

Table S1. PCR and sequencing primers used for confirmation of A/T-tracts and SNPs.

Gene	Primer	Primer sequence
CAMP0019	reverse	3' AAGTATTGCGGGATTTAGAA 5'
	forward	5' GCTATGGAATTTGCGGATTT 3'
CAMP0608	reverse	3' CCCAGTTTAATGTCTATCTT 5'
	forward	5' TTAAATGGAGCTTATGTCTT 3'
CAMP0624	reverse	3' TATCCGCTTTACTTACCT 5'
	forward	5' GCGTGAGTTTGCCTATTT 3'
CAMP0935	reverse	3' CTATTCGTTAGTACGGATTT 5'
	forward	5' GCCCTTATGGTACACTTTAT 3'
CAMP1031	reverse	3' GAAGCCGATATTGTTATTGC 5'
	forward	5' TAAACATCTATCCCTCCCTT 3'
CAMP1108	reverse	3' GTAAATGTTAGCGTAGTATTCG 5'
	forward	5' GCCTTGTTGCTGTTCTGC 3'
CAMP1113	reverse	3' TTGGTTCTTTCCGAATGGAC 5'
	forward	5' TATCGCATTGTTATTGGG 3'
CAMP1242	reverse	3' TATGGCTTCTTTGAGGATCG 5'
	forward	5' GGGGAATGATTTATTGTGAT 3'

Table S2. Distance matrix (numbers of allelic differences) of the six milk-borne *C. jejuni* outbreak-associated isolates and two references strains (*C. jejuni* PT14 and 1_12S) based on 1404-shared loci.

	1_12S	Le_204R	Le_755	Ma_1	Ma_B	Po_1	Po_2	PT14
1_12S	0							
Le_204R	420	0						
Le_755	418	9	0					
Ma_1	419	9	4	0				
Ma_B	418	9	3	6	0			
Po_1	418	12	9	10	9	0		
Po_2	419	9	4	2	5	8	0	
PT14	281	454	452	453	452	453	453	0

Table S3. Distance matrix (numbers of allelic differences) of the six milk-borne outbreak-associated *Campylobacter jejuni* isolates based on 1432-shared loci.

	Le_204R	Le_755	Ma_1	Ma_B	Po_1	Po_2
Le_204R	0					
Le_755	10	0				
Ma_1	10	4	0			
Ma_B	10	3	6	0		
Po_1	12	8	9	8	0	
Po_2	10	4	2	5	7	0