

Silicon Controls Bacterial Wilt Disease in Tomato Plants and Inhibits the Virulence-Related Gene Expression of *Ralstonia solanacearum*

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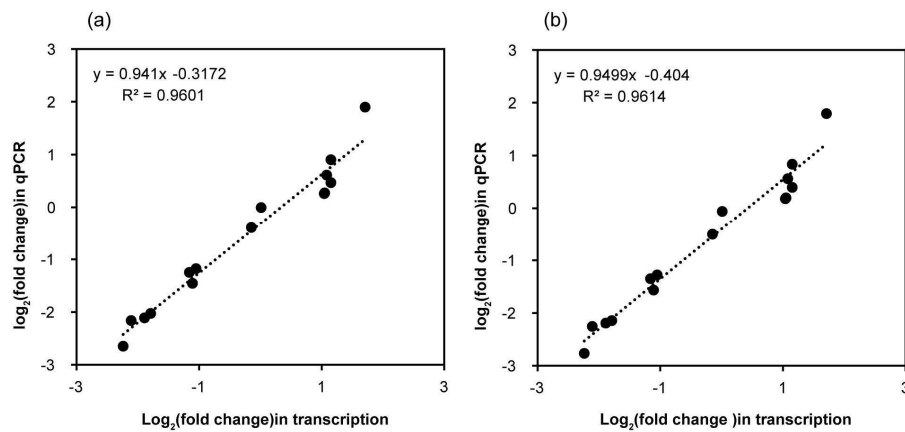


Figure S1. Correlation of transcription (x axis) and qPCR data (y axis) for a subset of 15 DEGs.

(a) *GAPDH* gene as internal control. (b) *thyA* gene as internal control.

KEGG pathway annotation

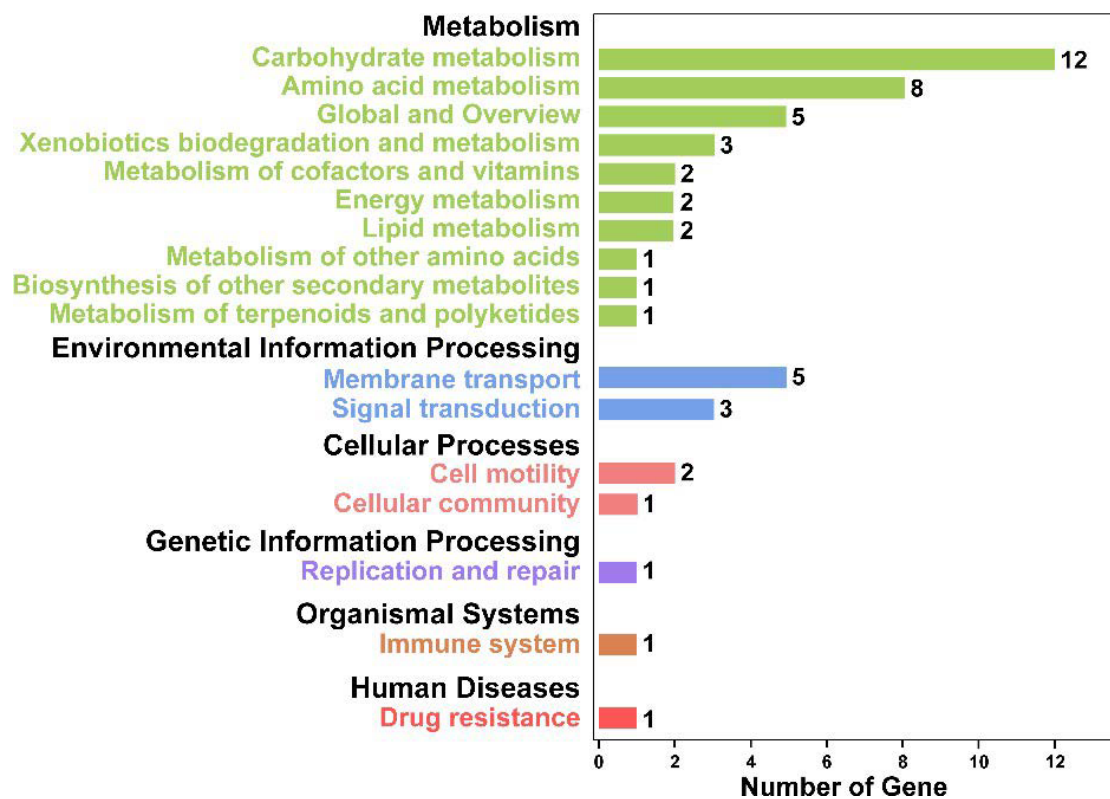


Figure S2. KEGG pathway annotation.

