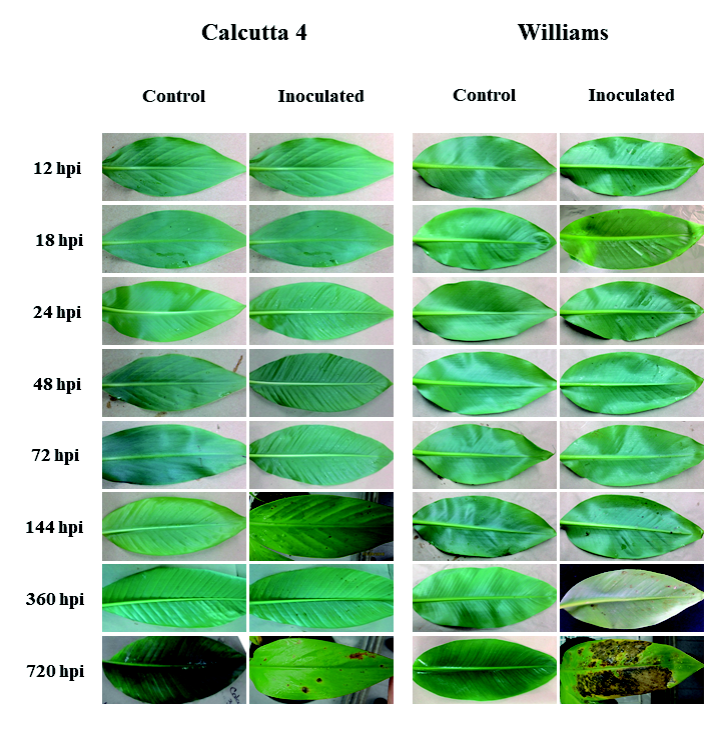
Table S1. Primer sequences for RT-qPCR. Oligonucleotide primer pairs for amplification of a fragment of approximately 150 bp with an optimum of 120 bp, were designed for each selected gene using the Primer3 software (Rozen and Skaletsky 2000) and their specificity was verified by doing a blast search in the GenBank database. Primer amplification was verified by conventional PCR using DNA template from Calcutta 4 and Williams before qRT-PCR. Primer pairs were designed with a one Celsius degree as a maximum melting temperature (Tm) difference between them. GC values of the primer sequences were between 45-65% with an optimum of 50%. Maximum Hairpin score 1.0 and Maximum primer-dimer score 1.0.

Gene	ID_Primer	type	Tm_qPCR	Sequence
Lipoxygenase (LOX)	LOX_fw[a]	Biosynthesis	62 ºC	5'-ACTACTTGCTCTTCCCCAGCGG-3'
	LOX_rv[b]	Biosynthesis	62 ºC	5'-CGTCCCTCACACCACACGC-3'
Allene Oxide Synthase (AOS)	AOS_fw	Biosynthesis	60 ºC	5'-CCACCTGCTTCAACTCCTTCGGC-3'
	AOS_rv	Biosynthesis	60 ºC	5'-ATCGCCCGCATCGTCACCTC-3'
Allene Oxide Cyclase (AOC)	AOC_fw	Biosynthesis	60 ºC	5'-CCCCGCCTACCTCCGCCT-3'
	AOC_rv	Biosynthesis	60 ºC	5'-CCGTGATGCCCACCCGCTTTT-3'
12-Oxophytodienoate Reductase 2 (OPR2)	OPR2_fw	Biosynthesis	60 ºC	5'-CCATTGTGGAAGGCAGGCG-3'
	OPR2_rv	Biosynthesis	60 ºC	5'-TCGGCAAGTCGGGGTTGGA-3'
3-Ketoacyl-CoA thiolase (Kat)	KAT_fw	Biosynthesis	60 ºC	5'-TGCTACAGGTGCCCGATGT-3'
	KAT_rv	Biosynthesis	60 ºC	5'-CGTCTCCACGCTCAAACACAG-3'
Jasmonate-amido synthetase (JAR1)	JAR1_fw	Signal transduction	60 ºC	5'-CCAGTTCAAGACACCACGCT-3'
	JAR1_rv	Signal transduction	60 ºC	5'-GGAAAGACGAATCACAGAAGAGG-3'
Transcription factor MYC4	Myc4_fw	Signal transduction	60 ºC	5'-CTCCCGCCCGCTCGTTCAAG-3'
	Myc4_rv	Signal transduction	60 ºC	5'-GCTCGCCCTGGATGTCGCTC-3'
Pathogenesis-Related Protein 4 (PR4)	PR-4_fw	Defense	60 ºC	5'-TGGGACGCCAATAAGCCCCT-3'
	PR-4_rv	Defense	60 ºC	5'-TCCTGACCGTAGCCTGAGTTCC-3'
26s subunit ribosomal	26s_fw	Housekeeping	60 ºC	5'-ACATTGTCAGGTGGGGAGTT-3'
	26s_rv	Housekeeping	60 ºC	5'-CCTTTTGTTCCACACGAGATT-3'

