



Article

Antimicrobial Resistance and Genomic Characterization of *Campylobacter jejuni* and *Campylobacter coli* Isolated from Retail Chickens in Beijing, China

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† The two authors contributed equally to this study.

Supplementary Materials

Table S1. Relationship between Susceptibility/resistance Patterns and Associated Antibiotic Resistance Genes and point mutations in *C. coli* isolates.

	GEN		ERY		CHL		DC		TET	
	OR	p-value	OR	p-value	OR	p-value	OR	p-value	OR	p-value
<i>aac(6')-aph(2'')</i>	1.0118E+26	0.999	4568241710	1	3.299	1	2.1625E+27	0.999	1.2584E+17	0.999
<i>aadE-Cc</i>	3795044.065	1	1989693.387	1	0	0.999	0.914	1	323094968.6	0.999
<i>ant(6)-Ia</i>	54861221.88	1	2.3834E+15	0.999	75297861.22	1	114224890	1	0.754	1
<i>aph(2'')-If</i>	0	0.998	0.635	0.784	0	0.999	0	0.999	0	0.999
<i>aph(3')-III</i>	0	0.999	0	0.998	0	0.998	0	0.998	0.371	1
<i>erm(B)</i>	0	0.999	70646893.47	0.998	0	0.999	0	0.999	0	0.999
<i>cat</i>	871838322.8	0.999	3.821	0.423	1.2931E+17	0.998	0	0.999	0	0.999
<i>fexA</i>	0	1	0	1	1014835424	1	0.243	1	560937444.5	1
<i>tet(L)</i>	0	1	0	1	1014835424	1	0.243	1	560937444.5	1
<i>tet(O)</i>	0	0.999	0	0.999	10.727 ^a	0.024	1.871	0.502		
<i>bla_{OXA-193}</i>	0	0.999	0	0.998	0	1	0	0.998	0	0.999
<i>bla_{OXA-489}</i>	0	0.999	0	0.999	27760879868	1	0	0.999	0	0.999
<i>RpsL (K43R)</i>	0	1	180416521.8	1	3.598	1	2.157	1	2.074	1
<i>23S (A2075G)</i>	0	0.999	0	0.999	0	0.999	0	0.999	0	1
<i>L4 V121A</i>	632801535.5	0.999	272171667.3	0.999	0.428	1	2.666	1	1.44	1
<i>L4 M192I</i>	0	0.999	0	0.999	27760879868	1	0	0.999	0	0.999

GEN: gentamicin, ERY: erythromycin, CHL: chloramphenicol, DC: doxycycline, TET: tetracycline, OR: Odds ratio ^a Indicates an association between antibiotics resistance and the associated-antibiotic resistance gene. ^b Indicates an association between antimicrobial susceptibility and the associated-antibiotic resistance gene. Antimicrobial resistance is defined as an OR > 1 and *p* < 0.05, and antimicrobial susceptibility is defined as an OR < 1 and *p* < 0.05.

Table S2. Relationship between Susceptibility/resistance Patterns and Associated Antibiotic Resistance Genes and point mutations in *C. jejuni* isolates.