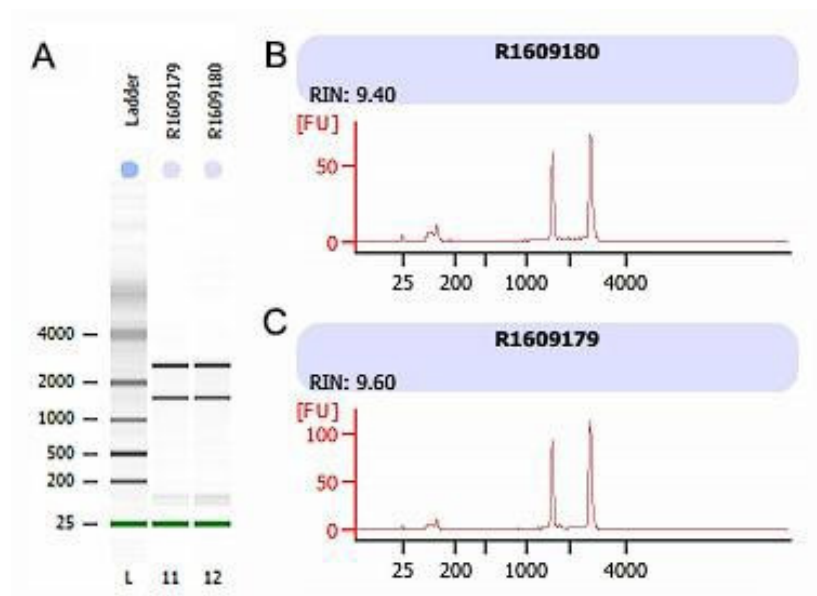


Figure S3. Quality of the extracted RNA. A: Capillary electrophoresis of the samples; B:

Integrity of CK samples; C: Integrity of Si samples.

Table S1 The genes significantly upregulated in Si treatment compared with CK

No.	Gene ID	log2(FC)	<i>p</i> -value	No.	Gene ID	log2(FC)	<i>p</i> -value
1	RSc0699	13.32	1.56E-02	30	RSc2519	1.21	1.67E-02
2	RSp1151	13.27	1.56E-02	31	RSc0199	1.2	5.42E-03
3	RSc3187	13.05	7.82E-03	32	RSc1963	1.2	7.78E-50
4	RSc1895	3.62	1.84E-03	33	RSc0583	1.2	6.67E-03
5	RSc3357	3.25	1.17E-02	34	RSc1325	1.19	1.38E-02
6	RSp0632	2.52	1.30E-02	35	RSp0002	1.15	4.54E-19
7	RSc1850	2.26	7.56E-03	36	RSc2080	1.15	1.02E-32
8	RSp1108	2.24	5.13E-77	37	RSc1057	1.15	1.76E-56
9	RSp1107	2.21	1.08E-14	38	RSc0609	1.13	4.75E-40
10	RSc1241	2.2	5.51E-04	39	RSp1106	1.12	1.87E-25
11	RSp0379	2.18	2.61E-03	40	RSc0593	1.12	2.96E-06
12	RSp0564	1.97	5.41E-41	41	RSc1254	1.12	2.65E-10
13	RSp1464	1.76	1.45E-04	42	RSp0602	1.09	4.13E-03
14	RSp1552	1.71	3.79E-11	43	RSc0723	1.09	1.88E-05
15	RSp0199	1.58	4.58E-03	44	RSc2740	1.09	1.21E-02
16	RSp1638	1.49	1.37E-07	45	RSc1614	1.08	3.53E-04
17	RSc0076	1.48	4.08E-12	46	RSc0374	1.08	1.56E-18
18	RSc1025	1.46	2.94E-04	47	RSc2780	1.06	6.08E-06
19	RSc2388	1.45	4.68E-04	48	RSp1449	1.06	8.09E-53
20	RSc1622	1.41	9.10E-03	49	RSc2680	1.05	1.46E-05
21	RSc1159	1.38	5.33E-04	50	RSc0722	1.04	2.25E-04
22	RSp0757	1.36	1.62E-02	51	RSc0719	1.03	1.55E-03
23	RSc0512	1.33	1.28E-03	52	RSc2528	1.02	4.68E-21
24	RSp0443	1.3	2.30E-08	53	RSc2880	1.01	1.49E-09
25	RSp0708	1.3	3.84E-03	54	RSc0570	1.01	4.37E-04
26	RSc3150	1.29	6.87E-11	55	RSc2725	1.01	3.44E-04
27	RSc2280	1.26	1.59E-06	56	RSc2629	1	3.61E-05
28	RSc2506	1.26	1.11E-03	57	RSc0980	1	4.71E-06
29	RSp0713	1.21	1.32E-03				

