

Table S2. sX13-regulated genes identified by microarray and qRT-PCR analysis.

Locus ^a	Annotated gene product ^b	4G-motif ^c	Microarray Fold-change (Δ sX13 / wt) ^d		qRT-PCR Fold-change (Δ sX13 / wt) ^e	
			NYG	MMA	NYG	MMA
Upregulated genes (ΔsX13 / wt)						
XCV0678	AlgR; two-component system regulatory protein	a,a,a	1.8	—	2.5 ± 0.23	n.t.
XCV0730	Prc; tail-specific protease	—	—	1.6	n.t.	n.t.
XCV0950	conserved hypothetical protein	a,a	1.6	—	n.t.	n.t.
XCV1274	putative secreted protein	a	—	2.7	n.t.	n.t.
XCV1528	putative secreted protein	—	—	1.8	n.t.	n.t.
XCV1626	peptidyl-prolyl cis-trans isomerase	—	—	1.6	n.t.	n.t.
XCV1768	Hfq; host factor-I protein	b	1.6	—	2.4 ± 0.08	1.6 ± 0.31
XCV2041	putative signal transduction protein	a	—	1.9	n.t.	n.t.
XCV2185	conserved hypothetical protein	—	3.7	—	n.t.	n.t.
XCV2186	methyl-accepting chemotaxis protein	a	7.7	—	2.1 ± 0.34	10.2 ± 4.63
XCV2302	conserved hypothetical protein	—	1.5	1.6	n.t.	n.t.
XCV2341	conserved hypothetical protein	—	—	1.5	n.t.	n.t.
XCV2357	conserved hypothetical protein	—	1.7	—	n.t.	n.t.
XCV2499	putative membrane protein	a,b	2.0	—	n.t.	n.t.
XCV2565	conserved hypothetical protein	b	—	1.6	n.t.	n.t.
XCV2608	type IV secretion system VirJ-like protein	b	1.7	2.5	n.t.	n.t.
XCV2814	PilE; type IV pilus pilin	—	2.8	—	3.3 ± 0.36	n.t.
XCV2815	type IV pilus adhesin	b	2.1	—	n.t.	n.t.
XCV2819	type IV pilus assembly protein PilW	a	3.7	4.0	3.4 ± 0.37	5.5 ± 3.0
XCV2820	type IV pilus assembly protein PilV	a	2.9	—	n.t.	n.t.
XCV2821	type IV pilus assembly protein FimT	a	4.3	7.4	4.2 ± 0.32	3.4 ± 1.27
XCV2917	hypothetical protein	—	2.9	—	n.t.	n.t.
XCV3059	putative secreted protein	b	—	2.1	n.t.	n.t.
XCV3067	PilU; type IV pilus assembly protein ATPase	a	1.8	—	1.7 ± 0.29	n.t.
XCV3096	ComEA-related DNA uptake protein	—	—	4.2	n.t.	1.9 ± 0.12
XCV3151	hypothetical protein	b,b	—	1.6	n.t.	n.t.
XCV3230	PilJ; type IV pilus methyl-accepting chemotaxis protein	a	2.2	—	n.t.	n.t.
XCV3233	PilG; type IV pilus response regulator	a,b	—	2.0	2.3 ± 0.26	4.1 ± 1.71
XCV3353	PilA; type IV pilus assembly protein, major pilin	a	—	2.9	n.t.	n.t.
XCV3371	conserved hypothetical protein	a,b	—	1.8	n.t.	n.t.
XCV3376	hypothetical protein	—	2.0	—	n.t.	n.t.
XCV3497	PilQ; type IV pilus assembly protein	a,b	—	1.6	n.t.	n.t.
XCV3498	PilP; type IV pilus assembly protein	—	2.5	—	n.t.	n.t.
XCV3499	PilO; type IV pilus assembly protein	a	2.4	—	n.t.	n.t.
XCV3500	PilN; type IV pilus assembly protein	—	2.7	—	2.7 ± 0.16	n.t.
XCV3629	putative amidohydrolase family protein	a	1.9	—	n.t.	n.t.
XCV3727	conserved hypothetical protein	a	—	2.3	n.t.	n.t.
XCV3730	type IV pilus assembly protein	a,a	2.0	—	n.t.	n.t.
XCV3927	putative secreted protein	a	—	1.7	5.6 ± 0.45	8.3 ± 4.54
XCV4099	conserved hypothetical protein	b	—	1.7	n.t.	n.t.
XCV4117	conserved hypothetical protein	b	—	1.5	n.t.	n.t.
XCV4382	putative acetyltransferase	—	—	1.5	n.t.	n.t.
Downregulated genes (ΔsX13 / wt)						
XCV0227	hypothetical protein	—	0.4	—	n.t.	n.t.
XCV0588	putative secreted protein; Ycel-like family	—	0.5	—	n.t.	n.t.
XCV1188	conserved hypothetical protein	—	0.5	—	n.t.	n.t.
XCV1315	HrpX; AraC-type transcriptional regulator	—	0.6	—	0.6 ± 0.01	0.7 ± 0.13
XCV1787	predicted ATPase related to phosphate starvation-inducible protein PhoH	—	0.6	—	n.t.	n.t.
XCV1945	methyl-accepting chemotaxis protein	—	0.5	—	n.t.	n.t.
XCV1956	CheA1; chemotaxis protein	—	0.6	—	n.t.	n.t.
XCV1957	CheY; chemotaxis response regulator	—	0.4	—	0.1 ± 0.04	n.t.
XCV1958	putative anti-sigma factor antagonist	—	0.4	—	n.t.	n.t.
XCV2021	FliD; flagellar capping protein	—	0.7	—	n.t.	n.t.
XCV2022	FliC; flagellin and related hook-associated proteins	—	0.2	—	0.06 ± 0.03	1.0 ± 0.39
XCV2037	conserved hypothetical protein	—	0.3	—	n.t.	n.t.
XCV2276	hypothetical protein	b	0.6	—	n.t.	n.t.
XCV2282	conserved hypothetical protein	—	0.6	—	n.t.	n.t.
XCV2535	CydA; cytochrome D ubiquinol oxidase, subunit II	a	0.3	—	n.t.	n.t.
XCV2537	putative membrane protein	—	0.1	—	n.t.	n.t.
XCV3119	sigma-54 modulation protein	—	0.6	—	n.t.	n.t.
XCV3206	TonB-dependent outer membrane receptor	—	0.4	—	n.t.	n.t.
XCV3572	TonB-dependent outer membrane receptor	a	0.2	—	0.2 ± 0.04	0.9 ± 0.24
XCV4119	putative secreted protein	—	0.2	—	n.t.	n.t.
XCVd0093	putative secreted protein	—	0.5	—	n.t.	n.t.

