

Supplementary material

Table S1. Screening of putative virulence genes in *C. jejuni* ST353CC isolates sequenced in this study. Compared to *C. jejuni* reference strains 11168 (GenBank AL111168.1), 81-176 (GenBank *CP000538.1 (chromosome) and **AY394561.1 (pTet plasmid), and 108 (Genbank #JX436460.1).

Function	Gene annotation in 11168, 81-176*/** or 108 [#]		Analysis of 353CC isolates		
	Locus tag	Gene name	Present in all isolates	Not found in any isolates	Differences
Capsule biosynthesis	cj1413c	<i>kpsS</i> , capsule polysaccharide modification protein	✓		
	cj1414c	<i>kpsC</i> , capsule polysaccharide modification protein	✓		
	cj1415c	<i>cysC</i> , putative adenylylsulfate kinase	✓		
	cj1423c	<i>hddC1</i> , putative D-glycero-D-manno-heptose 1-phosphate guanosyltransferase			Present in B30, B31 and B44
	cj1424c	<i>gmhA2</i> , phosphoheptose isomerase		✓	
	cj1425c	<i>hddA</i> , putative D-glycero-D-manno-heptose 7-phosphate kinase			Present in E00, E79, B30, B31 and B44
	cj1428c	<i>fcl</i> , GDP-L-fucose synthetase		✓	
	cj1430c	<i>rfbC</i> , putative dTDP-4-dehydrorhamnose 3,5-epimerase			Present in B30, B31 and B44
	cj1431c	<i>hddC2</i> , capsular polysaccharide heptosyltransferase		✓	
	cj1439c	<i>glf</i> , UDP-galactopyranose mutase		✓	
	cj1441c	<i>kfiD</i> , UDP-glucose 6-dehydrogenase		✓	
	cj1443c	<i>kpsF</i> , D-arabinose 5-phosphate isomerase	✓		
	cj1444c	<i>kpsD</i> , capsule polysaccharide export system periplasmic protein	✓		
	cj1445c	<i>kpsE</i> , capsule polysaccharide export system inner membrane protein	✓		
	cj1447c	<i>kpsT</i> , capsule polysaccharide export ATP-binding protein	✓		
	cj1448c	<i>kpsM</i> , capsule polysaccharide export system inner membrane protein	✓		
Motility and	cj0041	<i>fliK</i> , putative flagellar hook-length control protein	✓		
	cj0042	<i>flgD</i> , putative flagellar hook assembly protein	✓		

chemotaxis	cj0043	<i>flgE</i> , flagellar hook protein	✓
	cj0059c	<i>fliY</i> , putative flagellar motor switch protein	✓
	cj0060c	<i>fliM</i> , flagellar motor switch protein	✓
	cj0061c	<i>fliA</i> , RNA polymerase sigma factor for flagellar operon	✓
	cj0063c	<i>flhG</i> , flagellar biosynthesis protein, ATPase	✓
	cj0064c	<i>flhF</i> , flagellar biosynthesis protein	✓
	cj0195	<i>fliI</i> , flagellum-specific ATP synthase	✓
	cj0283c	<i>cheW</i> , chemotaxis protein	✓
	cj0284c	<i>cheA</i> , chemotaxis histidine kinase	✓
	cj0285c	<i>cheV</i> , chemotaxis protein	✓
	cj0318	<i>fliF</i> , flagellar M-ring protein	✓
	cj0319	<i>fliG</i> , flagellar motor switch protein	✓
	cj0320	<i>fliH</i> , putative flagellar assembly protein	✓
	cj0335	<i>flhB</i> , flagellar biosynthesis protein	✓
	cj0336c	<i>motB</i> , putative flagellar motor protein	✓
	cj0337c	<i>motA</i> , putative flagellar motor proton channel	✓
	cj0351	<i>fliN</i> , flagellar motor switch protein	✓
	cj0448c	<i>acfB</i> , accessory colonisation factor, MCP-type signal transduction protein	✓
	cj0526c	<i>fliE</i> , flagellar hook-basal body complex protein	✓
	cj0527c	<i>flgC</i> , flagellar basal body rod protein	✓
	cj0528c	<i>flgB</i> , flagellar basal body rod protein	✓
	cj0547	<i>flaG</i> , flagellar protein	✓
	cj0548	<i>fliD</i> , flagellar hook-associated protein	✓
	cj0549	<i>fliS</i> , flagellar protein	✓
	cj0670	<i>rpoN</i> , RNA polymerase sigma-54 factor	✓
	cj0687c	<i>flgH</i> , putative flagellar L-ring protein precursor	✓
	cj0697	<i>flgG2</i> , <i>flgF</i> , flagellar basal-body rod protein	✓
	cj0698	<i>flgG</i> , <i>flgG</i> , flagellar basal-body rod protein	✓
	cj0720	<i>flaC</i> , flagellin	✓

