

TABLE S1: Cell shape/cell cycle-related *E. coli* O157:H7 genes that were differentially expressed at 2 and 4 h exposure to cinnamaldehyde

Gene	Function	Fold change
		(log ₂)
		4 h
<i>alr</i>	alanine racemase 1	2.8
<i>ftsW</i>	cell division protein	2.8
<i>mrcA</i>	fused penicillin-binding protein 1a:murein transglycosylase	2.4
<i>mrda</i>	penicillin-binding protein 2	2.4
<i>mraY</i>	phospho-N-acetylmuramoyl-pentapeptide-transferase	2.5
<i>mreBCD</i> ¹	rod shape-determining protein	2.4/2.5/3.2
<i>murG</i>	undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase	2.5
<i>murE</i>	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase	2.7
<i>murF</i>	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase	2.3
<i>mukEF</i> ¹	chromosome condensin	2.0/2.0
<i>bcsQ</i>	hypothetical protein /cell division protein	2.6
<i>mraY</i>	phospho-N-acetylmuramoyl-pentapeptide transferase	2.5
<i>tig</i>	peptidyl-prolyl cis/trans isomerase (trigger factor)	2.4
<i>dicB</i>	putative inhibitor of cell division encoded by cryptic prophage CP-933P/DicB	-3.0
<i>dicF</i>	ncRNA	-2.8

¹Changes in expression for each gene of the complex or the same group are listed sequentially in respective order.

TABLE S2: *E. coli* O157:H7 genes that were highly upregulated only at 2 h exposure to cinnamaldehyde¹

Gene	Function	Fold change (log ₂)
Energy derivation and oxidation reduction		
<i>poxB</i>	pyruvate dehydrogenase	3.5
<i>cyoC</i>	cytochrome o ubiquinol oxidase subunit III	3.1
<i>nfnB</i>	dihydropteridine reductase, NAD(P)H-dependent, oxygen-insensitive	3.1
<i>acnA</i> ²	aconitate hydratase 1	3.0
<i>aceE</i> ²	pyruvate dehydrogenase, decarboxylase component E1, thiamin-binding	2.9
<i>mdaA/nfsA</i> ²	nitroreductase A, NADPH-dependent, FMN-dependent	2.9
<i>talA</i>	transaldolase A	2.9
<i>aceF</i> ³	dehydrogenase, dihydrolipoyltransacetylase component E2	2.8
<i>gcd</i>	glucose dehydrogenase	2.8
<i>fumC</i> ²	fumarate hydratase (fumarase C), aerobic Class II	2.4
<i>betA</i>	choline dehydrogenase	2.2
<i>betB</i>	betaine aldehyde dehydrogenase	2.0
<i>mltD</i>	membrane-bound lytic murein transglycosylase D	2.0
<i>gdhA</i>	glutamate dehydrogenase	2.0
<i>erpA</i>	iron-sulfur cluster insertion protein	2.0
<i>deoB</i>	Phosphopentomutase	2.4
<i>deoC</i>	2-deoxyribose-5-phosphate aldolase, NAD(P)-linked	2.3
Translation/ protein synthesis		
<i>rpsV</i>	30S ribosomal subunit S22 / Stationary-phase-induced ribosome-associated protein	2.5
<i>rnt</i>	ribonuclease T	2.4
Stress response		
<i>inaA</i> ²	conserved protein, acid-induced	3.9
<i>sodA</i> ²	superoxide dismutase, Mn	3.5

