

Supplemental Tables, Figures and Data.

Supplemental Table 1. Repository information for the genomes sequenced in this study.

SUBID	BioProject	BioSample	Localid	Accession	Organism
SUB9233512	PRJNA634604	SAMN15004773		CP071579	
			CjGB03		<i>Campylobacter jejuni</i> GB03
SUB9228550	PRJNA634604	SAMN15004774		CP071577	
			CjGB18		<i>Campylobacter jejuni</i> GB18
SUB9233606	PRJNA634604	SAMN15004775		CP071582	
			CjGB28		<i>Campylobacter jejuni</i> GB28
SUB9233607	PRJNA634604	SAMN15004776		CP071583	
			CjGB60		<i>Campylobacter jejuni</i> GB60
SUB9220467	PRJNA634604	SAMN15004779		CP071574	
			CjRM1510		<i>Campylobacter jejuni</i> RM1510
SUB9228496	PRJNA634604	SAMN15004780		CP071575	
			CjRM3147		<i>Campylobacter jejuni</i> RM3147
SUB9228544	PRJNA634604	SAMN15004781		CP071576	
			CjEnt12		<i>Campylobacter jejuni</i> R12
SUB9233595	PRJNA634604	SAMN15004782		CP071580	
			CjEnt23		<i>Campylobacter jejuni</i> R23
SUB9233601	PRJNA634604	SAMN15004783		CP071581	
			CjEnt31		<i>Campylobacter jejuni</i> R31
SUB9233425	PRJNA634604	SAMN15004784		CP071578	
			CjEnt72		<i>Campylobacter jejuni</i> R72
SUB9233611	PRJNA634604	SAMN15004785			
			CjEnt73	CP071584	<i>Campylobacter jejuni</i> R73
SUB9235759	PRJNA348673	SAMN05871073		CP071592	<i>Campylobacter jejuni</i> subsp. <i>jejuni</i>
			CjGB19		GB19
SUB9235759	PRJNA348673	SAMN05871073	CjGB19pGB19	CP071593	<i>Campylobacter jejuni</i> subsp. <i>jejuni</i>
					GB19
SUB9235875	PRJNA348675	SAMN05871074		CP071585	<i>Campylobacter jejuni</i> subsp. <i>jejuni</i>
			CjGB26		GB26

Supplemental Table 2. The presence of *Campylobacter jejuni* integrated elements (CJIE)s in strains with the capsular Penner serotype HS:19. Mauve alignment and BLASTn analysis was used to identify and characterise CJIEs in *C. jejuni*.

Strain	Disease	CJIE present	Homology with	Location in genome (bp)	Size (bp)	Integration site	Naturally transformable
GB03	GBS	yes	CJIE1	185,572-225,032	39.461	in a putative protease	no
GB18	GBS	no	-	-	-	-	yes
GB28	GBS	no	-	-	-	-	yes
GB60	GBS	no	-	-	-	-	yes
RM1245	GBS	no	-	-	-	-	no
RM1477	GBS	yes	CJIE1	1,500,862-1,538,087	37.226	after ABC transporter	no
RM1510	GBS	yes	CJIE1	821,493-858,403	36.911	after putative sulphotransferase	no
RM3147	GBS	no	-	-	-	-	yes
R12	Enteritis	yes	CJIE2	452,580-492,176	39.597	in tRNA Arg-CCT	yes
R23	Enteritis	no	-	-	-	-	yes
R31	Enteritis	no	-	-	-	-	yes
R72	Enteritis	no	-	-	-	-	yes
R73	Enteritis	no	-	-	-	-	yes
RM3420	Enteritis	yes	CJIE1	1,326,743-1,365,298	38.556	in putative periplasmic protein	no
RM1285	chicken isolate	yes	unique	879,831-919,449	39.619	in tRNA Leu-GAG	yes

Supplemental Table 3. Genes in *C. jejuni* strain CjjRM3420 that contain poly G/C-tracts.

Gene, gene product function, location of poly G/C-tract within the gene, status of the poly G/C-tract and numbers of poly G/C-tracts that are in an in-frame status (GBS vs non-GBS).

Grey rows indicate poly G/C-tract information for genes within a gene cluster involved in a similar function.

^a, non-annotated pseudogene between CjjRM3420_0171 and _0171 containing a poly G/C-tract;

^b, these genes are sometimes identical but can have different sizes and annotations, the largest annotated CDS is 2604;

^c, poly G-tract is close to the 3' end the CDS and produces products of varying size when variable; IF, CDS in frame; OOF, CDS out of frame; OOFB, CDS out of frame before poly G/C-tract; IF/OOF, variable poly G-tract with in frame and out frame CDS states; IF/no polyG, CDS in frame, no poly G/C-tracts; GGGGAGGGG, poly G/C-tract altered to sequence given; GGGCGGGGGG, poly G/C-tract altered to sequence given, 9bp, 10bp, 9/10bp, 10/11bp, 12/13bp, sizes of intragenic poly G/C- tract upstream off CjjRM3420_1407, NP, not present; AP, not applicable.

