

Table S1. Bacterial strains used in this study

Strain	Genotype	Source/Reference
DH5α	<i>E. coli</i> supE44 ΔlacU169 (ϕ 80lacZΔM15) hsdR17 recA1 endA1 gyrA96 thi-1 relA1	Invitrogen
DH5α/RK212.1	DH5α with conjugation transfer element	(1)
BL21 (DE3)	F ⁻ <i>ompT gal [dcm] [lon]</i> hsdS _B (<i>r_B</i> ⁻ <i>m_B</i> ⁻ ; an <i>E. coli</i> B strain) with DE3, a λ prophage carrying the T7 RNA polymerase gene	(2)
81-176	Wild-type <i>C. jejuni</i> clinical isolate	(3)
DRH212	81-176 <i>rpsL</i> ^{S_m}	(4)
DRH461	DRH212 ΔastA	(5)
DRH119	DRH212/pRY112	This study
PML242	DRH212 <i>Cjj1483</i> _{D58A}	This study
PML321	DRH212 <i>Cjj1484::cat-rpsL</i>	This study
PML322	DRH212 <i>Cjj1483::cat-rpsL</i>	This study
PML324	DRH461 <i>Cjj1483::cat-rpsL</i>	This study
PML335	DRH212 Δ <i>Cjj1483</i>	This study
PML337	DRH461 Δ <i>Cjj1483</i>	This study
PML360	DRH212 Δ <i>Cjj1484</i>	This study
PML624	DRH212 Δ <i>Cjj1483</i> /pPML533	This study
PML642	DRH212 Δ <i>Cjj1483</i> /pRY112	This study
PML739	DRH461 <i>Cjj1483</i> _{D58E}	This study
PML769	DRH461 <i>Cjj1483</i> _{D58N}	This study
PML973	DRH212 Δ <i>Cjj1484</i> /pPML968	This study
PML1129	DRH212 Δ <i>Cjj1484</i> /pPML1119	This study
PML1133	DRH212 Δ <i>Cjj1484</i> /pDAR1604	This study
PML1137	DRH212/pDAR1604	This study
PML1262	DRH212 <i>Cjj0064::cat-rpsL</i>	This study
PML1274	DRH212 <i>chuC::cat-rpsL</i>	This study
PML1280	DRH212 <i>Cjj1386::cat-rpsL</i>	This study
PML1305	DRH212 <i>Cjj1619::cat-rpsL</i>	This study