TABLE S2: continued

Gene	Function	Fold change (log ₂)
<i>katE</i>	hydroperoxidase II	2.7
<i>gshB</i> ²	glutathione synthetase	2.1
<i>sufA</i>	iron-sulfur cluster assembly scaffold protein	1.9
<i>otsB</i>	trehalose-6-phosphate phosphatase	3.3
<i>treF</i>	cytoplasmic trehalase	2.4
<i>osmY</i>	osmotically inducible periplasmic protein	2.3
<i>hchA</i>	chaperone protein HchA	2.4
Antibiotic resistance		
<i>acrA</i> ²	acriflavin resistance protein A	2.9
<i>mdlAB</i> ¹	fused predicted multidrug transporter	2.9/2.3
Membrane/membrane transport		
<i>bhsA</i>	biofilm, cell surface and signaling protein	4.6
<i>chaC</i>	cation transport protein	3.7
ECs2055	putative outer membrane receptor for iron transport	2.6
<i>ompX</i> ²	outer membrane protein X	1.9
<i>ylaC</i>	inner membrane protein, DUF1449 family	2.2
<i>nlpD</i>	activator of AmiC murein hydrolase activity, lipoprotein (S-phase)	2.0
Amino acid synthesis/metabolism		
<i>shiA</i>	shikimate transporter	2.8
<i>ltaE</i>	L-allo-threonine aldolase	2.5
Transcriptional regulators		
<i>yqhC</i>	putative ARAC-type regulatory protein	3.8
<i>fnr</i>	fumarate/nitrate reduction transcriptional regulator	2.0
Other genes		
<i>yhbW</i>	predicted enzyme	3.8
<i>hemB</i> ²	delta-aminolevulinic acid dehydratase	2.3
<i>idi/</i>	isopentenyl-diphosphate delta-isomerase (isoprenoid	2.3
ECs3761	biosynthesis)	

¹Changes in expression for each gene of the complex or the same group are listed sequentially in respective order.

²Genes that are directly or indirectly controlled by MarA (Barbosa and Levy, 2000; Ruiz et al., 2008).

TABLE S3: *E. coli* O157:H7 genes that were highly downregulated only at 2 h exposure to cinnamaldehyde¹

Gene	Function	Fold change (log ₂)
Energy derivation and oxidation reduction		
<i>hycABCDEFHI</i> ²	hydrogenase 3/ formate hydrogenlyase	-3.9/-2.3/-3.1/-5.0/-4.5/-3.5/-2.0/-2.0
<i>hyaABC</i> ²	hydrogenase-1	-4.0/-3.1/-1.9
<i>hydN</i>	electron transport protein HydN	-4.1
<i>fdhF</i>	formate dehydrogenase H	-3.4
<i>frdABCD</i> ²	fumarate reductase flavoprotein subunit (anaerobic)	-2.7/-3.2/-2.2/-3.4
<i>dmsABC</i> ²	anaerobic dimethyl sulfoxide reductase	-2.8/-3.0/-2.0
<i>nuoA</i>	NADH dehydrogenase subunit A	-2.1
<i>nrfA</i>	cytochrome c552 /nitrite reductase	-2.0
<i>hypB</i>	hydrogenase nickel incorporation protein HypB	-2.1
<i>nrdG</i>	anaerobic ribonucleotide reductase activating protein	-2.1
<i>dcuAB</i> ²	anaerobic C4-dicarboxylate transporter	-2.1/-3.5
DNA metabolism		
<i>priB</i>	primosomal replication protein N	-2.7
<i>cnu</i>	oriC-binding nucleoid-associated protein	-2.4
Translation/ protein synthesis		
<i>tdcF</i>	predicted L-PSP (mRNA) endoribonuclease	-2.1
<i>rpmEG</i> ²	50S ribosomal protein L31/L33	-2.1/-2.9
<i>rplOP</i> ²	50S ribosomal protein L15/16	-2.1/-2.2
<i>rpsHRS</i> ²	30S ribosomal protein S8/S18/S19	-3.2/-2.2/-2.3
<i>rpsH</i>	30S ribosomal protein S8	-3.2
Stress response		
<i>gadE</i> ³	DNA-binding transcriptional activator involved in acid resistance	-3.6
<i>gadAB</i> ^{2,3}	glutamate decarboxylase alpha	-4.1/-4.8
<i>gadC</i> ³	glutamate:gamma-aminobutyric acid antiporter/ acid sensitivity protein	-3.5
<i>hdeAB</i> ^{2,3}	acid-resistance protein	-4.8/-6.0