Gene	Gene product function	CjRM3420		CDS status														(partial) F GBS	(partial) F Enteritis/Food	p (Fisher exact)	
				GBS-related (n = 8)								Enteritis/food-related (n = 7)									
		gene length (bp)	start G/C-ratio	GB03	GB18	GB28	GB60	RM1245	RM1477	RM1510	RM1417	R12	R23	R31	R72	R73	RM1285	RM3420			
CjRM3420_0039	DNA cleavage	3738	2563	F/no polyG	F/no polyG	IF	F/no polyG	F/OOF	F/OOF	F/OOF	F/no polyG	OOFB	F/no polyG	F/no polyG	F/GGGGAGGGG	F/no polyG	F/no polyG	F/OOF	8	6	0.4667
CjRM3420_0053	hypothetical protein	720 ²	708	F	OOFB	F	OOFB	F	F/OOF	F	F	F	OOFB	OOFB	F	OOFB	F	IF	6	4	0.6084
CjRM3420_0171-0172 ⁴	pseudogene	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CjRM3420_0472 ⁵	unknown n	1170	30	F/OOF	F/OOF	OOF	F	F/OOF	F/OOF	F/OOF	F/OOF	OOF	OOFGGGAGGGG	F/OOF	OOFGGGAGGGG	IF	OOFGGGAGGGG	OOF	6	2	0.1319
CjRM3420_0590	DUF2920 domain protein	1263	584	OOF	IF	IF	IF	F/OOF	F/OOF	F/OOF	F/OOF	IF	OOF	IF	IF	IF	F/OOF	IF	7	6	1
CjRM3420_0649	capsule modification	1395	835	F/OOF	IF	IF	F/OOF	F/OOF	F/OOF	F/OOF	IF	IF	IF	F/OOF	F/OOF	F/OOF	IF	IF	8	7	1
CjRM3420_0931 ⁶	unknown n	1170	30	F/OOF	F/OOF	F/OOF	F/OOF	F/OOF	F/OOF	IF	OOFGGGAGGGG	OOF	OOFGGGAGGGG	F/OOF	OOFGGGAGGGG	F/OOF	OOFGGGAGGGG	IF	7	4	0.2821
CjRM3420_1249	flagella biosynthesis	1308	143	IF	F/OOF	F/OOF	F/OOF	F/OOF	F/OOF	IF	IF	IF	IF	F/OOF	F/OOF	F/OOF	IF	IF	8	7	1
CjRM3420_1250		794	309	OOF	F/OOF	F/OOF	F/OOF	F/OOF	F/OOF	OOF	IF	OOF	F/OOF	OOF	OOF	OOF	IF	OOF	6	2	0.1319
CjRM3420_1258		1215	587	F/OOF	F/OOF	F/OOF	F/OOF	IF	IF	OOF	OOF	IF	F/OOF	F/OOF	IF	F/OOF	IF	IF	6	7	0.4667
CjRM3420_1260		1209	576	NP	F/OOF	F/OOF	NP	IF	IF	IF	IF	NP	NP	NP	IF	NP	F/OOF	OOF	6	2	0.1319
CjRM3420_1264		1215	578	IF	IF	OOF	F/OOF	IF	IF	OOF	IF	IF	OOF	IF	IF	IF	IF	OOF	6	5	1
CjRM3420_1278		1245	560	IF	F/OOF	F/OOF	F/OOF	IF	F/OOF	OOF	IF	IF	IF	IF	IF	F/OOF	IF	IF	7	7	1
CjRM3420_1407	capsule biosynthesis	1407	-21	10/11bp	10/11bp	9/10bp	10/11bp	12/13bp	10/11bp	10bp	9bp	10bp	10/11bp	10bp	10/11bp	10/11bp	10/11bp	9bp	NA	NA	NA
CjRM3420_1414	capsule modification (MeOPh)	774	393	IF	IF	OOF	IF	IF	F/OOF	IF	OOF	F/OOF	IF	IF	IF	IF	IF	IF	6	7	0.4667
CjRM3420_1415		1833	93	IF	F/OOF	F/OOF	IF	F/OOF	F/OOF	OOF	OOF	F/OOF	IF	IF	F/OOF	IF/OOF	F/OOF	IF/OOF	6	7	0.4667
CjRM3420_1434	sialylation	1278	1206	F/OOF	IF	F/OOF	F/OOF	F/no polyG	F/GGGGAGGGG	F/GGGGAGGGG	IF	F/GGGGAGGGG	F/OOF	F/OOF	IF	IF	F/OOF	F/GGGGAGGGG	8	7	1
CjRM3420_1439	sulfation	1203 ³	1146	IF	IF	IF	IF	IF	IF	IF	IF	IF	IF	IF	IF	IF	IF	IF	8	7	0.4667
CjRM3420_1441	methylation	960	138	IF	IF	IF	F/OOF	F/OOF	IF	IF	IF	F/OOF	OOF	F/OOF	IF	F/OOF	F/OOF	IF	8	6	0.4667
CjRM3420_1448		1137	539	IF	F/OOF	IF	IF	IF	F/OOF	IF	IF	IF	IF/OOF	IF	F/OOF	F/OOF	OOF	F/OOF	8	6	0.4667
CjRM3420_1454		methylation	1203	126	F/OOF	F/OOF	F/OOF	F/OOF	F/OOF	F/OOF	F/OOF	F/OOF	IF/OOF	IF/OOF	IF/OOF	OOF	IF/OOF	OOF	OOF	8	5
CjRM3420_1567	putative 4Fe-4S dicluster domain dimethylsulfoxide (pseudogene)	673	153	IF	F/OOF	F/OOF	F/OOF	OOF	OOF	OOF	OOF	OOFGGGGGGGGG	IF	F/OOF	OOF	OOF	OOF	OOF	4	2	0.6084

Supplemental Table 4. Blast analysis of ST-22 strains derived from PubMLST. To determine whether ST-22 genomes generally have capsular Penner serotype HS:19, LOS class A1 and the clusters identified in this study, ST-22 genomes with a core genome MLST (cgMLST) that had less than 200 cgMLST allelic differences were selected in PubMLST and blasted (BLASTn) against sequences relevant for this study (Supplemental data 1). Green, indicates that the queried sequence was present; yellow, indicates that the queried sequence was absent (based on >98% identity and >60% query coverage).