	cj0769c	<i>flgA</i> , putative flagellar protein	✓	
	cj0793	<i>flgS</i> , signal transduction histidine kinase	✓	
	cj0820c	<i>fliP</i> , flagellar biosynthesis protein	✓	
	cj0882c	<i>flhA</i> , flagellar biosynthesis protein	✓	
	cj0887c	<i>flaD</i> , <i>flgL</i> , flagellar hook-associated protein	✓	
	cj0923c	<i>cheR</i> , putative MCP protein methyltransferase	✓	
	cj0924c	<i>cheB</i> , putative MCP protein-glutamate methylesterase	✓	
	cj1024c	<i>flgR</i> , sigma-54 associated transcriptional activator	✓	
	cj1118c	<i>cheY</i> , chemotaxis regulatory protein	✓	
	cj1179c	<i>fliR</i> , flagellar biosynthesis protein	✓	
	cj1189c	<i>cetB</i> , bipartate energy taxis response protein	✓	
	cj1198	<i>luxS</i> , S-ribosylhomocysteine lyase	✓	
	cj1190c	<i>cetA</i> , bipartate energy taxis response protein	✓	
	cj1312	<i>pseG</i> , nucleotidase	✓	
	cj1313	<i>pseH</i> , N-acetyltransferase	✓	
	cj1331	<i>ptmB</i> , acylneuraminate cytidylyltransferase	✓	
	cj1332	<i>ptmA</i> , putative oxidoreductase	✓	
	cj1338c	<i>flaB</i> , flagellin		Missing in E00
	cj1339c	<i>flaA</i> , flagellin		Missing in E00
	cj1408	<i>fliL</i> , putative flagellar protein	✓	
	cj1462	<i>flgI</i> , flagellar P-ring protein	✓	
	cj1466	<i>flgK</i> , putative flagellar hook-associated protein	✓	
	cj1506c	<i>tlpI</i> , putative MCP-type signal transduction protein	✓	
	cj1565c	<i>pflA</i> , paralysed flagellum protein	✓	
	cj1675	<i>fliQ</i> , flagellar biosynthesis protein	✓	
	cj1729c	<i>flgE2</i> , flagellar hook subunit protein	✓	
adhesion	cj0289c	<i>peb3</i> , major antigenic peptide	✓	
	cj0921c	<i>peb1A</i> , aspartate/glutamate-binding ABC transporter protein	✓	
	cj0983	<i>jlpA</i> , surface-exposed adhesin		Missing in E00

	cj1259	<i>porA</i> , major outer membrane protein	✓	
	cj1279c	<i>flpA</i> , putative fibronectin domain-containing lipoprotein	✓	
	cj1351	<i>pldA</i> , phospholipase A	✓	
	cj1478c	<i>cadF</i> , outer membrane fibronectin-binding protein	✓	
	*CJJ81176_0067	<i>ggt</i> , gamma-glutamyltransferase		✓
invasion	cj0914c	<i>ciaB</i> , invasion antigen B	✓	
	cj1647	<i>iamA</i> , putative ABC transport system ATP-binding protein	✓	
stress response	cj0012c	<i>rrc</i> , non-haem iron protein	✓	
	cj0020c	cytochrome C551 peroxidase	✓	
	cj0334	<i>ahpC</i> , alkyl hydroperoxide reductase	✓	
	cj0358	putative cytochrome C551 peroxidase	✓	
	cj0779	<i>tpx</i> , thiol peroxidase	✓	
	cj1260c	<i>dnaJ</i> , chaperone	✓	
	cj1272c	<i>spoT</i> , putative guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase	✓	
	cj1385	<i>katA</i> , catalase	✓	
	*CJJ81176_1121	<i>csrA</i> , carbon storage regulator	✓	
iron acquisition	cj0178	putative TonB-dependent outer membrane receptor	✓	
	cj0755	<i>cfrA</i> , ferric enterobactin uptake receptor	✓	
	cj1355	<i>ceuE</i> , enterochelin uptake periplasmic binding protein	✓	
	cj1614	<i>chuA</i> , haemin uptake system outer membrane receptor	✓	
toxin	cj0077c	<i>cdtC</i> , cytolethal distending toxin C	✓	
	cj0078c	<i>cdtB</i> , cytolethal distending toxin B	✓	
	cj0079c	<i>cdtA</i> , cytolethal distending toxin A	✓	
type IV	**	<i>cmgB4</i> , putative type IV secretion system component, <i>virB4</i>		Present in B30, B31 and B44
secretion	**	<i>cmgB5</i> , putative type IV secretion system component, <i>virB5</i>		“
system	**	<i>cmgB6</i> , putative type IV secretion system component, <i>virB6</i>		“
(T4SS)	**	<i>cmgB7</i> , putative type IV secretion system component, <i>virB7</i>		“
	**	<i>cmgB8</i> , putative type IV secretion system component, <i>virB8</i>		“
	**	<i>cmgB9</i> , putative type IV secretion system component, <i>virB9</i>		“