TABLE S3: continued

Gene	Function	Fold change (log ₂)
<i>hdeD</i> ³	acid-resistance membrane protein	-4.8
Membrane/membrane transport		
<i>malEG</i> ²	maltose transporter	-4.0/-2.5
<i>wbdNO</i> ²	putative glycosyl transferase	-3.1/-2.0
<i>manXYZ</i> ²	PTS system mannose-specific transporter	-2.3/-2.3/-2.7
<i>lamB</i>	maltose outer membrane porin (malto porin)	-2.5
<i>afuB</i>	putative permease component of transport system for ferric iron	-2.1
<i>ydeQRS</i> ²	predicted fimbrial-like protein	-2.5/-3.8/-3.6
<i>wzx</i>	O antigen flippase	-2.0
<i>wzy</i>	O antigen polymerase	-3.0
<i>wbdR</i>	acetyl transferase; O-antigen biosynthesis	-2.1
<i>ompF</i> ³	outer membrane protein F	-2.2
<i>ompC</i>	outer membrane porin protein C	-2.8
<i>pgaAB</i>	biofilm adhesin polysaccharide PGA export/ PGA export lipoprotein with a polysaccharide deacetylase activity needed for export	-2.6/-2.3
<i>ycdT</i>	diguanylate cyclase	-2.8
<i>etk</i>	cryptic autophosphorylating protein tyrosine kinase Etk	-2.1
Transcription		
<i>nhaR</i>	DNA-binding transcriptional activator	-2.0
Amino acid synthesis/metabolism		
<i>cysW</i>	sulfate/thiosulfate transporter permease subunit	-2.7
<i>cysD</i>	sulfate adenylyltransferase subunit 2	-3.2
<i>aspA</i>	aspartate ammonia-lyase	-4.2

¹ Genes with expression value ≤ -1.9 are presented.

² Changes in expression for each gene of the complex or the same group are listed sequentially in respective order.

³Genes that are directly or indirectly controlled by MarA (Barbosa and Levy, 2000; Ruiz et al., 2008).

References:

Barbosa TM, Levy SB. 2000. Differential expression of over 60 chromosomal genes in *Escherichia coli* by constitutive expression of MarA. *J. Bacteriol.* 182:3467-3474.

Ruiz C, McMurry LM, Levy SB. 2008. Role of the multidrug resistance regulator MarA in global regulation of the *hdeAB* acid resistance operon in *Escherichia coli*. *J. Bacteriol.* 190:1290-1297.

TABLE S4: *E. coli* O157:H7 genes that were highly upregulated only at 4 h exposure to cinnamaldehyde¹

Gene	Function	Fold change (log ₂)
Motility and chemotaxis		
<i>motB</i>	flagellar motor protein	6.8
<i>motA</i>	flagellar motor protein	6.7
<i>fliC</i>	flagellin	5.6
<i>fliD</i>	flagellar capping protein	5.2
<i>tap</i>	methyl-accepting protein IV	5.6
<i>cheA</i>	chemotaxis protein	5.6
<i>cheZ</i>	chemotaxis regulator CheZ	4.5
<i>cheW</i>	purine-binding chemotaxis protein	4.5
<i>cheY</i>	chemotaxis regulator transmitting signal to flagellar motor component	4.0
<i>tar</i>	methyl-accepting chemotaxis protein II	4.8
<i>fliS</i>	flagellar protein potentiates polymerization	4.6
<i>flgK</i>	flagellar hook-filament junction protein 1	4.1
<i>flgN</i>	flagella synthesis protein	3.6
<i>fliT</i>	flagellar biosynthesis protein	3.4
<i>flgM</i>	anti-sigma factor for FliA	3.2
<i>cheR</i>	chemotaxis methyltransferase	3.1
<i>flhC</i>	transcriptional activator FlhC	2.2
<i>tsr</i>	methyl-accepting chemotaxis protein I	2.6
<i>fliA</i>	flagellar biosynthesis sigma factor (σ^{28})	2.6
<i>flhD</i>	transcriptional activator FlhD	2.6
<i>flgM</i>	anti-sigma factor for FliA (σ^{28})	3.2
<i>yhjH</i>	cyclic-di-GMP phosphodiesterase, FlhDC-regulated	4.2
Energy generation and oxidation reduction		
<i>atpABDEFGH</i> ²	F ₀ F ₁ ATP synthase	2.9/2.0/2.7/2.7/2.8/2.8/ 3.0
<i>nuoEHIJKL</i> ²	NADH:ubiquinone oxidoreductase	2.0/2.0/2.7/2.0/2.4/2.5