Isolate id	Isolate	Country	Year	Disease	MLST-ST	MLST-CC	HS:19	LOS class A1	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster VI	Cluster X
1818	D5476	USA	1998	enteritis	22	ST-22	1	1	1	1	1	1	1	1
1820	D0445	USA	1983	enteritis	22	ST-22	1	1	1	1	1	1	1	1
6199	OXC342	UK [England]	2004	enteritis	22	ST-22	1	1	1	1	1	1	1	1
14651	OXC2413	UK [England]	2007	enteritis	22	ST-22	1	1	1	1	1	1	1	1
16061	OXC6264	UK [England]	2011	enteritis	22	ST-22	1	1	1	1	1	1	1	1
16390	OXC6641	UK [England]	2011	enteritis	22	ST-22	1	1	1	1	1	1	1	1
18201	OXC6644	UK [England]	2011	enteritis	22	ST-22	1	1	1	1	1	1	1	1
18202	OXC6645	UK [England]	2011	enteritis	22	ST-22	1	1	1	1	1	1	1	1
21585	OXC6866	UK [England]	2012	enteritis	22	ST-22	1	1	1	1	1	1	1	1
22083	OXC6887	UK [England]	2012	enteritis	22	ST-22	1	1	1	1	1	1	1	1
22084	OXC6888	UK [England]	2012	enteritis	22	ST-22	1	1	1	1	1	1	1	1
22097	OXC6902	UK [England]	2012	enteritis	22	ST-22	1	1	1	1	1	1	1	1
22269	OXC7085	UK [England]	2012	enteritis	22	ST-22	1	1	1	1	1	1	1	1
22669	OXC7178	UK [England]	2012	enteritis	22	ST-22	1	1	1	1	1	1	1	1
23903	OXC7364	UK [England]	2012	enteritis	22	ST-22	1	1	1	1	1	1	1	1
23906	OXC7367	UK [England]	2012	enteritis	22	ST-22	1	1	1	1	1	1	1	1
23913	OXC7375	UK [England]	2012	enteritis	22	ST-22	1	1	1	1	1	1	1	1
23992	OXC7463	UK [England]	2012	enteritis	22	ST-22	1	1	1	1	1	1	1	1
24018	OXC7490	UK [England]	2012	enteritis	22	ST-22	1	1	1	1	1	1	1	1
24607	OXC7809	UK [England]	2013	enteritis	22	ST-22	1	1	1	1	1	1	1	1
24635	OXC7838	UK [England]	2013	enteritis	22	ST-22	1	1	1	1	1	1	1	1
24945	OXC7697	UK [England]	2013	enteritis	22	ST-22	1	1	1	1	1	1	1	1
25568	OXC7942	UK [England]	2013	enteritis	22	ST-22	1	1	1	1	1	1	1	1
25593	OXC8043	UK [England]	2013	enteritis	22	ST-22	1	1	1	1	1	1	1	1
25980	Dg253	UK			22	ST-22	1	1	1	1	1	1	1	1
26044	Dg258	UK			22	ST-22	1	1	1	1	1	1	1	1
30554	OXC8868	UK [England]	2014	enteritis	22	ST-22	1	1	1	1	1	1	1	1
30815	OXC9136	UK [England]	2014	enteritis	22	ST-22	1	1	1	1	1	1	1	1