Table S2. Plasmids used in this study

Plasmid	Genotype/Description	Source/Reference
pUC19	Amp ^r	New England Biolabs
pGEX-4T-2	Amp ^R ; Tc ^R	GE Healthcare
pRY108	Km ^R ; <i>E. coli-C. jejuni</i> shuttle vector	(6)
pRY112	Cm ^R ; <i>E. coli-C. jejuni</i> shuttle vector	(6)
pET28-6XHis MalE	Km ^R ; pET28 containing a 6xHis-maltose binding protein fusion upstream of a TEV cleavage site	(7)
pDRH265	pUC19::cat-rpsL	(4)
pDAR812	pUC19 with the <i>Cjj1484-Cjj1483</i> locus from 81-176 cloned into the BamHI site	This study
pDAR1604	pRY108 with the promoter and start codon of <i>flaA</i> from 81-176 with an in-frame fusion of codons for a FLAG-tag cloned into the XbaI and BamHI sites	This study
pLKB156	pUC19 with the <i>chuCD</i> genes grom 81-176 cloned into the BamHI site	This study
pPML101	pDAR812 with a mutation to generate a HpaI site in <i>Cjj1484</i>	This study
pPML102	pDAR812 with a <i>cat-rpsL</i> cassette cloned into the EcoRV site of <i>Cjj1483</i>	This study
pPML107	Same as pPML106 with <i>cat-rpsL</i> cloned into the HpaI site of <i>Cjj1484</i> in opposite orientation	This study
pPML113	pDAR812 with an in-frame deletion of codons 2-225 of <i>Cjj1483</i>	This study
pPML165	pGEX-4T-2 with codons 2 – stop codon of <i>Cjj1483</i> cloned into the BamHI site	This study
pPML239	pDAR812 with a mutation to encode <i>Cjj1483</i> _{D58A}	This study
pPML278	pGEX-4T-2 with codons 2 – stop codon of <i>Cjj1483</i> _{D58A} cloned into the BamHI site	This study
pPML334	pDAR812 with an in-frame deletion of codons 2-402 of <i>Cjj1484</i>	This study
pPML340	pDAR812 with a mutation encode <i>Cjj1483</i> _{D58E}	This study
pPML533	pRY112 with a fragment containing 400 bp upstream of <i>Cjj1483</i> through the stop codon inserted into the BamHI site	This study
pPML732	pDAR812 with a mutation to encode <i>Cjj1483</i> _{D58N}	This study
pPML757	pGEX-4T-2 with codons 2 – stop codon of <i>Cjj1483</i> _{D58E} cloned into the BamHI site	This study
pPML758	pGEX-4T-2 with codons 2 – stop codon of <i>Cjj1483</i> _{D58E} cloned into the BamHI site	This study
pPML770	pUC19 with the <i>Cjj0063</i> locus from 81-176 cloned into the BamHI site	This study
pPML771	pUC19 with the <i>Cjj1386</i> locus from 81-176 cloned into the BamHI site	This study
pPML772	pUC19 with the <i>Cjj1619</i> locus from 81-176 cloned into the BamHI site	This study

pPML817	pDAR812 with a mutation to encode <i>Cjj1484</i> _{H195A}	This study
pPML848	pET28-6xHis-MalE with codons 2 – stop codon of <i>Cjj1484</i> cloned into the BamHI site	This study
pPML968	pDAR1604 with codons 2 – stop codon of <i>Cjj1484</i> cloned into the BamHI site	This study
pPML1119	pDAR1604 with codons 2 – stop codon of <i>Cjj1484</i> _{H195A} cloned into the BamHI site	This study
pPML1247	pPML772 with a mutation to generate a HpaI site in <i>Cjj1619</i>	This study
pPML1249	pLKB156 with a <i>cat-rpsL</i> cassette cloned into the ClaI site of <i>chuC</i>	This study
pPML1253	pPML770 with a <i>cat-rpsL</i> cassette cloned into the EcoRV site of <i>Cjj0064</i>	This study
pPML1254	pPML771 with a <i>cat-rpsL</i> cassette cloned into the HpaI site of <i>Cjj1386</i>	This study
pPML1261	pPML1247 with a <i>cat-rpsL</i> cassette cloned into the HpaI site of <i>Cjj1619</i>	This study

Table S3. Complete list of genes differentially expressed in *C. jejuni* 81-176 Sm^R Δ1484 compared to WT *C. jejuni* 81-176 Sm^{Ra}

Locus Tag	Gene Name	Putative Function	Ratio WT/ mutant	Reference
81176_0315	<i>peb3</i>	glycoprotein; putative adhesin or transport protein	3.52	(8-10)
81176_1619	<i>exbB2</i>	ferric enterobactin transport protein	3.44	(11)
81176_1339	<i>flaA</i>	major flagellin	2.87	(12)
81176_0211		possible transferrin transport protein	2.70	(13, 14)
81176_1620	<i>exbD2</i>	ferric enterobactin transport protein	2.62	(11)
81176_0210		possible transferrin transport protein	2.51	(13, 14)
81176_0722	<i>glnA</i>	glutamine synthetase	2.35	
81176_0580		hypothetical inner membrane protein	2.06	
81176_0438		gluconate dehydrogenase, subunit III	0.07	(15)
81176_0439		gluconate dehydrogenase, subunit I	0.08	(15)
81176_0885		putative cytochrome c	0.33	

^a Expression of genes was increased or decreased by two-fold in the *C. jejuni* ΔCjj1484 mutant.