Table S2 The genes significantly downregulated in Si treatment compared with CK

No.	Gene ID	log2(FC)	p-value	No.	Gene ID	log2(FC)	p-value
1	RSp0937	-12.58	3.91E-03	32	RSc0093	-1.26	0.00E+00
2	RSc0626	-2.88	4.20E-03	33	RSc1093	-1.26	8.01E-03
3	RSc3301	-2.24	0.00E+00	34	RSp0479	-1.24	2.01E-09
4	RSp0106	-2.1	8.82E-55	35	RSp1001	-1.22	2.35E-92
5	RSp1373	-2.07	1.19E-02	36	RSp1005	-1.21	9.87E-07
6	RSc2984	-1.99	1.13E-16	37	RSc2313	-1.21	1.94E-04
7	RSp1510	-1.94	3.74E-03	38	RSp0306	-1.2	1.59E-03
8	RSc2641	-1.91	1.00E-04	39	RSc2981	-1.2	1.06E-35
9	RSc2983	-1.89	1.25E-79	40	RSp0836	-1.17	4.34E-08
10	RSp1002	-1.87	0.00E+00	41	RSc2756	-1.16	2.47E-11
11	RSp0982	-1.85	3.02E-11	42	RSc3232	-1.16	1.34E-02
12	RSp1003	-1.79	0.00E+00	43	RSp1249	-1.14	4.90E-07
13	RSp0319	-1.78	8.93E-42	44	RSp0837	-1.13	3.61E-06
14	RSp0482	-1.75	1.08E-03	45	RSp0838	-1.13	2.37E-05
15	RSp0377	-1.73	1.47E-02	46	RSp0829	-1.11	1.28E-02
16	RSc0190	-1.73	1.47E-02	47	RSp1016	-1.11	4.10E-15
17	RSp1526	-1.71	2.05E-18	48	RSp0140	-1.11	6.53E-03
18	RSc0931	-1.65	1.26E-02	49	RSc2980	-1.1	1.09E-14
19	RSp1004	-1.56	0.00E+00	50	RSc2113	-1.1	3.11E-03
20	RSp1268	-1.55	1.74E-21	51	RSc2755	-1.08	7.61E-11
21	RSp1366	-1.52	2.92E-03	52	RSp0971	-1.07	1.77E-02
22	RSc2982	-1.47	1.26E-59	53	RSp0650	-1.07	5.22E-03
23	RSp0484	-1.4	3.64E-43	54	RSc0538	-1.05	2.55E-12
24	RSp1000	-1.39	0.00E+00	55	RSp1633	-1.05	4.03E-85
25	RSc0597	-1.37	5.95E-04	56	RSp0485	-1.04	5.42E-05
26	RSp0696	-1.37	2.22E-03	57	RSc1825	-1.03	8.74E-03
27	RSc1750	-1.36	9.54E-03	58	RSp0649	-1.02	1.28E-02
28	RSp1527	-1.35	2.97E-59	59	RSp1636	-1.02	5.85E-24
29	RSp1401	-1.33	3.22E-03	60	RSp0995	-1.01	2.55E-04
30	RSc3128	-1.31	2.37E-36	61	RSp1011	-1.01	3.95E-23
31	RSp0483	-1.28	7.65E-46	62	RSp1530	-1	2.86E-42