30821	OXC9142	UK [England]	2014	enteritis	22	ST-22	1	1	1	1	1	1	1
30918	OXC9245	UK [England]	2014	enteritis	22	ST-22	1	1	1	1	1	1	1
31162	OXC9343	UK [England]	2014	enteritis	22	ST-22	1	1	1	1	1	1	1
31420	OXC9601	UK [England]	2015	enteritis	22	ST-22	1	1	1	1	1	1	1
31500	OXC9681	UK [England]	2015	enteritis	22	ST-22	1	1	1	1	1	1	1
31556	H144520622	UK [England]	2014	enteritis	22	ST-22	1	1	1	1	1	1	1
32554	H150260421	UK [England]	2015	enteritis	22	ST-22	1	1	1	1	1	1	1
32824	OXC9768	UK [England]	2015	enteritis	22	ST-22	1	1	1	1	1	1	1
34427	OXC9895	UK [England]	2015	enteritis	22	ST-22	1	1	1	1	1	1	1
34441	OXC9909	UK [England]	2015	enteritis	22	ST-22	1	1	1	1	1	1	1
35305	Cj1997-11	USA			22	ST-22	1	1	1	1	0	1	1
38448	ARI1517	UK [Scotland]	2012		22	ST-22	1	1	1	1	1	1	1
38473	ARI1544	UK [Scotland]	2012		22	ST-22	1	1	1	1	1	1	1
38514	ARI1591	UK [Scotland]	2012		22	ST-22	1	1	1	1	1	1	1
38680	ARI1786	UK [Scotland]	2012		22	ST-22	1	1	1	1	1	1	1
38682	ARI1788	UK [Scotland]	2012		22	ST-22	1	1	1	1	1	1	1
38728	ARI1836	UK [Scotland]	2012		22	ST-22	1	1	1	1	1	1	1
39288	ARI2483	UK [Scotland]	2013		22	ST-22	1	1	1	1	1	1	1
40905	ARI3321	UK [Scotland]	2014	enteritis	22	ST-22	1	1	1	1	1	1	1
41650	C1018	UK [Scotland]	2014		22	ST-22	1	1	1	1	1	1	1
42172	ARI3891	UK [Scotland]	2015	enteritis	22	ST-22	1	1	1	1	1	1	1
43814	NWC161	UK [England]	2016	enteritis	8118	ST-22	1	1	1	1	1	1	1
47373	41974	USA	2011		22	ST-22	1	1	1	1	1	1	1
47709	NWC256	UK [England]	2016	enteritis	22	ST-22	1	1	1	1	1	1	1
47767	NWC280	UK [England]	2015	enteritis	22	ST-22	1	1	1	1	1	1	1
47791	OXC10181	UK [England]	2015	enteritis	22	ST-22	1	1	1	1	1	1	1
47794	NWC266	UK [England]	2015	enteritis	22	ST-22	1	1	1	1	1	1	1
48259	ARI3902	UK [Scotland]			22	ST-22	1	1	1	1	1	1	1
48304	ARI4172	UK [Scotland]	2015		22	ST-22	1	1	1	1	1	1	1
50282	NWC529	UK [England]	2015	enteritis	22	ST-22	1	1	1	1	1	1	1
50854	ACP163	UK	2016		22	ST-22	1	1	1	1	1	1	1
50932	ACP1278	UK	2016		22	ST-22	1	1	1	1	1	1	1
57331	OXC10470	UK [England]	2016	enteritis	22	ST-22	1	1	1	1	1	1	1
58092	NWC1010	UK [England]	2017	enteritis	22	ST-22	1	1	1	1	1	1	1
58157	ARI3973	UK [Scotland]	2015		22	ST-22	1	1	1	1	1	1	1
59035	OXC10639	UK [England]	2017	enteritis	22	ST-22	1	1	1	1	1	1	1
59520	OXC10732	UK [England]	2017	enteritis	22	ST-22	1	1	1	1	1	1	1
59522	NWC1327	UK [England]	2017	enteritis	22	ST-22	1	1	1	1	1	1	1
59617	NWC1280	UK [England]	2017	enteritis	22	ST-22	1	1	1	1	1	1	1
61015	M00214	USA	2007		22	ST-22	1	1	1	1	1	1	1
