

Expression of *kdgR* in intact tomatoes and soft rots

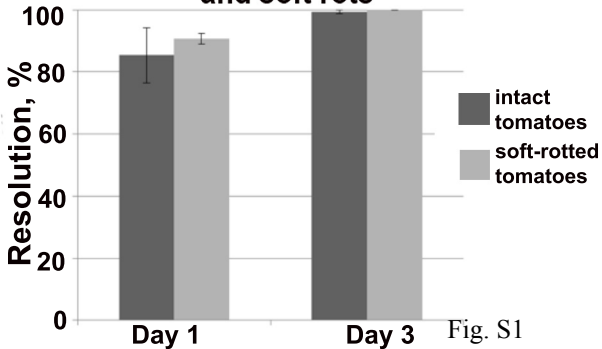


Fig. S1. Regulation of the *kdgR* RIVET reporter in intact and soft rotted tomatoes.

A *kdgR::tnpR-lacZY* reporter in *S. enterica* sv Typhimurium 14028 was inoculated into tomatoes with or without *Pectobacterium carotovorum* SR38. Following 1 or 3 days of incubation, samples were plated and scored for the loss of the tetracycline marker. Error bars were standard errors

Color key and histogram

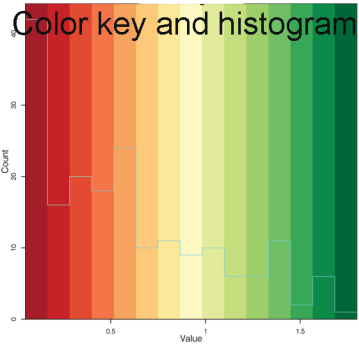
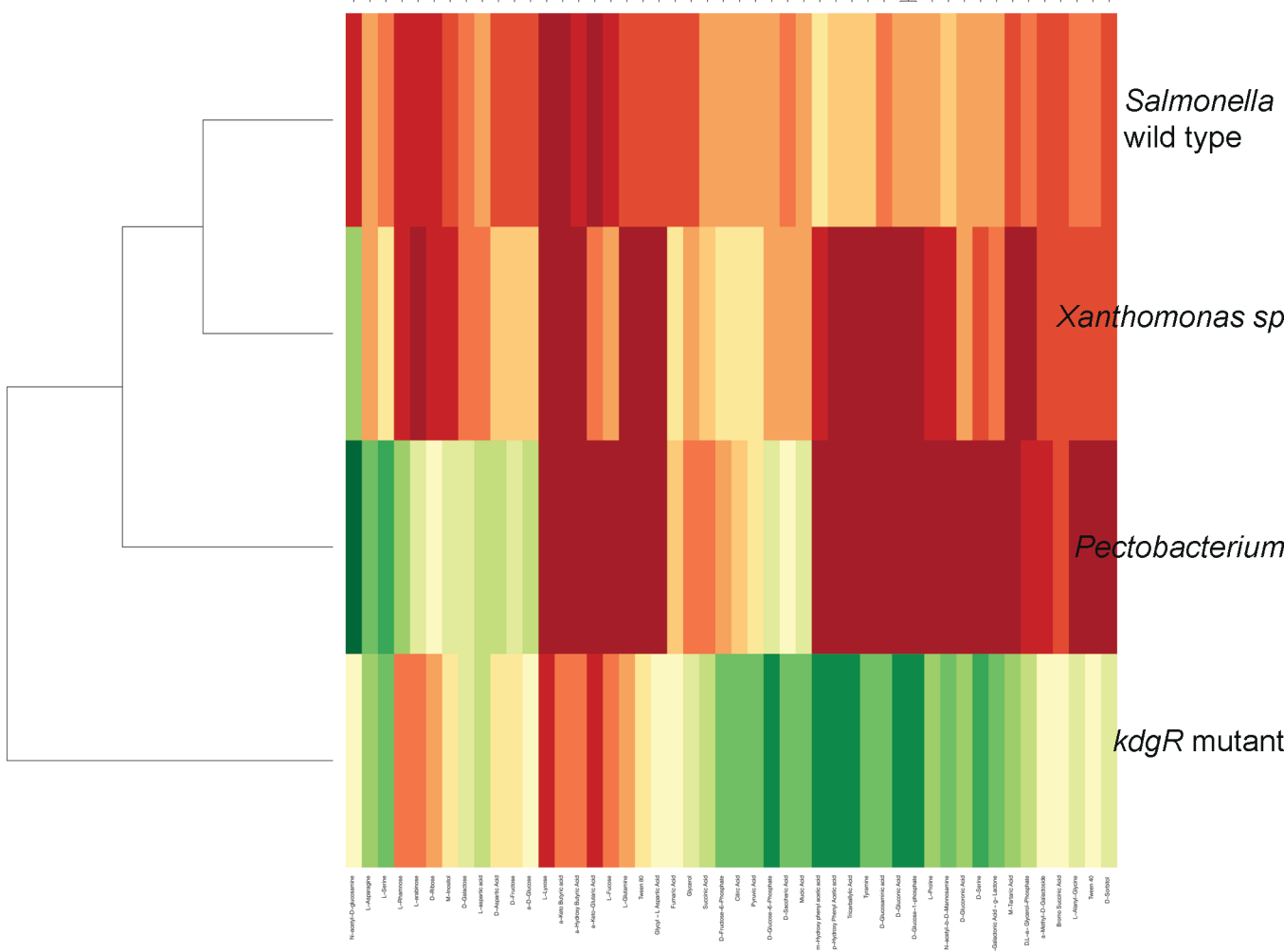
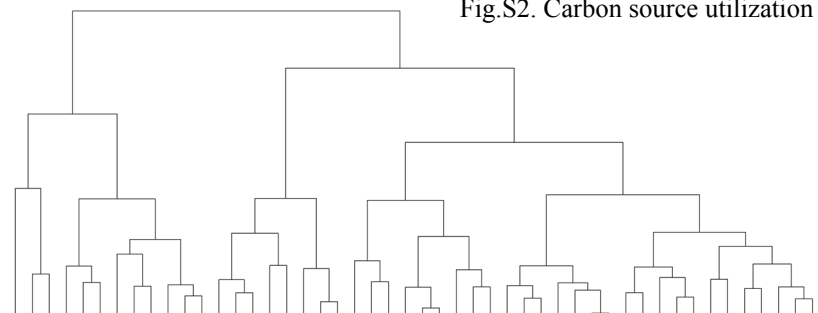