	**	<i>cmgB10</i> , putative type IV secretion system component, <i>virB10</i>			“
	**	<i>cmgB11</i> , putative type IV secretion system component, <i>virB11</i>			“
	**	<i>cmgD4</i> , putative type IV secretion system component, <i>virD4</i>			“
	**pTet	pTet plasmid			“
	** <i>tetO</i>	<i>tetO</i> , tetracyclin resistance gene	✓		
type VI secretion system (T6SS)	#	<i>tssA</i> , <i>VasJ</i>	✓		
	#	<i>tssB</i> , <i>VipA</i>	✓		
	#	<i>tssC</i> , <i>VipB</i>	✓		
	#	<i>tssD</i> , <i>Hcp</i>	✓		
	#	<i>tssE</i>	✓		
	#	<i>tssF</i> , <i>VasA</i>	✓		
	#	<i>tssG</i> , <i>VasB</i>	✓		
	#	<i>tagH</i> , <i>VasC</i>	✓		
	#	<i>tssI</i> , <i>VgrG</i>	✓		
	#	<i>tssJ</i> , <i>VasD</i>	✓		
	#	<i>tssK</i> , <i>VasE</i>	✓		
	#	<i>tssL</i>	✓		
	#	<i>tssM</i>	✓		
LOS class	A			✓	
	B				E38, E01, E03,
	C			✓	
	D				E79
	E				E00, B30, B31, B44
	F			✓	

Table S2. Results from comparative genomic analyses identifying genes unique for *C. jejuni* ST353CC isolates of different sequence types.

Annotation from BLAST of protein sequence	COG
Unique genes for ST-9438 isolates	
PseF, pseudaminic acid cytidyltransferase, CMP-N-acetylneuraminic acid synthetase	[M] Cell wall/membrane/envelope biogenesis
restriction endonuclease subunit S, type I SS modification system specificity (S) subunit	[V] Defence mechanisms
class I SAM-dependent methyltransferase	[H] Coenzyme transport and metabolism
dihydroorotase, pyrimidine biosynthesis	[F] Nucleotide transport and metabolism
YeeE/YedE family protein, uncharacterized membrane protein	[R] General function prediction only
peptidase C39	[R] General function prediction only
HmcD domain-containing protein	[C] Energy production and conversion
relaxase/mobilisation nuclease domain-containing protein	[X] Mobilome: prophages, transposons
NTPase	[F] Nucleotide transport and metabolism
protein kinase family protein	[T] Signal transduction mechanisms
RadB, RecA-family ATPase	[L]* Replication, recombination and repair
resolvase, site-specific DNA recombinase	[L]* Replication, recombination and repair
VirB4, type IV secretion system conjugal transfer ATPase	[U] Intracellular trafficking, secretion, and vesicular transport
Rha family transcriptional regulator	[X] Mobilome: prophages, transposons
single-stranded DNA-binding protein	[L]* Replication, recombination and repair
VirB5, type IV secretion system P-type DNA transfer protein	[U] Intracellular trafficking, secretion, and vesicular transport
VirB6, type IV secretion system plasmid conjugal transfer protein	[U] Intracellular trafficking, secretion, and vesicular transport
VirB8, type IV secretion system DNA transporter protein	[U] Intracellular trafficking, secretion, and vesicular transport
VirB9, type IV secretion system P-type conjugative transfer protein	[U] Intracellular trafficking, secretion, and vesicular transport
VirB10, type IV secretion system protein	[U] Intracellular trafficking, secretion, and vesicular transport
VirB11, type IV secretion system P-type DNA transfer ATPase	[U] Intracellular trafficking, secretion, and vesicular transport
VirD4, type IV secretion system conjugative DNA transfer protein, TraG/TraD family ATPase	[U] Intracellular trafficking, secretion, and vesicular transport
type IV secretion system protein	[U] Intracellular trafficking, secretion, and vesicular transport
TrbM, conjugal transfer protein	[U] Intracellular trafficking, secretion, and vesicular transport
DNA topoisomerase III	[L]* Replication, recombination and repair

chaperone of the DnaK-DnaJ-GrpE chaperone system
repA, plasmid replication protein
ParA family protein implicated in chromosome segregation
type I restriction modification system DNA methylase
GNAT family N-acetyltransferase

Unique genes for ST-9336, ST-9437 and ST-3515 isolates

TnpV, transposon-encoded protein
MerR family of transcription regulatory protein
transposase
class I SAM-dependent methyltransferase
DNA methyltransferase
dihydroorotase

[E] Protein fate, Protein folding and stabilization
[L]* Replication, recombination and repair
[L]* Replication, recombination and repair
[V] Defense mechanisms
[G] Carbohydrate transport and metabolism

[X] Mobilome: prophages, transposons
[K] Transcription
[X] Mobilome: prophages, transposons
[H] Coenzyme transport and metabolism
[R] General function prediction only
[F]* Nucleotide transport and metabolism

*Involved in information storage and processing

Figure S1. BRIG analysis of plasmids identified in *C. jejuni* ST353CC isolates B30, B31 and B44 (all ST-9438) compared to the pTet plasmid from *C. jejuni* 81-176. Outer ring shows consensus sequence with arrows indicating ORFs.