TABLE S4: continued

Gene	Function	Fold change (log ₂)
<i>torA</i>	trimethylamine-N-oxide reductase 1	5.5
<i>torC</i>	trimethylamine N-oxide (TMAO) reductase I cytochrome c-type subunit	6.2
<i>torD</i>	chaperone involved in maturation of TorA subunit of trimethylamine N-oxide reductase system I	5.3
<i>rsxABC</i> ²	electron transport complex	4.1/4.1/3.8
DNA metabolism		
<i>dnaB</i>	replicative DNA helicase	3.2
<i>fimB</i>	tyrosine recombinase/inversion of on/off regulator of fimA	2.3
<i>yjvV</i>	predicted DNase	3.5
<i>nrdA</i>	ribonucleotide-diphosphate reductase subunit alpha	3.0
<i>dnaE</i>	DNA polymerase III subunit alpha	2.5
<i>hola</i>	DNA polymerase III subunit delta	2.1
ECs4325	putative O-methyltransferase	5.0
Translation/ Protein synthesis		
<i>hemK</i>	N5-glutamine S-adenosyl-L-methionine- dependent methyltransferase	3.6
<i>tgt</i>	queuine tRNA-ribosyltransferase	3.1
<i>rlmH</i>	rRNA large subunit methyltransferase	2.7
<i>rhIE</i>	ATP-dependent RNA helicase RhIE	3.1
<i>rpsJP</i> ²	30S ribosomal protein S10/S16	2.5/2.1
<i>rplBDV</i> ²	50S ribosomal protein L2/L4/L22	2.4/2.3/2.1
<i>rpmH</i>	50S ribosomal protein L34	2.0
<i>glyS</i> ²	Glycyl-tRNA synthetase	2.0
<i>pheST</i> ²	Phenylalanyl-tRNA synthetase	2.8/2.2
<i>prfAC</i> ²	Peptide chain release factor 1/2/3	3.2/2.2
<i>rnpA</i>	protein C5 component of RNase P	3.4

TABLE S4: continued

Gene	Function	Fold change (log ₂)
Stress response		
<i>cadA</i>	lysine decarboxylase, acid-inducible	4.0
<i>cadB</i>	lysine/cadaverine antiporter	4.0
<i>adiA</i>	biodegradative arginine decarboxylase	3.7
<i>adiC</i>	arginine:agmatin antiporter	3.2
<i>cpxP</i>	periplasmic repressor CpxP	4.3
<i>degP</i>	serine endoprotease	3.1
<i>gppA</i>	guanosine pentaphosphate phosphohydrolase	3.0
Antibiotic resistance		
<i>acrB</i>	acriflavin resistance protein B	2.8
<i>acrD</i>	aminoglycoside/multidrug efflux system	2.6
<i>ampC</i>	beta-lactamase	2.2
<i>emrAD</i> ²	multidrug resistance secretion protein	2.2/1.8
<i>mdtIJ</i> ²	multidrug efflux system protein	2.7/4.6
Membrane/membrane transport		
<i>spr</i>	mutational suppressor of <i>prc</i> thermosensitivity, outer membrane lipoprotein	4.7
<i>lpxT</i>	Lipid A 1-diphosphate synthase/ lipid A 1- phosphate phosphotransferase	4.4
<i>eptB</i>	KDO phosphoethanolamine transferase, Ca ²⁺ - inducible	4.3
<i>waaL</i>	lipid A-core:surface polymer ligase	4.2
<i>gfcE</i>	predicted lipoprotein required for formation of the O-antigen capsule	3.7
ECs4327	putative phospholipid biosynthesis acyltransferase	3.9
ECs4324	lipoprotein	4.1
ECs4329	acyl carrier protein	3.9
ECs4332	putative (3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase	3.6
<i>ddg</i>	lipid A biosynthesis palmitoleoyl acyltransferase	3.0