61177	OXC10848	UK [England]	2017	enteritis	22	ST-22	1	1	1	1	1	1	1

62693	NWC1741	UK [England]	2017	enteritis	22	ST-22	1	1	1	1	1	1	1
62696	NWC1738	UK [England]	2017	enteritis	22	ST-22	1	1	1	1	1	1	1
62729	NWC1740	UK [England]	2017	enteritis	22	ST-22	1	1	1	1	1	1	1
62917	NWC1877	UK [England]	2017	enteritis	8118	ST-22	1	1	1	1	1	1	1
62933	OXC11201	UK [England]	2017	enteritis	22	ST-22	1	1	1	1	1	1	1
69389	NWC1993	UK [England]	2017	enteritis	22	ST-22	1	1	1	1	1	1	1
69398	OXC11267	UK [England]	2017	enteritis	22	ST-22	1	1	1	1	1	1	1
69415	OXC11266	UK [England]	2017	enteritis	22	ST-22	1	1	1	1	1	1	1
69452	NWC1958	UK [England]	2017	enteritis	22	ST-22	1	1	1	1	1	1	1
69502	NWC1925	UK [England]	2017	enteritis	22	ST-22	1	1	1	1	1	1	1
70407	2010D-7920	USA		enteritis	22	ST-22	1	1	1	1	1	1	1
70410	2010D-7921	USA		enteritis	22	ST-22	1	1	1	1	1	1	1
70412	2005782	USA		enteritis	22	ST-22	1	1	1	1	1	1	1
70413	20070225	USA		enteritis	22	ST-22	1	1	1	1	1	1	1
70414	20070697	USA		enteritis	22	ST-22	1	1	1	1	1	1	1
70415	PNUSAC000105	USA	2015	enteritis	22	ST-22	1	1	1	0	1	1	1
70416	PNUSAC000107	USA	2015	enteritis	22	ST-22	1	1	1	1	1	1	1
70421	PNUSAC000310	USA	2016	enteritis	22	ST-22	1	1	1	1	1	1	1
70809	NWC2343	UK [England]	2018	enteritis	8118	ST-22	1	1	1	1	1	1	1
76108	CjRM1477	USA		GBS	22	ST-22	1	1	1	1	1	1	1
76110	CjRM1510	Japan		GBS	22	ST-22	1	1	1	1	1	1	1
76878	OXC11712	UK [England]	2018		22	ST-22	1	1	1	1	1	1	1
76960	NWC2662	UK [England]	2018	enteritis	22	ST-22	1	1	1	1	1	1	1
76976	NWC2661	UK [England]	2018	enteritis	22	ST-22	1	1	1	1	1	1	1
77030	NWC2694	UK [England]	2018	enteritis	22	ST-22	1	1	1	1	1	1	1
77069	NWC2715	UK [England]	2018	enteritis	22	ST-22	1	1	1	1	1	1	1
77157	OXC11837	UK [England]	2018		22	ST-22	1	1	1	1	1	1	1
77254	OXC11872	UK [England]	2018		22	ST-22	1	1	1	1	1	1	1
78185	FDI670	UK	2018		22	ST-22	1	1	1	1	1	1	1
78273	OXC11922	UK [England]	2018		22	ST-22	1	1	1	1	1	1	1
78465	NWC2908	UK [England]	2018	enteritis	22	ST-22	1	1	1	1	1	1	1
79189	CVM N17C205	USA	2017		22	ST-22	1	1	1	1	1	1	1
79244	PS00268	USA	2017		22	ST-22	1	1	1	1	1	1	1
80426	npCAMPY38	Peru	2013	carrier	22	ST-22	1	1	1	1	1	1	1
80470	p3H2	Peru	2012	carrier	22	ST-22	1	1	1	1	1	1	0
80828	CVM N18C436	USA	2018		22	ST-22	1	1	1	1	1	1	1
80871	PNUSAC009624	USA			22	ST-22	1	1	1	1	1	1	0
80937	PNUSAC009814	USA			22	ST-22	1	1	1	1	1	1	1
80957	PNUSAC009671	USA			22	ST-22	1	1	1	1	0	1	0
80958	PNUSAC009677	USA			22	ST-22	1	1	1	1	1	1	1
81073	PNUSAC009524	USA			22	ST-22	1	1	1	1	1	1	1