[a]fw: Forward.

[b]rv: Reverse.


Calcutta 4
Williams
Control
Inoculated
Control
Inoculated
12 hpi
18 hpi
24 hpi
48 hpi
72 hpi
144 hpi
360 hpi
720 hpi

Time	Metabolites
12 hpi	gibberellin A24
12 hpi	gibberellin A9
12 hpi	*cis* -zeatin-7-*N* -glucoside
12 hpi	*cis* -zeatin-9-*N* -glucoside
12 hpi	2-*cis* -abscisate
12 hpi	violaxanthin
24 hpi	gibberellin A44 (closed lactone form)
24 hpi	gibberellin A9
24 hpi	*trans* -zeatin-7-*N* -glucoside
24 hpi	indole-3-acetyl-phenylalanine
24 hpi	indole-3-acetyl-valine
24 hpi	α-linolenate
24 hpi	13(S)-HPOTE
72 hpi	gibberellin A44 (closed lactone form)
72 hpi	salicylate 2-O-β-D-glucoside
72 hpi	salicylate β-D-glucose ester
72 hpi	salicylate 2-O-β-D-glucoside
72 hpi	salicylate β-D-glucose ester
72 hpi	β-D-glucopyranosyl abscisate
72 hpi	indole-3-acetyl-L-aspartate
72 hpi	6-hydroxy-indole-3-acetyl-valine
72 hpi	gibberellin A8-catabolite
72 hpi	12,13(S)-epoxylinolenate
72 hpi	9'-*cis* -neoxanthin
144 hpi	dihydrozeatin-9-*N* -glucoside-*O* -glucoside
144 hpi	dihydrozeatin-7-*N* -glucose
144 hpi	adenosine
144 hpi	*trans* -zeatin riboside
144 hpi	indole-3-acetyl-glutamate
144 hpi	2-*cis* -abscisate
144 hpi	β-D-glucopyranosyl abscisate
144 hpi	9'-*cis* -neoxanthin

144 hpi	*ent* -kaur-16-en-19-oate
144 hpi	12,13(S)-epoxylinolenate
144 hpi	12-oxo-cis-10,15-phytodienoate
144 hpi	linoleate
360 hpi	dihydrozeatin-9-N-glucoside-O-glucoside
360 hpi	dihydrozeatin-7-N-glucose
360 hpi	adenosine
360 hpi	dihydrozeatin-O-glucoside
360 hpi	isopentenyladenine-9-N-glucoside
360 hpi	chorismate
360 hpi	salicylate
360 hpi	salicylate β-D-glucose ester
360 hpi	UDP
360 hpi	1-aminocyclopropane-1-carboxylate
360 hpi	S-adenosyl-L-methionine
360 hpi	s-methyl-5'-thioadenosine
360 hpi	3-hydroxy-indole-3-butyryl-CoA
360 hpi	indole-3-acetyl-CoA
360 hpi	indole-3butyrate
360 hpi	(+)-cis-abscisic aldehyde
360 hpi	2-cis-abscisate
360 hpi	2-cis,4-trans-xanthoxin
360 hpi	α-linolenate
360 hpi	12,13(S)-epoxylinolenate
360 hpi	12-oxo-cis-10,15-phytodienoate
360 hpi	13(S)-HPOTE
360 hpi	3-oxo-2-[cis-2'-pentenyl]-cyclopentane-1-octanoate
360 hpi	gibberellin A12
360 hpi	gibberellin A12-aldehyde