TABLE S4: continued

Gene	Function	Fold change (log ₂)
<i>lgt</i>	prolipoprotein diacylglyceryl transferase	3.0
<i>acpT</i>	holo-(acyl carrier protein) synthase 2	2.8
<i>mipA</i>	scaffolding protein for murein synthesizing machinery	3.1
<i>prc</i>	carboxy-terminal protease for penicillin-binding protein 3	3.3
<i>setB</i>	lactose/glucose efflux system	3.4
<i>oppCD</i> ²	oligopeptide transport system	3.3/2.9
<i>lpxB</i>	lipid-A-disaccharide synthase	2.7
<i>miaF</i>	ABC transporter maintaining OM lipid asymmetry, ATP-binding protein	2.7
<i>accBC</i> ²	acetyl-CoA carboxylase carboxyltransferase	2.5/2.1
<i>aaeB</i> ²	p-hydroxybenzoic acid efflux system	2.0
<i>nupC</i>	permease of transport system for 3 nucleosides	2.6
<i>yejE</i>	putative transport system permease protein	2.4
Transcription		
<i>fis</i>	global DNA-binding transcriptional dual regulator	2.9
<i>malT</i>	transcriptional regulator MalT	3.1
<i>mcbR</i>	colanic acid and biofilm gene transcriptional regulator, MqsR-controlled	3.3
<i>grlR</i>	negative regulator GrlR	2.2

¹ Genes with expression value ≥ 1.8 are presented.

² Changes in expression for each gene of the complex or the same group are listed sequentially in respective order.

TABLE S5: *E. coli* O157:H7 genes that were highly downregulated only at 4 h exposure to cinnamaldehyde¹

Gene	Function	Fold change (log ₂)
Stress response		
<i>ibpAB</i> ²	Small heat shock protein	-2.9/-3.6
<i>htpG</i>	heat shock protein 90	-2.7
<i>rmf</i>	ribosome modulation factor (heat resistant)	-2.5
<i>hspQ</i>	heat shock protein HspQ	-2.0
<i>grxA</i>	glutaredoxin 1	-5.0
<i>gadY</i>	ncRNA (acid resistant)	-3.0
<i>cspD</i>	stationary phase/starvation inducible regulatory protein CspD	-2.8
<i>uspBDF</i> ²	universal stress protein	-2.1/-2.2/-3.0
<i>ldhA</i>	fermentative D-lactate dehydrogenase, NAD-dependent	-2.2
ECs1120	putative copper/zinc-superoxide dismutase	-2.5
<i>osmC</i>	osmotically inducible protein	-2.1
<i>osmB</i>	osmotically inducible lipoprotein	-3.4
Translation/protein synthesis		
<i>higAB</i> ²	HigB-HigA toxin-antitoxin system	-2.3/-4.0
<i>rdlB</i>	ncRNA	-3.3
<i>sokC</i>	ncRNA	-2.6
Membrane/membrane transport		
<i>macB</i>	macrolide transporter ATP-binding permease protein	-3.3
<i>cysP</i>	thiosulfate transporter subunit	-2.9
<i>slp</i>	membrane protein induced after carbon starvation	-2.9
<i>ygdl</i>	lipoprotein ygdI precursor	-4.2
<i>yggA</i>	arginine exporter protein	-2.1
<i>ybhL</i>	inner membrane protein, UPF0005 family	-2.3
<i>yohC</i>	inner membrane protein	-2.2
<i>ydhC</i>	inner membrane transport protein YdhC	-2.2
<i>ydhC</i>	inner membrane transport protein YdhC	-2.2

TABLE S5: continued

Gene	Function	Fold change (log ₂)
Transcription		
<i>zntR</i>	DNA-binding transcriptional activator in response to Zn(II)	-3.6
<i>glnK</i>	nitrogen regulatory protein P-II	-2.3
<i>yafC</i>	putative transcriptional regulator YafC	-2.1
Biofilm formation		
<i>bdm</i>	biofilm-dependent modulation	-2.3
<i>bssR</i>	biofilm formation regulatory protein BssR	-3.5
Others		
<i>ryjA</i>	ncRNA	-3.1

¹Genes with expression value ≤ -2.0 are presented.

²Changes in expression for each gene of the complex or the same group are listed sequentially in respective order.