Fig.S2. Carbon source utilization



Supplemental Figure 2. Utilization of carbon sources in BIOLOG PM1 and PM2 by *S. enterica* sv Typhimurium 14028, *S. enterica* sv Typhimurium AG1 (*kdgR::frit*), *P. carotovorum* SR38 and *Xanthomonas sp.* Carbon sources that were not utilized by any of the strains are not shown. Heat maps indicate intensity of the respiration on a given carbon source (dark red – no utilization, dark green – strong respiration), color key is shown in the top left corner. The heat map was constructed using `heatmap.2` from the R package *gplots*. The dendrogram imposed over the rows and columns was constructed with a complete linkage hierarchical clustering using the Euclidean distance between the mean absorbance values.

Table S1. Primers used in this study.

Primer Name	Sequence	Description
JTN177	TCGTAGCTGCTTTTTTTTAAACGTCATGCTAATAACGTTGCTGTAGGCTGGAGCTGCTTCG	<i>kdgR</i> deletion forward primer
JTN178	TCGTTCTGAATTTTATAAAACGCTCGTAATGAGGTGATAACATATGAATATCCTCCTTAG	<i>kdgR</i> deletion reverse primer
JTN179	TTTCCGACTGTCCCAITTTTCAGAA	<i>kdgR</i> verification forward primer
JTN180	GCGACCTGGCGTGAAATTATAATA	<i>kdgR</i> verification reverse primer
JTN163	CGCACACTAACGCTAAITTTTTACAGATCAGGTTCCAGACTTGTAGGCTGGAGCTGCTTCG	<i>kdgK</i> deletion forward primer
JTN164	GGCCCGGTAAGCGCAGCGCCACCGGCAAGAGCGAATGACCATATGAATATCCTCCTTAG	<i>kdgK</i> deletion reverse primer
JTN165	CGTAGCTGCTGGATAACCTGCTTT	<i>kdgK</i> verification forward primer
JTN166	CAAGCGGACCGGAATTTAATATG	<i>kdgK</i> verification reverse primer
JTN167	AAGCGTCGATTTTCCAGAAAACGCAATTTGTGTCAGTAGCGGATGTAGGCTGGAGCTGCTTCG	<i>kduID</i> deletion forward primer
JTN168	ATTTTGTGCCATTGCGATCGATTTATCATTGGAGGAAAACATATGAATATCCTCCTTAG	<i>kduID</i> deletion reverse primer
JTN169	TTTATCAGTTTTTTTCGGCCAAAGC	<i>kduID</i> verification forward primer
JTN170	TCAAITTCGCACATCAGACCTCGTT	<i>kduID</i> verification reverse primer
AG7	TTTAAATACAAAAATAAAGTTAATTGATGAGCGGAGTATTTTATGTgtaggctggagctgcttcg	<i>kdgM</i> deletion forward primer
AG8	TATGAATACTAAGCAAAGATTAGTACAGTAACTCTTTAACTTTCCATATGAATATCCTCCTTAG	<i>kdgM</i> deletion reverse primer
AG33	GCGTTGTTGATGGTGTGTTTTG	<i>kdgM</i> verification forward primer
AG34	CGCAGGTCATCACCAAGTAA	<i>kdgM</i> verification reverse primer
AG64	GTTTGTGATCTTAATTTGATTGAATATAATCGTTATGATTTTATTTCAATTgtaggctggagctgcttcg	<i>kdgT</i> deletion forward primer
AG65	GTATCATTGATCCGGTAAAATCATCGGCGATAACTATCAITTCATATGAATATCCTCCTTAG	<i>kdgT</i> deletion reverse primer
AG66	AACGAAGTCGCCAAACATTC	<i>kdgT</i> verification forward primer
AG67	GGCAAATTCGGTTTCCAGTA	<i>kdgT</i> verification reverse primer
AG92	CAGTTTTTCATCGGAATCTTCTCTCGCCTGATTACTAGTGTGTCATCTgtaggctggagctgcttcg	<i>eda</i> deletion forward primer
AG93	CCTGAAACGATTTTGCCCAATTATCACCGGACATCATGTATTTCACTGCATATGAATATCCTTAG	<i>eda</i> deletion reverse primer
AG94	CATCGGAATCTTCTCTCGC	<i>eda</i> verification forward primer
AG95	GGTCGTTCTGTGGAATGAGTT	<i>eda</i> verification reverse primer
AG72	ATTGAGCTGTCGCAGAAAGG	<i>kdgK</i> qPCR forward primer
AG73	CCTGACGGGCAATATAAACG	<i>kdgK</i> qPCR reverse primer
AG74	CGGTGAGTCCATACTGAGC	<i>kduID</i> qPCR forward primer
AG75	CGTCACCTTAGGCGATAACC	<i>kduID</i> qPCR reverse primer
AG76	TCTGGCGGAAAGGGTTAGC	<i>araH</i> qPCR forward primer
AG77	TCCGGAAGGTGTCTATGTGG	<i>araH</i> qPCR reverse primer
AG78	CTGCGGGAATTGAAAGACC	<i>fruF</i> qPCR forward primer
AG79	CAAACCTCGACCTTTCTTGG	<i>fruF</i> qPCR reverse primer
AG82	GCCTGGAAGTGGTTAATGTCC	<i>edd</i> qPCR forward primer
AG83	TCAACTGGGATGACTTCTCG	<i>edd</i> qPCR reverse primer
AG84	CCATAGTCCATGCCAACAT	<i>eda</i> qPCR forward primer
AG85	GACTGACTGAGCCACTGCTG	<i>eda</i> qPCR reverse primer
AG88	CGAATAATATCGCAAGATCG	<i>iroN</i> qPCR forward primer
AG89	CGCCGAGCAAGTATTAAGC	<i>iroN</i> qPCR reverse primer
AG90	GGAAAACCTGCCTGAGTTTG	<i>soda</i> qPCR forward primer
AG91	GACTGACTGAGCCACTGCTG	<i>soda</i> qPCR reverse primer

Table S2. *Salmonella* genomes used in the bioinformatics analysis to define consensus KdgR binding sites