Locus ^a	Annotated gene product ^b	4G-motif ^c	Microarray Fold-change ($\Delta sX13$ / wt) ^d		qRT-PCR Fold-change ($\Delta sX13$ / wt) ^e	
			NYG	MMA	NYG	MMA
Additional genes tested by qRT-PCR						
XCV0173	putative secreted protein	a,b,b,b	—	—	1.9 ± 0.19	0.8 ± 0.26
XCV0612	ATPase of the AAA+ class	a	—	—	1.0 ± 0.06	0.8 ± 0.26
XCV1533	AsnB2; asparagine synthase	b	—	—	1.0 ± 0.04	1.0 ± 0.17
XCV3232	PilH; type IV pilus response regulator	a	—	—	2.2 ± 0.07	1.9 ± 0.67
XCV3573	putative transcriptional regulator, AraC family	a	—	—	0.2 ± 0.11	n.t.
XCV0324	type III effector protein XopS	—	—	—	0.6 ± 0.05	n.t.

^a, bold letters indicate genes with known TSS [1]. ^b, refers to Thieme *et al.* (2005) [2]. ^c, presence of a 4G-motif within the 5'-UTR or 100 bp upstream of translation start codon if TSS is unknown (a) and within 100 bp downstream of the start codon (b) (see Figure S4). ^d, genes not detected as expressed are marked with —. ^e, values represent mean fold-change and standard deviation (see Figure 4); n.t. - not tested.

References

- Schmidtke C, Findeiss S, Sharma CM, Kuhfuss J, Hoffmann S, et al. (2012) Genome-wide transcriptome analysis of the plant pathogen *Xanthomonas* identifies sRNAs with putative virulence functions. *Nucleic Acids Res* 40: 2020-2031.
- Thieme F, Koebnik R, Bekel T, Berger C, Boch J, et al. (2005) Insights into genome plasticity and pathogenicity of the plant pathogenic bacterium *Xanthomonas campestris* pv. *vesicatoria* revealed by the complete genome sequence. *J Bacteriol* 187: 7254-7266.