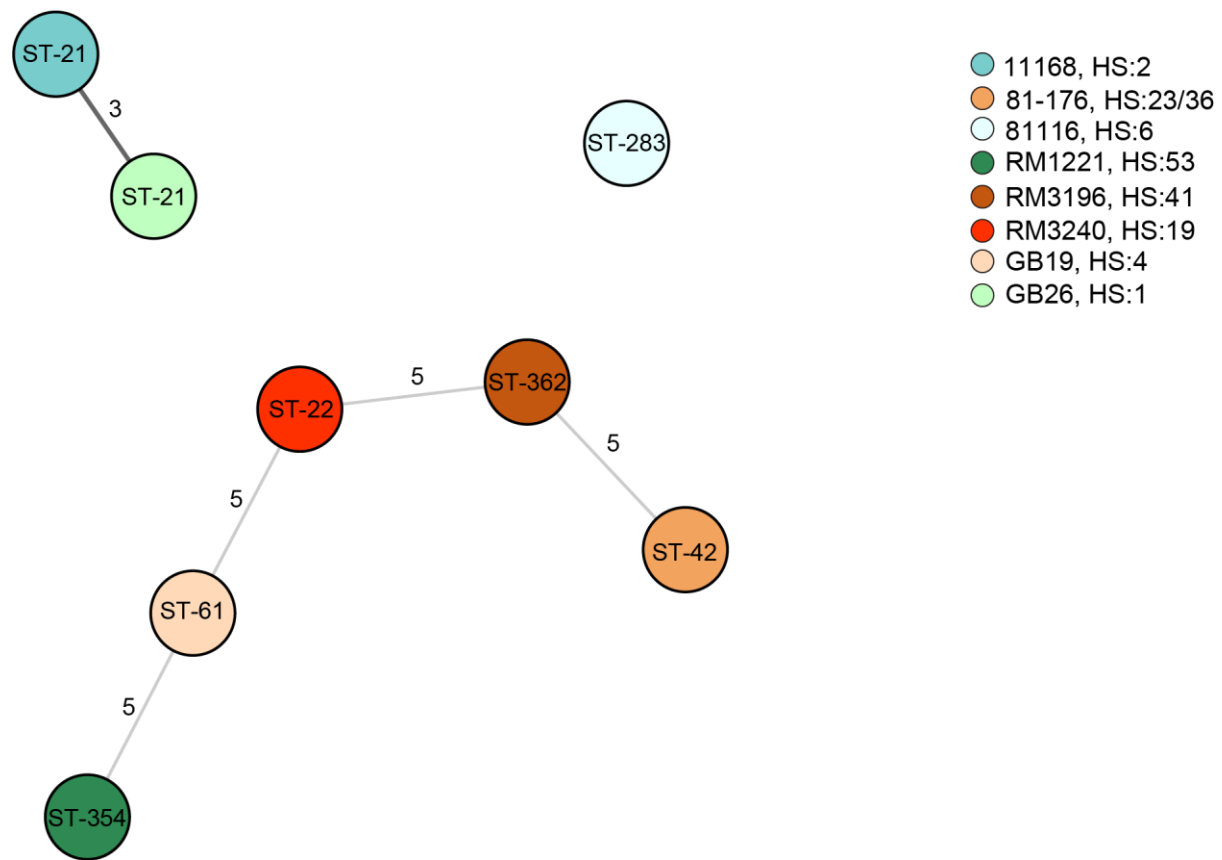
81074	PNUSAC009523	USA	22	ST-22	1	1	1	1	1	1	1	1
81101	PNUSAC009435	USA	22	ST-22	1	1	1	1	1	1	1	0
81126	PNUSAC009493	USA	22	ST-22	1	1	1	1	1	1	1	1
81212	PNUSAC005995	USA	22	ST-22	1	1	1	1	1	1	1	0
81409	PNUSAC005599	USA	22	ST-22	1	1	1	1	1	1	1	1
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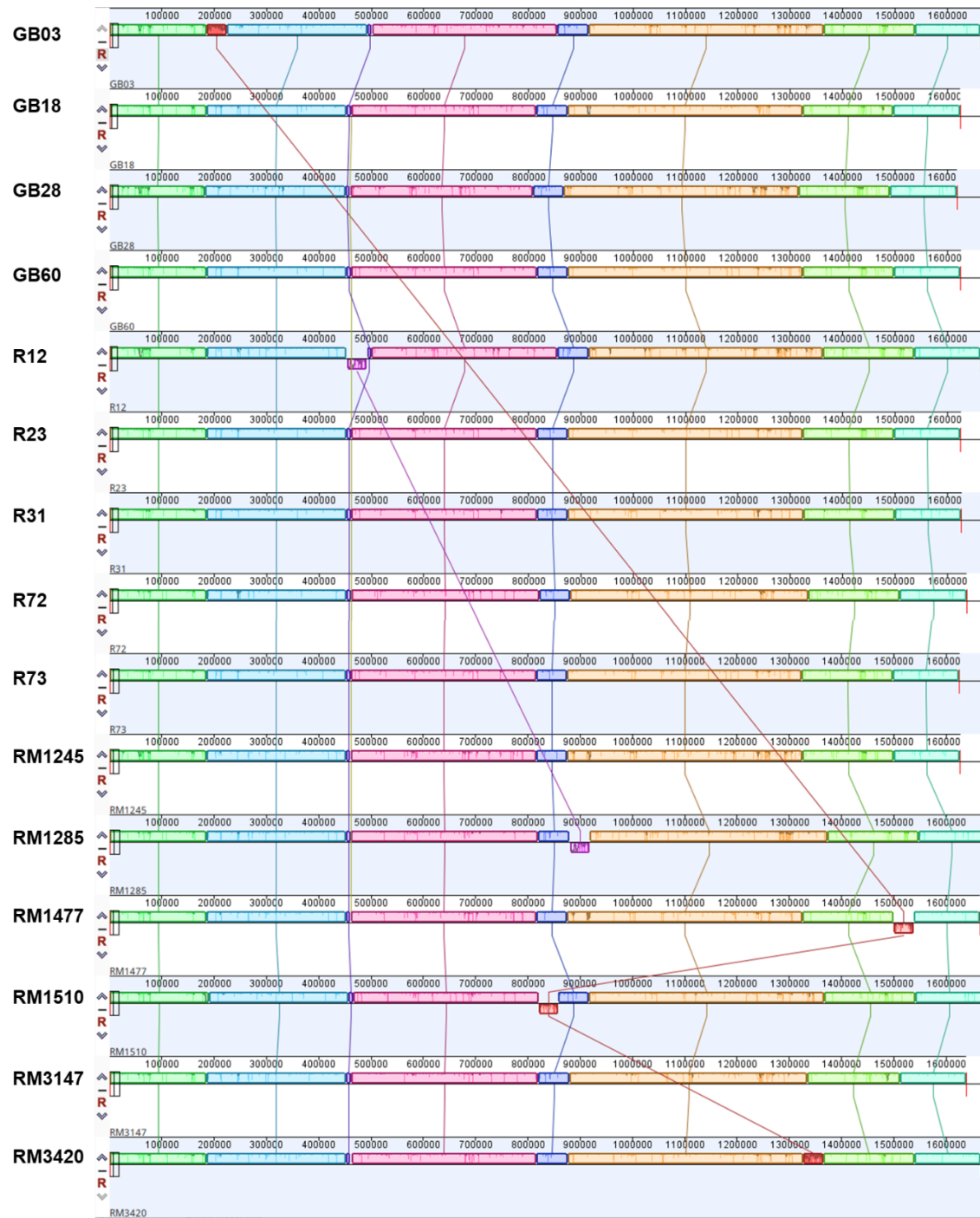
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Total present						287	287	286	287	281	287	286	274
Percentage (%)						100	100	99.7	100	97.9	100	99.7	95.5