Table S3 Gene primer sequence for qPCR

Accession	Gene	Primer Sequence (5'-3')	
RSc2749	<i>GAPDH</i>	F	CGCCATCGCCAACTTCAA
		R	GTTGACGACCAGCGTATTGC
RSc0947	<i>thyA</i>	F	GGCGACTGCCATCTCTACAAC
		R	GCGGGATGGCTTTCGTAG
RSc2553	<i>argG</i>	F	CCTATGCCTACACCGCCAA
		R	CGTGGTGTTGAAGTAGGTGATG
RSc0374	<i>rpoH</i>	F	GCCGAGATGCACGAGTACA
		R	CCACCGCATCGACTTCGT
RSc0722	<i>fimT</i>	F	AAGCAGCCGCAGGTCAC
		R	GACAAGGAGGTGAGGCAGG
RSc1057	<i>rseB</i>	F	GGTGGCATTCTCGCAAGTC
		R	AGCCCGTCACGCTCTTCA
RSc2680	<i>pilE</i>	F	CGGTTCTGGCGTATCCCT
		R	TCGTGAGGTCCGAGGCAT
RSc2748	<i>phcA</i>	F	CCTACAACCTCAACGCCTTCC
		R	CAGCATCGGGTGCGTGTT
RSc2756	<i>araH</i>	F	TGATCGCCCGGCTGAAG
		R	TGGTGTGCCCAGGTCG
RSc2983	<i>rpoE</i>	F	GCGTGGCTGTTGACCATCA
		R	TCGGTAGGCCAGTTGCTCC
RSc3301	<i>putA</i>	F	CGCCATGACGGAAGAGGA
		R	GCTTGATCGAGATGCCCCG
RSp0002	<i>cspD3</i>	F	AAAGGCTTCGGCTTCATCA
		R	CTTGATACCCGAGGCTTGC
RSp0106	<i>modA</i>	F	GACCAATGCCTTCAAGACGC
		R	GCCTTGTCATCGCTTCCT
RSp1003	<i>xpsR</i>	F	CGGTGGCAATCGCATCA
		R	CTTCCAGTCGCATTGCTCT
RSp1016	<i>epsD</i>	F	ATCGCCTTCGCCAATGAG
		R	GGCTTGGCATCGTTGACC
RSp1552	<i>degP</i>	F	ACCTCCATCCAGGGTTTGC
		R	ATTGCTTGTCACCCCCA
RSp1633	<i>xylF</i>	F	GGGCATCAAGGTGGTCTCG
		R	GGCGTTGTTGTCGGTGGA

Table S4 DEGs function definition in KEGG database

No.	Gene ID	KEGG ID	Gene Name	Function Definition	Patten
1	RSc0093	K01251	<i>ahcY</i>	adenosylhomocysteinase	down
2	RSc0190	K01420	<i>fnr</i>	CRP/FNR family transcriptional regulator, anaerobic regulatory protein	down
3	RSc0626	K07302	<i>iorA</i>	isoquinoline 1-oxidoreductase subunit alpha	down
4	RSc1093	K08195	<i>pcaK</i>	4-hydroxybenzoate transporter branched-chain amino acid	down
5	RSc1750	K01999	<i>livK</i>	transport system substrate-binding protein	down
6	RSc1825	K00450		gentisate 1,2-dioxygenase	down
7	RSc2755	K13874	<i>araB</i>	L-arabinonolactonase	down
8	RSc2756	K10538	<i>araH</i>	L-arabinose transport system permease protein	down
9	RSc2980	K17247	<i>msrQ</i>	methionine sulfoxide reductase heme-binding subunit	down
10	RSc2981	K07147	<i>msrP</i>	methionine sulfoxide reductase catalytic subunit	down
11	RSc2983	K03088	<i>rpoE</i>	RNA polymerase sigma-70 factor, ECF subfamily	down
12	RSc3128	K00138	<i>aldB</i>	aldehyde dehydrogenase	down
13	RSc3301	K13821	<i>putA</i>	RHH-type transcriptional regulator, proline utilization regulon repressor	down
14	RSp0106	K02020	<i>modA</i>	molybdate transport system substrate-binding protein	down
15	RSp0319	K01534	<i>zntA</i>	Cd-exporting ATPase	down
16	RSp0377	K02417	<i>fliNY</i>	flagellar motor switch protein FliN/FliY	down
17	RSp0479	K02028		polar amino acid transport system ATP-binding protein	down
18	RSp0483	K01750	<i>ocd</i>	ornithine cyclodeaminase	down
19	RSp0485	K01091	<i>gph</i>	phosphoglycolate phosphatase	down
20	RSp0649	K00020	<i>mmsB</i>	3-hydroxyisobutyrate dehydrogenase	down
21	RSp0650	K00140	<i>mmsA</i>	methylmalonate-semialdehyde dehydrogenase	down
22	RSp0696	K04127	<i>cefD</i>	isopenicillin-N epimerase	down
23	RSp0829	K01706	<i>gudD</i>	glucarate dehydratase	down