Strain	Type	RefSeq ID	Total genes	Length (mb)
Agona SL483	Chromosome	NC_011149.1	4881	4.8
	Plsm unnamed	NC_011148.1	53	0.037978
Arizonae 62:z4,z23	Chromosome	NC_010067.1	4671	4.6
Choleraesuis SC-B67	Chromosome	NC_006905.1	4641	4.76
	pSC138	NC_006856.1	170	0.138742
	pSCV50	NC_006855.1	51	0.049558
Dublin CT_02021853	Chromosome	NC_011205.1	4952	4.84
	PCT02021853_74	NC_011204.1	122	0.074551
Enteritidis P125109	Chromosome	NC_011294.1	4420	4.69
Gallinarum 287/91	Chromosome	NC_011274.1	4371	4.66
Gallinarum/pullorum RKS5078	Chromosome	NC_016831.1	4682	4.64
Heidelberg B182	Chromosome	NC_017623.1	4580	4.75
	pB182_37	NC_017624.1	44	0.037581
Heidelberg SL476	Chromosome	NC_011083.1	4904	4.89
	pSL476_3	NC_011082.1	4	0.003373
	pSL476_91	NC_011081.1	131	0.091374
Newport SL254	Chromosome	NC_011080.1	4809	4.83
	pSL254_3	NC_011079.1	5	0.003605
	pSN254	NC_009140.1	198	0.176473
Paratyphi A AKU_12601	Chromosome	NC_011147.1	4404	4.58
Paratyphi A ATCC 9150	Chromosome	NC_006511.1	4402	4.59
Paratyphi B SPB7	Chromosome	NC_010102.1	5771	4.86
Paratyphi C RKS4594	Chromosome	NC_012125.1	4827	4.83
	pSPCV	NC_012124.1	65	0.055414
Schwarzengrund CVM19633	Chromosome	NC_011094.1	4743	4.71
	pCVM19633_110	NC_011092.1	129	0.110227
	pCVM19633_4	NC_011093.1	5	0.004585
Typhi CT18	Chromosome	NC_003198.1	4455	4.81
	pHCM1	NC_003384.1	246	0.21816
	pHCM2	NC_003385.1	129	0.106516
Typhi P-stx-12	Chromosome	NC_016832.1	4885	4.77
	Plsm unnamed	NC_016825.1	236	0.181431
Typhi Ty2	Chromosome	NC_004631.1	4678	4.79
Typhi Ty21a	Chromosome	NC_021176.1	4601	4.79
Typhimurium 14028S	Chromosome	NC_016856.1	5516	4.87
	Plsm unnamed	NC_016855.1	103	0.093832
Typhimurium 798	Chromosome	NC_017046.1	4471	4.88

	p798_93	NC_017054.1	104	0.093877
Typhimurium D23580	Chromosome	NC_016854.1	4556	4.88
Typhimurium LT2	Chromosome	NC_003197.1	4631	4.86
	pSLT	NC_003277.1	112	0.093939
Typhimurium SL1344	Chromosome	NC_016810.1	4622	4.88
	pRSF1010_SL1344	NC_017719.1	12	0.008688
	pSLT_SL1344	NC_017720.1	102	0.093842
	pCol1B9_SL1344	NC_017718.1	101	0.086908
Typhimurium ST4/74	Chromosome	NC_016857.1	4775	4.88
	TY474p1	NC_016858.1	116	0.093842
	TY474p2	NC_017675.1	90	0.086908
	TY474p3	NC_016859.1	11	0.008688
Typhimurium T000240	Chromosome	NC_016860.1	4823	4.95
	pSTMDT12_S	NC_016862.1	10	0.00867
	pSTMDT12_L	NC_016861.1	139	0.10651
Typhimurium U288	Chromosome	NC_021151.1	4682	4.85
	pSTU288-1	NC_021155.1	200	0.148711
	pSTU288-2	NC_021156.1	12	0.011067
	pSTU288-3	NC_021157.1	5	0.004675
Typhimurium UK-1	Chromosome	NC_016863.1	4582	4.82
	pSTUK-100	NC_016864.1	101	0.093277