Supplemental figure 1. Minimal spanning tree of *C. jejuni* strains with unrelated capsular Penner serotypes and genetically diverse genetic backgrounds based on multi locus sequence typing (MLST) clonal complexes. The 3 and 5 indicate the number of MLST alleles that were different (7 genes MLST).



Supplemental figure 2. The presence of *Campylobacter jejuni* integrated elements (CJIE)s in the genomes of *C. jejuni* HS:19 strains. To identify large gene insertions and gene rearrangements in the genomes, a Mauve alignment was performed on the complete genome sequences. The CJIEs are indicated in red and violet and connected with a red and violet line.

Genomic map of the *kps* operon region on chromosome 1. The map shows the *kpsS* and *kpsH* genes, and the locations of various restriction sites (RM3420, R72, GB03, R73, GB28, RM1245, RM1477, GB60, R31, R12, RM1510, RM3147, RM1285, R23, GB18) across a 25,183 bp scale.

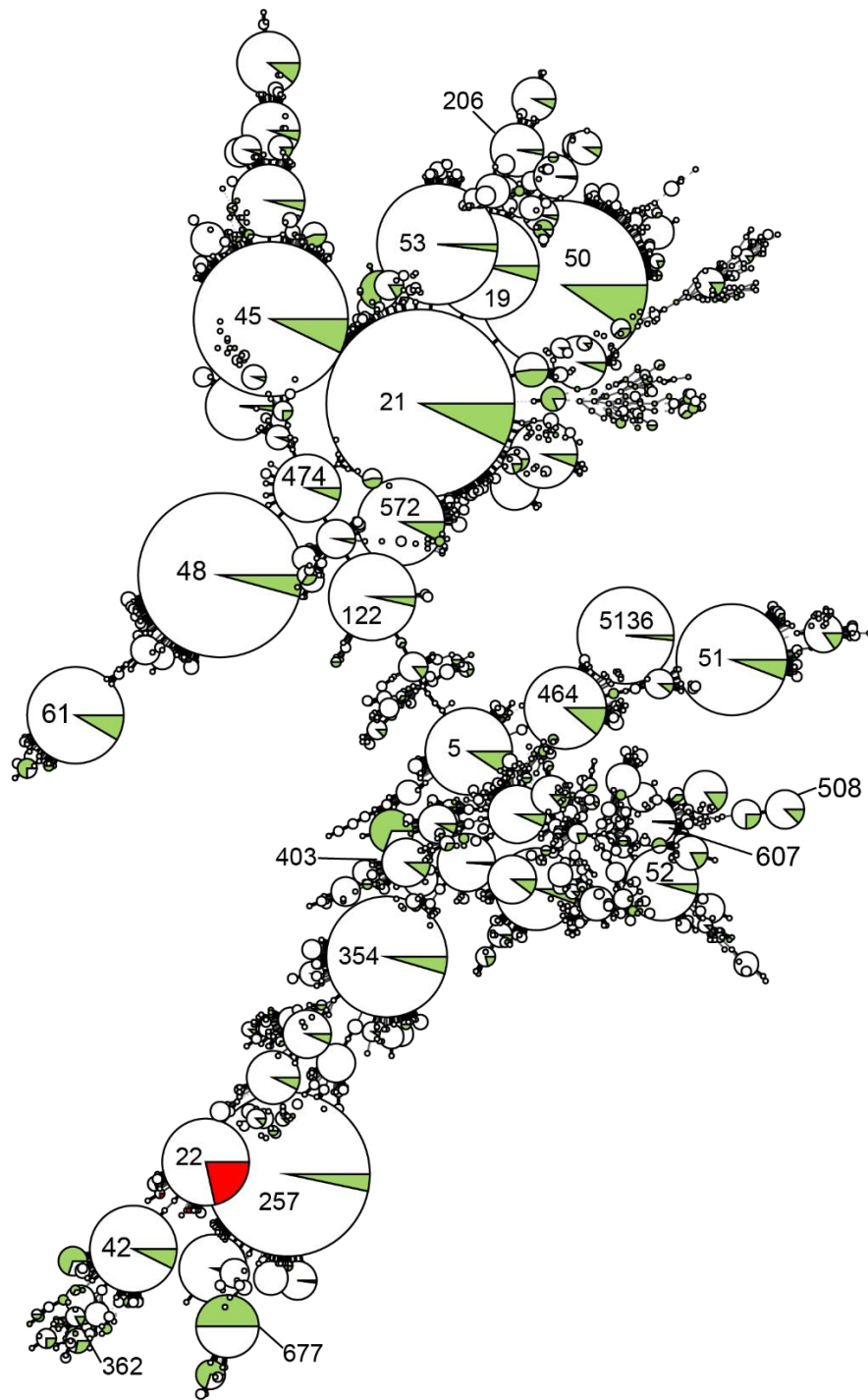
Phylogenetic tree showing relationships between various *Salmonella enterica* serotype Enteritidis strains. The tree is rooted at the top left. Bootstrap values are indicated at the nodes: 86, 62, 61, 88, and 77. The strains are listed on the right, with their serotype and country of origin. The strains are: RM1245 (GBS, USA (CA)), R31 (Enteritis, Netherlands), GB18 (GBS, Netherlands), GB03 (GBS, Netherlands), R23 (Enteritis, Netherlands), GB60 (GBS, Netherlands), R73 (Enteritis, Netherlands), RM3420 (Enteritis, Canada), RM1510 (GBS, Japan), R12 (Enteritis, Netherlands), GB28 (GBS, Bonaire), RM1477 (GBS, USA (FL)), RM1285 (Chicken, USA (CA)), RM3147 (GBS, Mexico), and R72 (Enteritis, Netherlands). A scale bar at the bottom left indicates 3.0E-5.