24	RSp0836	K03462		nicotinamide phosphoribosyltransferase	down
25	RSp0937	K02160		acetyl-CoA carboxylase biotin carboxyl carrier protein	down
26	RSp0995	K11103	<i>dctA</i>	aerobic C4-dicarboxylate transport protein	down
27	RSp1003	K19667	<i>xpsR</i>	transcriptional activator of eps genes	down
28	RSp1016	K02472	<i>epsD</i>	UDP-N-acetyl-D-mannosaminuro nic acid dehydrogenase	down
29	RSp1366	K03734	<i>apbE</i>	FMN transferase	down
30	RSp1373	K19342	<i>NosL</i>	copper chaperone	down
31	RSp1401	K03414	<i>cheZ</i>	chemotaxis protein	down
32	RSp1633	K10543	<i>xylF</i>	D-xylose transport system substrate-binding protein	down
33	RSc0199	K12262	<i>cybB</i>	cytochrome b561	up
34	RSc0374	K03089	<i>rpoH</i>	RNA polymerase sigma-32 factor	up
35	RSc0570	K05786	<i>rarD</i>	chloramphenicol-sensitive protein	up
36	RSc0583	K03753	<i>mobB</i>	molybdopterin-guanine dinucleotide biosynthesis protein	up
37	RSc0722	K08084	<i>fimT</i>	type IV fimbrial biogenesis protein	up
38	RSc0980	K07240	<i>chrA</i>	chromate transporter	up
39	RSc1025	K04755	<i>fdx</i>	ferredoxin, 2Fe-2S	up
40	RSc1057	K03598	<i>rseB</i>	sigma-E factor negative regulatory protein	up
41	RSc1241	K17213	<i>IbpA</i>	inositol transport system substrate-binding protein	up
42	RSc1963	K03832	<i>tonB</i>	periplasmic protein TonB	up
43	RSc2506	K00567	<i>ogt</i>	methylated-DNA-[protein]-cystei ne S-methyltransferase	up
44	RSc2528	K03561	<i>exbB</i>	biopolymer transport protein	up
45	RSc2680	K02655	<i>pilE</i>	type IV pilus assembly protein PilE	up
46	RSc2780	K03181	<i>ubiC</i>	chorismate--pyruvate lyase	up
47	RSp0002	K03704	<i>cspA</i>	cold shock protein	up
48	RSp0379	K02415	<i>fliL</i>	flagellar Flil protein	up
49	Rsp1151	K01821		4-oxalocrotonate tautomerase	up
50	RSp1464	K02003		putative ABC transport system ATP-binding protein	up
51	RSp1552	K04771	<i>degP</i>	serine protease Do	up

Table S5. DEGs in KEGG BRITE database annotation

No.	KOID	Function Orthology	GeneNo.
1	ko01000	Enzymes	23
2	ko02000	Transporters	13
3	ko02035	Bacterial motility proteins	4
4	ko03000	Transcription factors	4
5	ko03021	Transcription machinery	3
6	ko02044	Secretion system	3
7	ko03400	DNA repair and recombination proteins	1
8	ko04147	Exosome	1
9	ko03110	Chaperones and folding catalysts	1
10	ko01002	Peptidases	1
11	ko01009	Protein phosphatases	1

Table S6. DEGs in virulence genes of *R. solanacearum*.

No.	Gene ID	Gene name	Pattern	Pathogenesis
1	RSp1016	<i>EpsD</i>	down	EPS synthesized key genes
2	RSp1003	<i>xpsR</i>	down	Transcription regulator protein
3	RSp0140	<i>HrpB2</i>	down	Type III effector
4	RSp0838	<i>SpaO</i>	down	Type III effector
5	RSp0837	<i>EscR</i>	down	Type III effector
6	RSp1002	<i>tek</i>	down	EPS transmembrane transport
7	RSc2755		down	EPS synthesis-related genes
8	RSp1004		down	EPS synthesis-related genes
9	RSc2680	<i>pilE2</i>	up	type-4 fimbrial biogenesis transmembrane protein
10	RSc0719	<i>PilX</i>	up	type-4 fimbrial biogenesis pilx-related signal peptide
11	RSc0722	<i>FimT</i>	up	type-4 fimbrial pilin related transmembrane protein
12	RSc0723	<i>PilE</i>	up	type-4 fimbrial pilin-related transmembrane protein