Pathway(s) Involved	Dysregulation	Fold Change	p-value
gibberellin biosynthesis I (non C-3, non C-13 hydroxylation)	UP	1.9	1.5e-5
gibberellin biosynthesis I (non C-3, non C-13 hydroxylation)	UP	1.7	8.5e-7
gibberellin inactivation I (2β-hydroxylation)			
gibberellin inactivation II (methylation)			
cytokinins 7-N-glucoside biosynthesis	UP	1.6	3.3e-5
cytokinins 9-N-glucoside biosynthesis	DOWN	5.3	6.1e-6
abscisic acid biosynthesis	DOWN	7.0	1.1e-7
abscisic acid biosynthesis	DOWN	1.7	1.2e-5
gibberellin inactivation I (2β-hydroxylation)	UP	4.3	2.9e-6
gibberellin biosynthesis I (non C-3, non C-13 hydroxylation)	DOWN	1.4	2.8e-5
gibberellin inactivation I (2β-hydroxylation)			
gibberellin inactivation II (methylation)			
cytokinins 7-N-glucoside biosynthesis	UP	3.1	7.9e-4
	UP	2.9	6.9e-4
indole-3-acetate degradation	UP	2.9	6.9e-4
indole-3-acetyl-amide conjugate biosynthesis			
indole-3-acetate degradation V	UP	2.3	7.3e-4
indole-3-acetyl-amide conjugate biosynthesis			
jasmonic acid biosynthesis	UP	1.4	3.3e-4
jasmonic acid biosynthesis	UP	1.2	1.8e-4
gibberellin inactivation I (2β-hydroxylation)	UP	9.8	5.2e-6
salicylate glucosides biosynthesis IV	UP	5.3	3.8e-5
salicylate glucosides biosynthesis III	UP	5.3	3.8e-5
salicylate glucosides biosynthesis IV	DOWN	2.3	8.9e-5
salicylate glucosides biosynthesis III	DOWN	2.3	8.9e-5
abscisic acid glucose ester biosynthesis	UP	2.7	9.7e-5
indole-3-acetate degradation IV	DOWN	5.8	1.3e-5
indole-3-acetyl-amide conjugate biosynthesis			
indole-3-acetate degradation V	DOWN	4.5	4.6e-5
gibberellin inactivation I (2β-hydroxylation)	DOWN	2.5	4.5e-7
jasmonic acid biosynthesis	DOWN	2.0	5.9e-6
abscisic acid biosynthesis	DOWN	1.3	1.6e-5
cytokinin-O-glucosides biosynthesis	DOWN	10.3	6.9e-5
cytokinins 7-N-glucoside biosynthesis	DOWN	9.6	4.2e-5
cytokinins degradation	DOWN	2.8	5.8e-6
cytokinins degradation	DOWN	2.1	7.5e-5
indole-3-acetyl-amide conjugate biosynthesis	DOWN	2.4	6.5e-5
abscisic acid biosynthesis	DOWN	2.2	2.2e-6
abscisic acid glucose ester biosynthesis			
phaseic acid biosynthesis			
abscisic acid glucose ester biosynthesis	DOWN	2.0	4.7e-7
abscisic acid biosynthesis	DOWN	1.8	8.6e-6