Table S4. Complete list of genes differentially expressed in *C. jejuni* 81-176 Sm^R Δ1483 compared to WT *C. jejuni* 81-176 Sm^{Ra}

Locus Tag	Gene Name	Putative Function	Ratio WT/ mutant	Reference
81176_0204		putative periplasmic glycoprotein	5.87	(16)
81176_0075		putative cytochrome c subfamily protein	3.95	
81176_0206		phase-variable motility protein	3.77	(17, 18)
81176_1312		phase-variable flagellin glycosylation protein	3.73	(19)
81176_1208		putative periplasmic protein	3.17	
81176_1435		capsular polysaccharide modification protein	2.93	(20)
81176_0283	eptC	lipid A phosphoethanolamine transferase	2.51	(21, 22)
81176_0722	glnA	putative glutamine synthetase	2.37	
81176_1257	ciaC	invasion protein	2.23	(23)
81176_1422	hddC	capsular polysaccharide biosynthesis	2.13	(24)
81176_1603	chuC	hemin transport ATP-binding protein	0.09	(25)
81176_1386		hypothetical protein	0.11	
81176_0439		gluconate dehydrogenase, subunit I	0.13	(15)
81176_0438		gluconate dehydrogenase, subunit III	0.14	(15)
81176_0463	mfrA	methylmenaquinol:fumurate reductase protein A	0.16	(26)
81176_1385		hypothetical protein	0.19	
81176_1604	chuD	hemin transport substrate-binding protein	0.22	(25)
81176_0063		hypothetical protein	0.27	
81176_0464	mfrB	methylmenaquinol:fumurate reductase protein B	0.28	(26)
81176_0433	frdA	fumarate reductase/succinate dehydrogenase flavoprotein subunit	0.32	(27)
81176_0064		cytochrome c family protein	0.32	
81176_1619	exbB2	ferric enterobactin transport protein	0.33	(11)
81176_1602	chuB	hemin transport permease protein	0.34	(25)
81176_		hypothetical protein	0.36	
81176_	metC	hypothetical protein	0.38	
81176_1620	exbD2	ferric enterobactin transport protein	0.39	(11)
81176_1353	ceuD	enterochelin transport, ATP-binding protein	0.39	(28)
81176_1699	rplV	50S ribosomal protein L22	0.39	
81176_0123	dcuA	C4-dicarboxylate transporter	0.40	(29)
81176_0122	aspA	aspartate ammonia-lyase	0.41	(29)
81176_0561	oorA	2-oxoglutarate:acceptor oxidoreductase	0.41	
81176_1693	rplX	50S ribosomal protein L24	0.42	
81176_0471	cfrB	enterobactin receptor	0.42	(30)

81176_0432	<i>frdC</i>	fumarate reductase, cytochrome b subunit	0.42	(27)
81176_0291		putative endoribonuclease L-PSP	0.43	
81176_0478	<i>thiC</i>	thiamine biosynthesis protein	0.45	
81176_1600	<i>chuZ</i>	heme oxygenase	0.45	(25)
81176_1580	<i>rplsK</i>	30S ribosomal protein S11	0.45	
81176_0211		possible transferrin transport protein	0.45	(13)
81176_1160		LOS biosynthesis	0.45	
81176_1162		LOS biosynthesis	0.46	
81176_0128		putative periplasmic protein	0.46	
81176_0465	<i>mfrE</i>	methylmenaquinol:fumurate reductase protein E	0.47	(26)
81176_0210		possible transferrin transport protein	0.47	
81176_0758		putative periplasmic protien	0.47	
81176_0066		putative cytochrome c	0.48	
81176_0655	<i>hypE</i>	hydrogenase isoenzyme formation protein	0.50	

^a Expression of genes was increased or decreased by two-fold in the *C. jejuni* Δ *Cjj1483* mutant.

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