	GEN		ERY		CHL		CIP		DC		TET	
	OR	p-value	OR	p-value	OR	p-value	OR	p-value	OR	p-value	OR	p-value
<i>ant(6)-Ia</i>	1.792	1	4.386	1	1.968	1	0	0.999	0.888	1	0.001	1
<i>aph(2'')-If</i>	1.0137E+1 6	0.998	52.495 ^a	0.023	1.7113E+1 6	0.998	0.276	1	0	0.999	7.609	1
<i>aph(3')-III</i>	16.812	1	16731979. 27	0.999	16.376	1	247665265.0 71	1	4.313	1	0	1
<i>cat</i>	16.812	1	16731979. 27	0.999	16.376	1	247665265.0 71	1	4.313	1	0	1
<i>tet(O)</i>	0.46	0.455	20.541 ^a	0.026	0.503	0.445	0	0.999	0.705	0.653	1.5268E+1 5	0.997
<i>bla_{OXA-184}</i>	11.428	1	133379917 .5	1	11.395	1	5.2048E+17	0.999	4.995	1	0.173	1
<i>bla_{OXA-185}</i>	0.288	1	0	1	0.516	1	31610E+10	1	0	0.999	0	1
<i>bla_{OXA-193}</i>	207840075 .4	1	107056993 7	1	365844883 .9	1	2.100E+10	1	127772821 4	1	1134099.4 46	1
<i>bla_{OXA-465}</i>	1.121	1	0.459	1	2.02	1	0	1	0	0.999	0	1
<i>RpsL</i> (K43R)	0	1	0	0.999	0	1	1.856	1	6.342	0.301	0	0.999
<i>L4 V82I</i>	0	0.999	0	0.999	0	0.999	0	0.999	204249910 0	0.999	0	0.999
<i>L4 T91K</i>	0	1	0	1	0	1	0	1	0	0.998	0	0.999
<i>L4 V121A</i>	2.591	0.5	0.453	0.537	1.472	0.772	242392669.4 37	0.999	988041491 .1	0.999	11368174. 31	1
<i>L4 V176I</i>	0	1	0	1	0	1	0	1	0	0.998	0	0.999
<i>L4 T177S</i>	0	1	0	1	0	1	0	1	0	0.998	0	0.999
<i>L4 M192I</i>	10.333 ^a	0.001	2.019	0.253	8.286 ^a	0.03	2.585	0.697	0.636	0.458	2.270	0.466
<i>GyrA</i> (S22G)	0.19	0.282	0.113	0.247	0.319	0.45	0	0.999	0	0.998	0	0.999
<i>GyrA</i> (T86I)	133694456 7	0.999	979075588 .4	0.999	155564243 3	0.999	1236642433	1	0.207	0.171	4.0700E-09	0.999

GEN: gentamicin, ERY: erythromycin, CHL: chloramphenicol, CIP: ciprofloxacin, DC: doxycycline, TET: tetracycline, OR: Odds ratio ^a Indicates an association between antibiotics resistance and the associated-antibiotic resistance gene. ^b Indicates an association between antimicrobial susceptibility and the associated-antibiotic resistance gene. Antimicrobial resistance is defined as an OR > 1 and *p* < 0.05, and antimicrobial susceptibility is defined as an OR < 1 and *p* < 0.05.

Table S3. Relationship between Susceptibility/resistance Patterns and Associated Virulence Genes in *C. coli* isolates.

	GEN		ERY		CHL		DC		TET	
	OR	p-value	OR	p-value	OR	p-value	OR	p-value	OR	p-value
<i>cheA</i>	756362537.1	1	1150324865	1	323618950.7	1	1263792058	1	0	1
<i>Cj1135</i>	1.017	0.982	0.251	0.166	0.897	0.88	0.037 ^b	0.001	0.547	0.514
<i>htrB</i>	2.341	0.602	0.053	0.094	1.986	0.643	9.017	0.153	180178356.7	0.999
<i>kpsM</i>	0.09 ^b	0.002	0.098 ^b	0.003	0.167 ^b	0.035	0.307	0.102	2.279	0.472
<i>flaA</i>	0	1	0	1	0	1	0	1	0	1
<i>flaB</i>	311040269.3	1	221852055.5	1	1343515266	1	633182942.5	1	322034793.9	1

GEN: gentamicin, ERY: erythromycin, CHL: chloramphenicol, DC: doxycycline, TET: tetracycline, OR: Odds ratio ^a Indicates an association between antibiotics resistance and the associated-virulence

gene. ^b Indicates an association between antimicrobial susceptibility and the associated-virulence gene. Antimicrobial resistance is defined as an OR > 1 and $p < 0.05$, and antimicrobial susceptibility is defined as an OR < 1 and $p < 0.05$.

Table S4. Relationship between Susceptibility/resistance Patterns and Associated Virulence genes in *C. jejuni* isolates.