GA12 biosynthesis	DOWN	1.6	1.8e-5
jasmonic acid biosynthesis	DOWN	2.4	8.2e-5
jasmonic acid biosynthesis	DOWN	2.0	1.2e-5
jasmonic acid biosynthesis	DOWN	5.7	1.7e-5
cytokinin-O-glucosides biosynthesis	UP	23.0	9.5e-5
cytokinins 7-N-glucoside biosynthesis	UP	19.0	4.8e-5
cytokinins degradation	UP	13.4	2.4e-5
cytokinin-O-glucosides biosynthesis	DOWN	8.8	3.1e-8
cytokinins 9-N-glucoside biosynthesis	DOWN	8.8	3.1e-8
salicylate biosynthesis I	UP	12.5	3.8e-5
salicylate glucosides biosynthesis III	UP	3.1	1.8e-6
salicylate glucosides biosynthesis III	UP	10.3	1.3e-5
salicylate glucosides biosynthesis III	UP	1.5	7.6e-5
ethylene biosynthesis I (plants)	DOWN	3.2	1.7e-5
ethylene biosynthesis I (plants)	DOWN	2.5	4.1e-5
ethylene biosynthesis I (plants)	UP	9.0	9.2e-6
IAA biosynthesis VII	UP	12.9	5.7e-5
IAA biosynthesis VII	DOWN	5.6	5.2e-5
IAA biosynthesis VII	UP	4.8	8.1e-6
abscisic acid biosynthesis	DOWN	3.5	1.6e-5
abscisic acid biosynthesis	UP	14.0	1.5e-5
abscisic acid biosynthesis	DOWN	2.0	1.6e-5
jasmonic acid biosynthesis	UP	4.3	2.7e-5
jasmonic acid biosynthesis	DOWN	1.7	7.8e-5
jasmonic acid biosynthesis	UP	1.7	5.2e-5
jasmonic acid biosynthesis	DOWN	3.4	4.5e-5
jasmonic acid biosynthesis	DOWN	1.6	8.5e-6
GA12 biosynthesis	UP	5.8	4.5e.5
GA12 biosynthesis	DOWN	1.7	7.2e.5

m/z	Retention Time	Adducts
185,0867	3.47	M+H+Na[2+]
170,0812	12.42	M+H+Na[2+]
404,1554	5.57	M+Na[1+]
364,1618	4.81	M-H2O+H[1+]
282,1703	9.48	M+NH3+H[1+]
583,416	18.39	M-H2O+H[1+]
185,0866	3.58	M+H+Na[2+]
170,0812	12.54	M+H+Na[2+]
382,1714	3.68	M+H[1+]
305,0658	5.21	M+H[1+]
305,0658	5.21	M+H[1+]
257,1287	5.00	M-H2O+H[1+]
296,2587	11.83	M+NH3+H[1+]
293,2114	13.09	M-H2O+H[1+]
185,0867	3.55	M+H+Na[2+]
323,074	5.14	M+Na[1+]
323,074	5.14	M+Na[1+]
301,0923	2.37	M+H[1+]
301,0923	2.37	M+H[1+]
444,2208	2.38	M+NH3+H[1+]
274,0712	6.09	M-NH3+H[1+]
274,1079	3.60	M-NH3+H[1+]
182,0759	3.54	M+2H[2+]
310,2379	13.27	M+NH3+H[1+]
301,2165	15.26	M+2H[2+]
568,2243	3.50	M+Na[1+]
384,188	1.86	M+H[1+]
285,1313	6.40	M+NH3+H[1+]
374,1447	5.46	M+Na[1+]
164,0509	5.78	M+H+Na[2+]
247,1333	6.57	M-H2O+H[1+]
449,1785	6.57	M+Na[1+]
301,2164	12.35	M+2H[2+]

