome P-450	SALK_053817C	0,04	0,63
21	2	8588043	4,775429	At2g19880	GCS	Glucosylceramide synthase			
24	5	22814448	4,681923	At5g56360	PSL4	defense response to bacterium,	SALK_039458C	0,27	0,87
29	3	8300660	4,529327	At3g23240	ERF1	ethylene response factor			
31	5	18036619	4,440517	At5g44620	CYP706A3	cytochrome P-450			
				At5g44630		Sesquiterpene synthase	SALK_151777C	0,33	0,92
33	1	17866252	4,406965	At1g48370	YSL8	metal-nicotianamine transporter	SALK_076262_10	0,03	0,54
				At1g48380	RHL1	ROOT HAIRLESS 1			
34	1	5062465	4,403505	At1g14700	PAP3	purple acid phosphatase 3	SALK_081178	0,04	0,67
49	3	18002103	4,228665	At3g48560	AHAS	Acetohydroxy Acid Synthetase			
50	1	22960034	4,21292	At1g62180	APR2	APS reductase 2	GABI_108G02	0,16	1
54	5	8429895	4,146978	At5g24655	LSU2	Low Sulfur 2	SALK_069114	0,04	0,73
				At5g24660	LSU4	Low Sulfur 4	SALK_031648C	1,17	
59	2	8586121	4,092993	At2g19860	HXK2	hexokinase 2			
68	1	6895487	4,029585	At1g19920	ATPS2	ATP sulfurylase 2	SAIL775D12	0,49	1
69	5	1557906	4,024213	At5g05260	CYP79A2	cytochrome P-450	GK-913H04	0,13	0,74

Supplementary Table S4. T-DNA lines used for analysis

gene	annotation	homozygous T-DNA line	primers for verification of T-DNA insertion	
At2g20780	Major facilitator superfamily protein	SAIL_759_E05	gcgatgtagacaggagcg	gaatcttccggaggttgg
At5g45875	family of small, secreted, cysteine rich proteins	SALK_089063	ttagcaaggagaatatggaaa	atgaagtctactaccttgttc
At2g14750	APS kinase 1	SALK_053427	gctttcgatggcttcttc	gacccaaatcacacatcc
At1g15950	cinnamoyl CoA reductase	GK-622C01	gtcgacgtagcctcacc	cttgaccttggcctcagc
At4g20235	cytochrome P-450	SALK_064792C	cctgccgaggagatgg	gcttcaccactttcttagc
At4g20240	cytochrome P-450	SALK_053817C	ttccaatcttctccgtagg	gtctccttcccaagcgag
At5g56360	defense response to bacterium,	SALK_039458C	ccttcagctgctggctc	aattgagaaggtagaggag
At5g44630	Sesquiterpene synthase	SALK_151777C	gggacttggagagattgg	tctacgagcaaaagcctc
At1g48370	metal-nicotianamine transporter	SALK_076262_10	gccatcgaatagcagacc	tagcgacagctatgaacac
At1g14700	purple acid phosphatase 3	SALK_081178	ctaatctctcaatggctacc	aaggtttctgcaagctcg
At1g62180	APS reductase 2	GABI_108G02	gtgctcttaagggtcttaaa	ctcacacccgattgacac
At5g24655	Low Sulfur 2	SALK_069114	gatccaacaatctaagaacc	gaaaaggaggaaactatgtg
At5g24660	Low Sulfur 4	SALK_031648C	agccgataagaggatacatc	ttagatcaaagtaaaatggtcc
At1g19920	ATP sulfurylase 2	SAIL775D12	tctcaatttggtctataaacg	ttaaaggactagcccaacc
At5g05260	cytochrome P-450	GK-913H04	ttcgtccgacagagtagg	cattaactatgaagcgtaagg
		SALK LB primer	attttgccgatttcggaac	
		GABI LB primer	atattgaccatcatactcattgc	

Supplementary Table S5. Bacterial strains used.

