

Supplementary Table S1 Primer sequences used in this work

No.	Primer name	Sequence 5'—3'	Function
1	<i>AtUBP22 F</i>	ACAACATATGACCCGTTTATCGA	Endogenous control
2	<i>AtUBP22 R</i>	TGTTTAGGCGGAACGGATACT	
3	<i>AtSUS1 F</i>	GCGCGTCCACAGCCAACGTG	Sucrose synthase
4	<i>AtSUS1 R</i>	ACCAGGCCTTGGCCTCACAGC	
5	<i>AtSUS2 F</i>	AGGGTGTACCAAATCTCAT	Sucrose synthase
6	<i>AtSUS2 R</i>	CATAGTGAAAGCTGTGTGG	
7	<i>AtSUS3 F</i>	GAGCACGGGCTCTCGGGTTT	Sucrose synthase
8	<i>AtSUS3 R</i>	GCCGAGTCTCACGACGCTCC	
9	<i>AtSUS4 F</i>	CACACTTCCCGGGTTGTACCGT	Sucrose synthase
10	<i>AtSUS4 R</i>	GCGCAAGCGAGTGTTCTTACCG	
11	<i>AtSUS5 F</i>	GTCCTCGAAGCTCGGAGGGC	Sucrose synthase
12	<i>AtSUS5 R</i>	CTCCCTGCGCTTTCTCCCA	
13	<i>AtSUS6 F</i>	CGCCTTGATTGCAAGCCAGACC	Sucrose synthase
14	<i>AtSUS6 R</i>	TGGCCTGTCCTTGCTTCTGC	
15	<i>AtCINV1 F</i>	TCGAGGGCCATGAGTGGCGC	Cytosolic invertase
16	<i>AtCINV1 R</i>	CGCGCTCTTGCGATCTGCG	
17	<i>AtCINV2 F</i>	CGGTGGATCTTGCCAGTATTGC	Cytosolic invertase
18	<i>AtCINV2 R</i>	CCAGCAATCTCGGTGTAGCCGT	
19	<i>AtEIN3 F</i>	CATTCTCCAGTTACAATGAT	Transcription factor of AtERF1
20	<i>AtEIN3 R</i>	AGCTTGTTGAACAGGAC	
21	<i>AtERF1 F</i>	CGGCGGAGAGAGTTCAAGAGTC	Activator of AtPDF1.2
22	<i>AtERF1 R</i>	TCCCACTATTTTCAGAAGACCCC	
23	<i>AtPDF1.2 F</i>	CTGCTTTCGACGCACCGGCAA	Plant defense marker gene for JA/ET pathway
24	<i>AtPDF1.2 R</i>	ACCCCTGACCATGTCCCACTTGG	
25	<i>AtOXI1 F</i>	TCATCTACATTGGCCGTGTC	Protein kinase required for activation of AtMPK6
26	<i>AtOXI1 R</i>	CGTCGCTCCATACAACATCT	
27	<i>AtACS6 F</i>	CCGGGAATGTTTGAAGTCTCTTG	Substrate for AtMPK6
28	<i>AtACS6 R</i>	CGGTCTTAAGTCTGTGCACGG	
29	<i>AtPR3 F</i>	ATCACCGCTGCAAAGTCCTTC	Pathogenesis related gene (chitinase)
30	<i>AtPR3 R</i>	TGCTGTAGCCCATCCACCTG	
31	<i>AtBI1 F</i>	GCAGCAGCAATGTTAGCAAG	Attenuator of cell death
32	<i>AtBI1 R</i>	CACCACCATGTATCCACAA	
33	<i>SiTEF F</i>	ATCGTCGCTGTCAACAAGAT	Elongation factor 1 alpha
34	<i>SiTEF R</i>	ACCGTCTGGGGTTGTATCC	

Supplementary Table S2 Relative gene expression (ddCt) of *AtSUS* and *AtCINV* genes in systemic roots of *S. indica*-colonized *A. thaliana* plants in comparison to non-colonized controls ($n=3$; $\pm$ SE)

genes	Systemic roots of <i>S. indica</i> -colonized plants		
	3 dai	7 dai	14 dai
<i>AtSUS1</i>	-0.12 (± 0.13)	0.80 (± 0.31)	-0.21 (± 0.36)
<i>AtSUS2</i>	-0.09 (± 0.33)	-0.51 (± 0.31)	-0.26 (± 0.24)
<i>AtSUS3</i>	0.16 (± 0.55)	-0.19 (± 0.09)	-0.31 (± 0.33)
<i>AtSUS4</i>	-0.11 (± 0.41)	0.49 (± 0.25)	1.19 (± 0.43)
<i>AtSUS5</i>	0.38 (± 0.54)	-0.08 (± 0.26)	-0.53 (± 0.13)
<i>AtSUS6</i>	-0.14 (± 0.39)	0.00 (± 0.17)	-0.62 (± 0.33)
<i>AtCINV1</i>	0.00 (± 0.34)	0.27 (± 0.21)	-0.33 (± 0.30)
<i>AtCINV2</i>	0.10 (± 0.37)	0.59 (± 0.35)	-0.60 (± 0.24)