Figure S1

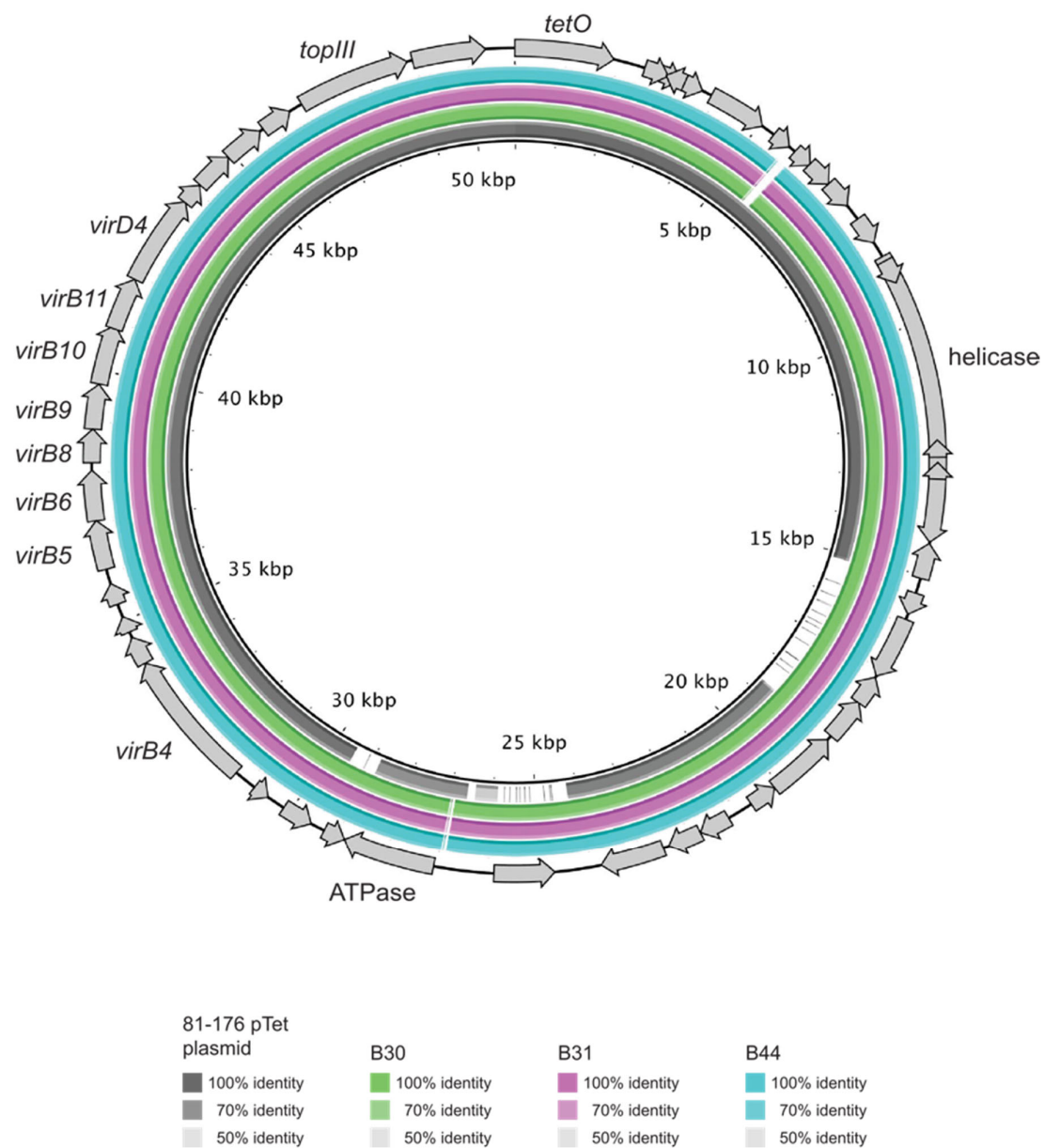


Figure S2. Chromosomal location of a 2862 nucleotide long fragment containing the tetO gene in non-ST-9438 isolates. The integration site contains several citrate transporters and is here theoretically demonstrated in the *C. jejuni* 11168 reference strain genome.