	NCBI Taxonomy ID	antibiotics resistance	sulfatase activity	ref.
Pseudomonas sp. CH267	1634009	ampicillin	+	(26)
Pseudomonas simiae WCS417r		rifampicin	-	(27)
Paraburkholderia phytofirmans PsJN	398527	gentamicin	-	(28)
Pseudomonas sp. Root9 (MPI9)	1736604		+	(4)
Rhizobium sp. Root491 (MPI491)	1736548		-	(4)
Burkholderia glumae PG1	595500	chloramphenicol	+	(29)

The NCBI Taxonomy number is included when available. Presence of sulfatase activity determined experimentally as production of p-nitrophenyl during growth on p-nitrophenyl sulfate.

Supplementary Table S6. Oligonucleotide primers used

qPCR					
TIP41	*AT4G34270*	TIP41-F	gaactggctgacaatggagtg	TIP41-R	atcaactctcagccaaaatcg
CYP71A12	*AT2G30750*	CYP71A12-F	tgtggtgtttggtccctatg	CYP71A12-R	ttgttcgtgagcagattgaga
CYP71A13	*AT2G30770*	CYP71A13-F	gatgttgtgtttgctccctatg	CYP71A13-R	ttgttggtgagcagattgaga
CYP71A27	*AT4G20240*	CYP71A27-F	ccctacggagaagattggaa	CYP71A27-R	ccagcttctctgtcattactttga
CYP71A28	*AT4G20235*	CYP71A28-F	ttctcctcctacggcgaata	CYP71A28-R	gaggagatggacagtgcataaa
GST6	*AT2G47730*	GST6-F	aagcaagaggcccacctt	GST6-R	tcttgactcgaaaagcgtca
GGP1	AT4G30530	GGP1-F	tgtcaagaaaattgatgagatgaag	GGP1-R	ccccttaccctggctatgat
CYP71B15	*AT3G26830*	CYP71B15-F	caccactgatcatctcaaagga	CYP71B15-R	cggtcattccccatagtgtt
MAM	At5g23020	MAM-F	ccgtgaacagtgttaagtacgc	MAM-R	cacccgcttttatcgattct
TSB	At5g54810	TSB-F	acgaagaagcgttggaagc	TSB-R	ggtaagctagtgcgtgtgagg
CYP79F1	*AT1G16410*	CYP79F1-F	agaccgatcttgccagctt	CYP79F1-R	ggtagattgccgaggatgg
CYP79B2	*AT4G39950*	CYP79B2-F	tgacggatcccaacaaaaag	CYP79B2-R	atgatcggccatcctgtg
MYB28	*AT5G61420*	MYB28-F	tggaccaactaccttaaacctga	MYB28-R	tctcgctatgaccgaccact
MYB51	*AT1G18570*	MYB51-F	ggccaattatcttagacctgaca	MYB51-R	ccacgagctatagcagaccatt
SUR1	*At2g20610*	SUR1-F	ggattctccccgcaagac	SUR1-R	catccagcggtcagaaaa
SOT16	*At1g74100*	SOT16-F	cgaagtcgtcgaactcacagagtt	SOT16-R	aaagaccttcgaggagacattcttg
SOT17	*At1g18590*	SOT17-F	ggaatccaaaaccataaacgacg	SOT17-R	cggatcttttggtctccagcc
UBQ5	*At3g62250*	AtUBI_F	ccaagccgaagaagatcaag	AtUBI_R	actccttcctcaaacgatga
PiTEF		03008_QPCR_F	gcaagttctccgagctcatc	03008_QPCR_R	ccaagtggtgggtactcgtt

cloning	
CYP27PROFOR	caccttt gacctatactttactacc
CYP27PROREV	attgtgcttatttaggaatgg
CYP27FOR	caccctatttaagtatttttattggac
CYP27REV	tcacaaggttggctagtgc