Strain	Disease	Country
RM1245	GBS	USA (CA)
R31	Enteritis	Netherlands
GB18	GBS	Netherlands
GB03	GBS	Netherlands
R23	Enteritis	Netherlands
GB60	GBS	Netherlands
R73	Enteritis	Netherlands
RM3420	Enteritis	Canada
RM1510	GBS	Japan
R12	Enteritis	Netherlands
GB28	GBS	Bonaire
RM1477	GBS	USA (FL)
RM1285	Chicken	USA (CA)
RM3147	GBS	Mexico
R72	Enteritis	Netherlands

3.0E-5

Supplemental figure 3. Alignment and phylogenetic tree of the capsule biosynthesis

locus of *C. jejuni* HS:19 strains. MUSCLE alignment (A) and UPGMA clustering (B) and of the capsule biosynthesis locus (genes *kpsS* - *kpsM*) of *C. jejuni* HS:19 strains. The sequence of the capsule biosynthesis locus was highly conserved in all strains with a maximum of 10 SNPs difference for RM1245 when compared to the reference RM3420 and a minimum of 2 SNPs for strain RM1510. UPGMA clustering of the sequence of the capsule biosynthesis locus did not lead to a separation of GBS- from enteritis-related strains



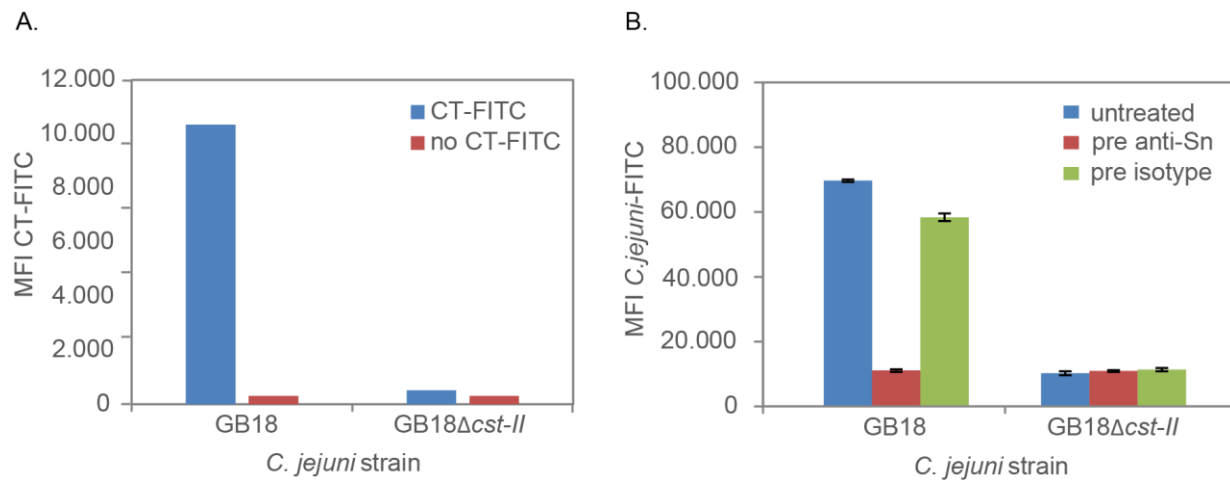
- MLST sequence type or clonal complex 22 from this study (n = 36)
- Other MLST sequence types from this study (n = 874)
- MLST sequence types from pubMLST (n = 10,000)

Supplemental figure 4. Minimal spanning tree of multi locus sequence type (MLST) data from this study and PubMLST. Comparison of multi locus sequence types of the sequenced HS:19 strains and the downloaded genomes from this study vs. a randomly downloaded subset from PubMLST.

The MLST sequence types of the sequenced HS:19 strains and the downloaded genomes from NCBI plotted together with a randomly downloaded subset of PubMLST sequence types.

Correlation MLST sequence type; this study vs PubMLST = 0.771, $p < 0.0001$ (Pearson).

Correlation MLST clonal complexes; this study vs PubMLST = 0.901, $p < 0.0001$ (Pearson).



Supplemental figure 5. Binding of a *C. jejuni* HS:19 wild type and knockout strain to cholera toxin and sialoadhesin. A *cst-II* knockout mutant was generated in the *C. jejuni* HS:19 strain GB18 through a natural transformation using DNA isolated from a previously generated *C. jejuni* knockout mutant strain GB11Δ*cst-II* (5). The GB18 wild type and knockout strain were incubated with FITC-labelled cholera toxin (CT-FITC) (A) or with sialoadhesin-expressing THP-1 cells (THP-1-Sn) (B) as described (1), and the binding was measured with FACS. Pre-anti-Sn, pre-treated with an antibody directed to Sn; pre isotype, pre-treated with an isotype control antibody.

Reference:

1. **Heikema AP, Koning RI, Duarte dos Santos Rico S, Rempel H, Jacobs BC et al.** Enhanced, sialoadhesin-dependent uptake of Guillain-Barre syndrome-associated *Campylobacter jejuni* strains by human macrophages. *Infect Immun* 2013;81(6):2095-2103.

Supplemental Data.

Supplemental Data 1. Sequence data relevant for this study.

>HS19 Cluster I *Campylobacter jejuni* subsp. *jejuni* str. RM3420

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>HS19 Cluster II *Campylobacter jejuni* subsp. *jejuni* str. RM3420

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>HS19 Cluster VI *Campylobacter jejuni* subsp. *jejuni* str. RM3420

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>LOSA Campylobacter jejuni subsp. jejuni str. RM3420

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>LOSA1 Campylobacter jejuni subsp. jejuni str. RM3420

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>HS19 CPS marker Campylobacter jejuni subsp. jejuni str. RM3420

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