303,2321	7.83	M+H[1+]
147,1099	2.30	M+2H[2+]
275,2009	11.12	M-H2O+H[1+]
319,2019	6.91	M+K[1+]
528,2291	5.80	M-H2O+H[1+]
366,1761	6.45	M-H2O+H[1+]
290,0873	5.52	M+Na[1+]
366,1763	10.29	M-H2O+H[1+]
366,1763	10.29	M+H[1+]
244,0817	2.34	M+NH3+H[1+]
139,0391	5.45	M+H[1+]
301,0922	2.33	M+H[1+]
442,9654	2.06	M+K[1+]
141,0178	1.87	M+K[1+]
401,1596	6.58	M+H[1+]
336,0514	5.72	M+K[1+]
485,106	4.89	M+2H[2+]
950,265	6.50	M+NH3+H[1+]
221,1287	2.52	M+NH3+H[1+]
249,1489	12.13	M+H[1+]
265,1438	5.07	M+H[1+]
233,1539	8.58	M-H2O+H[1+]
296,2587	11.70	M+NH3+H[1+]
293,2113	8.64	M+H[1+]
293,2113	9.62	M+H[1+]
328,2474	7.27	M+NH3+H[1+]
277,2165	12.55	M-H2O+H[1+]
333,207	5.99	M+H[1+]
317,2114	11.27	M+H[1+]

Time	Metabolites	Pathway(s) Involved
12 hpi	salicylate	salicylate glucosides biosynthesis II
		salicylate glucosides biosynthesis III
		salicylate glucosides biosynthesis IV
		volatile benzenoid biosynthesis I (ester formation)
12 hpi	dihydrozeatin	cytokinin-O-glucosides biosynthesis
		cytokinins 7-N-glucoside biosynthesis
		cytokinins 9-N-glucoside biosynthesis
12 hpi	UDP-α-D-galactose	galactose degradation I (Leloir pathway)
		galactose degradation III
		stachyose biosynthesis
		stachyose degradation
24 hpi	6-hydroxy-indole-3-acetyl-phenylalanine	indole-3-acetate degradation V
24 hpi	indole-3-acetyl-phenylalanine	indole-3-acetate degradation V
72 hpi	brassinolide	brassinosteroids inactivation
72 hpi	castasterone-23-O-glucoside	brassinosteroids inactivation
72 hpi	isopentenyl adenosine	cytokinins degradation
72 hpi	adenine	adenine and adenosine salvage II
		cytokinins degradation
72 hpi	kinetin	cytokinins 7-N-glucoside biosynthesis
		cytokinins 9-N-glucoside biosynthesis
72 hpi	dihydrozeatin-7-N-glucose	cytokinins 7-N-glucoside biosynthesis
72 hpi	*cis-zeatin-7-N-glucoside*	cytokinins 7-N-glucoside biosynthesis
72 hpi	*trans-zeatin* riboside	cytokinins degradation
72 hpi	gibberellin A36	gibberellin biosynthesis I
		gibberellin biosynthesis II
72 hpi	gibberellin A12-aldehyde	GA12 biosynthesis
72 hpi	gibberellin A12	GA12 biosynthesis
		gibberellin biosynthesis I
72 hpi	12,13(S)-epoxylinolenate	jasmonic acid biosynthesis
72 hpi	13(S)-HPOTE	jasmonic acid biosynthesis
		traumatin and (Z)-3-hexen-1-yl acetate biosynthesis
72 hpi	12-oxo-cis-10,15-phytodienoate	jasmonic acid biosynthesis
72 hpi	3-oxo-2-(cis-2'-pentenyl)-cyclopentane-1-octanoate	jasmonic acid biosynthesis
72 hpi	12,13(S)-epoxylinolenate	jasmonic acid biosynthesis
72 hpi	2-cis-abscisate	abscisic acid biosynthesis
		phaseic acid biosynthesis
72 hpi	2-cis,4-trans-xanthoxin	abscisic acid biosynthesis
144 hpi	α-linolenate	jasmonic acid biosynthesis
		traumatin and (Z)-3-hexen-1-yl acetate biosynthesis
144 hpi	OPC6-trans-2-enoyl-CoA	jasmonic acid biosynthesis
144 hpi	1-aminocyclopropane-1-carboxylate	ethylene biosynthesis I (plants)
144 hpi	*S-methyl-5'-thioadenosine*	ethylene biosynthesis I (plants)