Table S3. Predicted *Salmonella* gene targets of KdgR

	Gene, predicted function	End Position*	Start Position**	Weight Score	P-value
<i>kduI</i>	5-keto-4-deoxyuronate isomerase	-123	-103	17.9	1.20E-09
		-58	-38	10.7	1.30E-06
<i>yjgK</i>	hypothetical	-32	-12	16.4	1.10E-08
<i>ydiA</i>	(divergently transcribed from <i>pps</i>) phosphoenolpyruvate regulatory protein	-131	-111	16.3	1.20E-08
<i>pps</i>	(divergently transcribed from <i>ydiA</i>) phosphoenolpyruvate synthase	-226	-206	16.3	1.20E-08
<i>yjhH</i>	cyclic-di-GMP phosphodiesterase	-164	-144	15.7	2.30E-08
<i>kdgK</i>	ketodeoxygluconokinase	-85	-65	15.7	2.30E-08
<i>yeeO</i>	MATE-family multidrug exporter	-7	13	15.3	3.50E-08
STM1911	glycosyl (rhamnogalacturonyl) hydrolase	-189	-169	14.8	5.90E-08
STM1934	outermembrane lipoprotein	-168	-148	13.9	1.30E-07
STM1933	Ribose 5-phosphate isomerase	-108	-88	13.9	1.30E-07
<i>ftnB</i>	ferritin-like protein	-340	-320	13.9	1.30E-07
<i>araH</i>	arabinose permease	-231	-211	13.9	1.30E-07
<i>yifZ</i>	KDG permease	-34	-14	12.8	3.20E-07
<i>setB</i>	sugar efflux transporter	-108	-88	11.5	7.80E-07
<i>fruF</i>	PTS, fructose-specific IIA	-281	-261	11.5	7.80E-07
STM4509.S	hypothetical protein	-75	-55	10.8	1.20E-06
<i>thrS</i>	threonine tRNA ligase	-395	-375	10.3	1.60E-06
STM4051	hypothetical protein	-42	-22	9.8	2.20E-06
STM1043	attachment and invasion protein	72	92	9.3	2.90E-06
<i>deoB</i>	phosphopentomutase	-2	18	9.2	3.10E-06
<i>dpiB</i>	histidine sensor kinase	14	34	8.4	4.70E-06
<i>yebB</i>	uncharacterized protein	-212	-192	8.3	5.00E-06
STM0272	ATPase with chaperone activity	-215	-195	8.3	5.00E-06
STM0271	cytoplasmic protein	-173	-153	8.3	5.00E-06
<i>pdhR</i>	pyruvate dehydrogenase complex repressor	-162	-142	8.2	5.30E-06
STM4216	putative innermembrane protein	-2	18	8.1	5.50E-06
<i>clpA</i>	ATP-dependent protease	13	33	7.6	7.10E-06
<i>ddl</i>	D-alanine-D-alanine ligase	5	25	7.5	7.50E-06
<i>yjcB</i>	hypothetical protein	-120	-100	7.4	7.90E-06
<i>pykF</i>	pyruvate kinase	-286	-266	7.4	7.90E-06
STM4510	aspartate racemase	-78	-58	7.3	8.30E-06
<i>clpP</i>	ATP-dependent protease	-157	-137	7.3	8.30E-06
STM4435	2-keto-myo-inositol isomerase	56	76	7	9.70E-06
<i>iroN</i>	iron-enterobactin outer membrane transporter			7	1.00E-05
<i>yiaK</i>	2,3-diketo-L-gulonate reductase	-82	-62	6.9	1.00E-05

<i>yiaJ</i>	IclR family regulator	-168	-148	6.9	1.00E-05
<i>yehR</i>	lipoprotein	-19	1	6.9	1.00E-05
STM4054	hypothetical protein	-126	-106	6.9	1.00E-05
<i>sodA</i>	superoxide dismutase	-223	-203	6.9	1.00E-05

* Start of the predicted KdgR binding site

** End of the predicted KdgR binding site

Table S4. Utilization* of rhamnose, fructose and pyruvate by *S. enterica* sv. Typhimurium 14028 and *S. enterica* sv. Typhimurium AG1 ($\Delta kdgR$)

		0 hrs	24 hrs	48 hrs
Rhamnose	wild type	0.04±0.02	0.28±0.02	0.24±0.01
	<i>kdgR</i>	0.04±0.0	0.40±0.0	0.53±0.0
Fructose	wild type	0.04±0.0	0.31±0.01	0.30±0.02
	<i>kdgR</i>	0.04±0.0	0.41±0.01	0.51±0.01
Pyruvate	wild type	0.04±0.02	0.26±0.03	0.16±0.02
	<i>kdgR</i>	0.04±0.0	0.22±0.06	0.29±0.08

* measured as Absorbance at 590 nm