



Figure S1. Drawing scheme of tomato leaflets collected for counting bacterial population and for RNA extractions in this study.

Table S1. List of specific primer pairs used in this study.

Gene	Plant signaling pathway	Forward (5'-3') / Reverse (5'-3')	Slope	Efficiency (%)	Accession Number	Reference
<i>ICS1</i> (Isochorismate synthase)	Shikimate pathway for SA synthesis	GTTCCTCTCCAAGAAATGTCC TCCTTCAAGCTCATCAAAC	-3.32	100.12	XM_019214148	[45]
<i>PAL5</i> (Phenylalanine ammonia lyase)	Phenylpropanoid pathway for SA biosynthesis	ACGGGTTGCCATCTAATCTG TGGCTGAAATTAAAGCCCAAG	-2.92	119.97	M83314	This study
<i>PR1b1</i> (Pathogenesis-related (PR))	Salicylic acid (SA) response	GCACTAACCTAAAGAAAAATGGG AAGTTGGCATCCCAAGACATA	-3.17	106.94	Y08804	[37, 73]
<i>TomLoxC</i> (Lipoxygenase)	Jasmonic acid biosynthesis	TCCGGCAACACC GTTTACTC GTCAATGCCGGAAAATGTG	-3.44	95.28	U37839	[37]
<i>MYC2</i> (Transcription factor MYC2)	Jasmonates response	CTGAAAAGAAGCCGAGGAAGC GCATCTCCAAGAAGTGATGCC	-3.29	101.19	NM_001301178	[5]
<i>PINII</i> (Wound-induced)	Jasmonates response	GGCCAATGCTTGCACCTT	-3.21	104.69	K03291	[37, 73]

proteinase inhibitor)		CGTGGTACATCCGGTGGGATA					
<i>ERF-A2 (ERFI)</i> (Ethylene response factor)	Ethylene response	AAGTGGCTCGCCTAAGAGGA TAACATTGGTCCCCGGCTC	-3.21	105.09	NM_001329459	[74]	
<i>AREB2</i> (ABA-responsive element binding protein 2)	Abscisic acid (ABA) response	GGTATCCCTGATCCAGCACTC CACATAAGGAACTGGAGATACAG	-3.63	88.40	XM_026030430	[46]	
<i>LERBOH1</i> (NADPH oxidase)	Reactive oxygen species (ROS) biosynthesis	GTCAGGCTTCTACAGAAAAC GTTGATTACAGTAGGCCGGTTC	-3.12	109.08	AF088276	[75]	
Actin-7-like	---	CACCACTGCTGAACGGGAA GGAGCTGCTCCTGGCAGTT	-3.30	101.06	NM_001321306	[37, 73]	

Table S2. Effect of *Pst* and *Trichoderma* treatments on gene expression.

Gene	Treatment	Control		DC3000		DC3118		P x T***
		Control	0.83	a* C**	18.93	a A	3.00	
<i>ICS1</i>	Control	0.74	a C	5.76	b A	1.34	b B	<i>P < 0.05</i>
	T6	1.00	a C	15.92	a A	2.42	a B	
	T25	0.79	a C	6.60	b A	2.71	a B	
	T34							
<i>PAL5</i>	Control	1.77	ab C	56.09	a A	8.46	bc B	<i>P < 0.05</i>
	T6	0.69	b C	37.84	a A	4.25	c B	
	T25	2.90	a B	27.98	a A	16.50	ab A	
	T34	2.64	a B	36.46	a A	32.39	a A	
<i>PR1b1</i>	Control	0.80	a B	3.47	b A	3.35	a A	<i>P < 0.05</i>
	T6	1.17	a C	16.78	a A	3.87	a B	
	T25	1.23	a B	2.21	b B	4.77	a A	
	T34	0.75	a B	4.91	b A	2.87	a AB	
<i>TomLoxC</i>	Control	0.73	a A	0.73	ab A	0.44	a A	<i>P < 0.05</i>
	T6	0.28	b B	0.70	b A	0.15	b B	
	T25	1.06	a A	0.93	ab A	0.72	a A	
	T34	1.31	a A	1.34	a A	0.63	a B	
<i>MYC2</i>	Control	0.90	a B	6.23	a A	0.91	a B	<i>P < 0.05</i>
	T6	0.88	a B	1.68	c A	0.51	b C	
	T25	0.98	a B	1.96	bc A	0.47	b C	
	T34	0.97	a B	2.84	b A	0.98	a B	
<i>PINII</i>	Control	0.86	a C	190.73	a A	3.40	a B	<i>P < 0.05</i>
	T6	0.75	a B	44.80	b A	0.74	b B	
	T25	0.58	a C	169.08	a A	1.80	a B	
	T34	1.13	a B	96.54	ab A	2.19	a B	
<i>ERF-A2</i>	Control	0.90	b B	5.45	b A	3.28	b A	<i>P < 0.05</i>
	T6	2.30	a B	14.50	a A	3.40	b B	
	T25	2.46	a B	5.51	b A	3.24	b B	

	T34	1.90	a C	21.73	a A	6.18	a B	
<i>AREB2</i>	Control	0.94	a B	4.03	a A	0.76	a B	<i>P < 0.05</i>
	T6	0.33	b B	2.17	b A	0.58	a B	
	T25	0.39	b B	1.90	bc A	0.49	a B	
	T34	0.36	b B	1.65	c A	0.65	a B	
<i>LERBOH1</i>	Control	0.92	a B	1.88	a A	1.00	a B	<i>P > 0.05</i>
	T6	1.24	a B	3.62	a A	0.78	a B	
	T25	0.96	a B	4.91	a A	1.16	a B	
	T34	0.64	a B	2.95	a A	0.76	a B	

Data analysis was performed for each individual gene. *Different lowercase letters, for comparisons among columns (showing the effect among *Trichoderma* strains (T6 = *T. parareesei*, T25 = *T. asperellum*, and T34 = *T. harzianum*) for each *Pst* strain and control plants), indicate that the mean values are significantly different under Tukey's test ($p < 0.05$). **Different uppercase letters, for comparisons among rows (showing the effect of each *Trichoderma* treatment against both *Pst* strains and control plants), indicate that the mean values are significantly different under Tukey's test ($p < 0.05$). The data represents the average of four replicates as the relative quantity (RQ, $2^{\Delta\Delta Ct}$) of target genes compared to those of their basal condition (control plants untreated neither with *Trichoderma* nor with *Pst*). The expression values of each gene were normalized to the quantity of actin gene used as the endogenous gene. For statistical analysis, the data were transformed into log (x). ***Two-way analysis of variance (ANOVA) for interaction between factors (P = *Pst* and T = *Trichoderma* strains) (Tukey's test, $p < 0.05$).