	GEN		ERY		CHL		CIP		DC		TET	
	OR	<i>p</i> -value	OR	<i>p</i> -value	OR	<i>p</i> -value	OR	<i>p</i> -value	OR	<i>p</i> -value	OR	<i>p</i> -value
<i>porA</i>	0.41	0.208	0.296	0.142	0.412	0.196	3.942	0.216	0.832	0.777	0.227	0.226
<i>Cj1135</i>	5.139 ^a	0.036	23.801 ^a	0.009	2.659	0.156	13.316	0.38 ^a	1.345	0.636	10.214 ^a	0.017
<i>kpsM</i>	0.942	1	258777806 7	1	0.703	1	0.532	1	162005081 4	1	1.91	1
<i>NeuA1</i>	0.843	0.909	0.818	0.905	0.814	0.889	93267465.85	0.999	153139466 9	0.999	87609726.9 3	0.999
<i>wlaN</i>	0.843	0.909	0.818	0.905	0.814	0.889	93267465.85	0.999	153139466 9	0.999	87609726.9 3	0.999
<i>flaA</i>	1.129	0.838	0.39	0.154	2.214	0.171	6.430	0.136	0.994	0.992	0.338	0.263
<i>flaB</i>	1.129	0.838	0.39	0.154	2.214	0.171	6.430	0.136	0.994	0.992	0.338	0.263
<i>cdtA</i>	0	0.999	0.665	0.787	0	0.999	0	0.999	0.965	0.98	0	0.999
<i>cdtB</i>	2.4579E+1 8	0.999	258778147 3	1	1.8347E+1 8	0.999	0.532	1	162005095 6	1	1.91	1
<i>cdtC</i>	2.4579E+1 8	0.999	258778147 3	1	1.8347E+1 8	0.999	57886525.14 0	1	162005095 6	1	1.91	1

GEN: gentamicin, ERY: erythromycin, CHL: chloramphenicol, DC: doxycycline, TET: tetracycline, OR: Odds ratio ^a Indicates an association between antibiotics resistance and the associated-virulence gene. ^b Indicates an association between antimicrobial susceptibility and the associated-virulence gene. Antimicrobial resistance is defined as an OR > 1 and $p < 0.05$, and antimicrobial susceptibility is defined as an OR < 1 and $p < 0.05$.

Table S5. Reference ARGs sequences used in this study.