360 hpi	9'-cis-neoxanthin	abscisic acid biosynthesis
360 hpi	gibberellin A8-catabolite	gibberellin inactivation I
360 hpi	gibberellin A97	gibberellin inactivation I
360 hpi	gibberellin A98	gibberellin inactivation I
360 hpi	3-oxo-2-(cis-2'-pentenyl)-cyclopentane-1-octanoate	jasmonic acid biosynthesis
360 hpi	13(S)-HPOTE	jasmonic acid biosynthesis
360 hpi	(+)-7-iso-jasmonate	jasmonic acid biosynthesis
360 hpi	α-linolenate	jasmonic acid biosynthesis

Dysregulation	Fold Change	p-value	*m/z*	Retention Time	Adducts
UP	19.0	4.8e-6	176,994	3.26	M+K[1+]
DOWN	15.2	1.2e-6	204,1233	4.76	M-H2O+H[1+]
DOWN	5.2	2.4e-5	567,0632	2.16	M+H[1+]
UP	6.0	1.3e-5	181,0614	1.83	M+H+Na[2+]
	2.6	9.7e-5	322,1069	3.59	M-NH3+H[1+]
UP	7.8	1.6e-5	340,1659	4.32	M+NH3+H[1+]
UP	6.0	9.7e-7	498,3795	13.86	M+NH3+H[1+]
UP	2.4	1.3e-5	325,2012	11.11	M+H+Na[2+]
UP	4.0	3.4e-6	358,1482	7.78	M+Na[1+]
UP	2.9	2.9e-5	119,0348	2.48	M-NH3+H[1+]
DOWN	6.7	3.1e-5	233,1135	3.58	M+NH3+H[1+]
DOWN	6.5	1.7e-6	367,1603	6.69	M-NH3+H[1+]
DOWN	6.5	1.7e-6	367,1603	6.69	M-NH3+H[1+]
DOWN	2.6	1.2e-5	364,1604	3.73	M-H2O+H[1+]
DOWN	2.2	2.7e-5	334,1498	4.47	M-H2O+H[1+]
UP	3.4	6.1e-6	380,207	7.16	M+NH3+H[1+]
UP	2.0	9.5e-5	317,2114	11.31	M+H[1+]
DOWN	5.2	1.1e-6	316,1809	6.11	M-NH3+H[1+]
UP	3.1	1.2e-5	275,201	13.04	M-H2O+H[1+]
UP	3.0	9.0e-6	293,2114	12.31	M-H2O+H[1+]
UP	2.4	4.3e-5	275,2009	12.31	M-H2O+H[1+]
UP	2.4	3.7e-5	295,227	9.14	M+H[1+]
UP	2.2	4.2e-5	275,2009	14.17	M-H2O+H[1+]
UP	2.5	2.7e-5	265,1439	5.89	M+H[1+]
UP	2.2	2.9e-5	233,1539	10.84	M-H2O+H[1+]
DOWN	1.9	3.5e-3	261,2217	11.69	M-H2O+H[1+]
UP	5.1	1.6e-4	507,6448	7.01	M+2H[2+]
UP	1.9	4.6e-3	141,0184	3.05	M+K[1+]
DOWN	1.6	2.5e-4	336,0514	5.81	M+K[1+]

DOWN	1.6	7.4e-4	583,4158	18.38	M-H2O+H[1+]
DOWN	1.8	2.2e-3	182,0758	5.48	M+2H[2+]
DOWN	2.6	4.4E-4	182,076	4.55	M+2H[2+]
DOWN	6.0	3.2e-4	194,0926	2.33	M+H+Na[2+]
DOWN	6.0	3.2e-4	194,0926	2.33	M+H+Na[2+]
DOWN	6.9	1.0e-3	317,2074	5.44	M+Na[1+]
DOWN	3.4	1.4e-3	156,1138	21.69	M+2H[2+]
DOWN	4.6	1.5e-3	228,1597	5.27	M+nh3+H[1+]
DOWN	2.9	2.6e-3	261,2217	13.85	M-H2O+H[1+]