ID	ARG	Sequence (5'-3')
M13771	<i>aac(6')-aph(2'')_1</i>	ATGAATATAGTTGAAAATGAAATATGTATAAGAACCTTTAATAGATGATGATTTTCCTTTGATGTTAAAATGGTAACT GATGAAAGAGTATTAGAATTTTATGGTGGTAGAGATAAAAAATATACATTAGAATCATTAAAAAACATTATACAG AGCCTTGGAAGATGAAGTTTTAGAGTAATTATTGAATATAACAATGTTTCCTATTGGATATGGACAAATATATAAA ATGTATGATGAGTTATATACTGATTATCATTATCCAAAACTGATGAGATAGTCTATGGTATGGATCAATTTATAGG AGAGCCAAATTATTGGAGTAAAGGAATTGGTACAAGATATATTAAATTGATTTTTGAATTTTGAAAAAAGAAAGA AATGCTAATGCAGTTATTTAGACCCTCATAAAAAATAATCCAAGAGCAATAAGGGCATACCAAAAAATCTGGTTTTA GAATTATTGAAGATTTGCCAGAACATGAATTACACGAGGGCAAAAAAGAAGATTGTTATTTAATGGAATATAGATA TGATGATAATGCCACAAATGTTAAGGCAATGAAATATTTAATTGAGCATTACTTTGATAATTTCAAAGTAGATAGTA TTGAAATAATCGGTAGTGGTTATGATAGTGTGGCATATTTAGTTAATAATGAATACATTTTTAAACAAAATTTAGTA CTAATAAGAAAAAAGGTTATGCAAAAGAAAAAGCAATATATAATTTTTTAAATACAAATTTAGAACTAATGTAAA AATTCCTAATATTGAATATTCGTATATTAGTGATGAATTATCTATACTAGGTTATAAAGAAATTAAGGAACCTTTTT AACACCAGAAATTTATTCTACTATGTCAGAAGAAGAACAAAATTTGTTAAAACGAGATATTGCCAGTTTTTAAAGAC AAATGCACGTTTAGATTATACAGATATTAGTGAATGTACTATTGATAATAAACAAAATGTATTAGAAGAGTATATA TTGTTGCGTGAAACTATTTATAATGATTTAACTGATATAGAAAAAGATTATATAGAAAGTTTTATGGAAAGACTAAA TGCAACAACAGTTTTTGAGGGTAAAAAGTGTTTATGCCATAATGATTTTAGTTGTAATCATCTATTGTTAGATGGCAA TAATAGATTAACCTGGAATAATTGATTTTGAGATTCTGGAATTATAGATGAATATTGTGATTTTATATACTTACTTGA AGATAGTGAAGAAGAAATAGGAACAAATTTGGAGAAGATATATTAAGAATGTATGGAAATATAGATATTGAGAA AGCAAAAGAATATCAAGATATAGTTGAAGAATATTATCCTATTGAAACTATTGTTTATGGAATTAATAATATTAAC AGGAATTTATCGAAAAATGGTAGAAAAGAAATTTATAAAAGGACTTATAAAGATTGA
CP013733	<i>aadE-Cc_1</i>	ATGCAAAATCAAGATAAATTTTTAAAAACAATTTAAAAAATTAGCACTTTTAGATAAAAAATATACGCCTTGTTACACT TGAAGGCTCAAGGGTTAATAAAAAAGCGAAGAAAGATAAATATCAAGACTATGATATTTCATTTTTGTGCCACTTG ATAAAATGAAAGATTTTTTAGGGCTTAATGAAAAGCAAAATTTAACGAATGTAAAAACTTGCCAAAATGTATTTTA GAGCTTGAAAAATCTTCATATTTTAAAAAAATTTTAATGCTTCAAATGCCTGAATGTATGGAGTTTTATCCACCTGAT TTGCCACAAAATTGGATAAGTTTTTGTGCTTTTGAAGTGAGTGAGGCTTGATTAAACCATTATTCCTTTAGAA GATTTGAAAAATTACTATGAATTTGAGCCTTTAAGCCAAGCGCTTTGGATAAAAAATGGGCTTTTACGCACACTATT CCAAAAGCCCCATTTAGCATCACACACCTTAGCCAAAGAAGCTTTGATGATGTTTGCAATGAGTTTTATTTCTTTAT AGTTGCTTAAAAAAAGCTCTTTAAGAAAGCAGTTATTTTGTCAAATCATTTGCTAAATCTTTGAGAAAAGCACTT TTTGATTGCTTAGTTTTAAAATTGGCTTAAATTTTGGCTTTGAAATCTGGCTGGGAAAAGAATACACTAATATTTTA GAATTTTATAGAAAGAAAAGAAGTAAAAATCATCTTAAATCTTTTAAACCCGCCACGCTAGAACACATCAAAAAA GCAAGAAAAAAGCTTGAAATTTATTTTCAAAAAATGCTAAATTTGTAGCAAAAAAGAGTGATTTTAAAGCTTTTTCC TTACCGAAAAAATGTGAAAAGGTATTGTAAAATTTTAGGAAAATTGTAA

AF330699	<i>ant(6)-Ia_1</i>	<p>ATGAGATCAGAAAAAGAAATGATGGATTTAGTACTTTCTTTAGCAGAACAGGATGAACGTATTCTGAATTGTGACCC TTGAGGGGTCACGCGCAAATATTAATATACCTAAAGATGAATTTTCAGGATTATGATATTACATATTTTGTAAGTGAT ATAGAACCGTTTATATCTAATGATGACTGGCTTAATCAATTTGGGAATATAATAATGATGCAAAAAGCCGGAGGATAT GGAATTATTCCCACCTGAAGAAAAGGGATTTTCCTATCTTATGCTATTTGATGATTACAATAAAATTGATCTTACCTT ATTGCCCTTGGAAGAGTTAGATAAATTACCTAAAGGGCGATAAATTAATAAAAGGTTCTAATTGATAAAGATTGTAGA ATTAAAAGGGACATAGTTCCGACTGATATAGATTATCATGTAAGAAAGCCAAGCGCAAGGGAGTATGATGATTGCT GCAATGAATTTTGGAATGTAACACCTTATGTTATTAAGGATTGTGCCGTAAGGAAATTTTATTTGCTATTGATCATT TTAATCAGATTGTTTCGCCATGAGCTGCTGAGAATGATATCATGGAAGGTCGGCATCGAAACAGGCTTTAAATTAAGT GTAGGCAAGAACTATAAGTTTATTGAAAGGTATATATCCGAGGATTTGTGGGAGAACTTTTGTCCACCTACCGGAT GGATTCCTATGAAAACATATGGGAAGCATTATTTCTATGCCATCAATTGTTTCAGGGCGGTATCCGGTGAGGTGGCGG AAAGGCTTCATTATGCCTATCCGGAGTATGATAGGAATATAACAAAATATACCAGGGACATGTATAAAAAATACAC TGGTAAAACCGGCTGCCTGGATAGCACATATGCCGCTGATATAGAAGAGAGGCGGGAACAGTGA</p>
KF864551	<i>ant(6)-Ia_3</i>	<p>ATGAGATCAGAAAAGGAAGTTTATGATATTGTTTTGAATTTTGCAAAAACAGACAAACGCATTTCGCATGGTTACTTT GGAAGGATCTAGAACAAATACAAATATTCGCGCTGATGATTTTCAGGATTTTGATATTACTTTTTTTGTTACGGATAT GGACAGCTTCACAAGTGATGATAAATGGCTAGATATATTTGGTGAAAGGTTGATTCTGCAAAAGCCGGAAGATATG GAATTATTTCCAGCTGTAGAAAAGGGATTTTCATATTTAATGCTGTTTACTGATGATGTTAAGATAGATTAACTTTG CTGCCGCTGGAAGTATAGACGAGTATTTTACATGGGATAAACTGGTAAAGTTACTGTTGGATAAAGACAACCGTA TCGTAAAGCCGCCAATACCAACGGATATAGACTACCACTTGCAGAAGCCTACTCAAAGAATGTTTGACGATTGCTG TAATGAATTTTGGAATACTACAACATATGTAGTAAAGGGCTTATGCCGCAAAAGAAATTCCTTTTTGCTATTGACCATAT GAATGATATAGTACGAAAAGAATTGCTTCGCATGATTTCTGGCTGATTGGTATCAAACAGGGATTTTCATTTTCAGTTT GGGAAAAAACTATAAATTTATGAAGCAATATGTCCCAGAGGAATTGTGGGAACGACTTATGTCCACTTATAATATG GATTCCTATCCCCATATGTGGGAATCCTTTGAACAATGTATGGCATTGTTCCGGGAGGTTTCGTCAGAAGTGGCATG CCAGTTGGATTACCAGTATCCACTATATGATGAAAAAATCAGTAATTATGTGATTCCGGCAAAAGAAAAAATATGGC ATTGAAGATGATAACAAATAA</p>
AY701528	<i>aph(2'')-If_2</i>	<p>ATGGATATAAAAAAGATAATAGAAGAAAAATGCAATATAGTTGTTGATAGTATAAAAGTTGATTGGTGAGGGTTATG ACAGCAAAGCATACATTGTAAATAATGAATATGTTTTCAAAATCAAATTTAGTGCTAATAAGAAAAAAGGGTATGA AAAAGAAAAAGCAATATATGATTTTCTAAACAAAAAATTAATAACAAATATTAATAATACCAATATAGAATATTCA TATATAAGTGAAGAATTATCTATTTTAGGATATAAAGAAATTAAGGAACCTTTTTTAACACCAGAAATATATTTTGC CTTATCAAAAGAAAAGCAAGAATTATTAAGCAAGATATTGCTATGTTTTTAAGACAAATGCACGATTTAGATTATA GTGAAATAAGTTCATATACGATAGACAATAAACAAAATGTTTTAGAAGAATATCAATTACTTAAAGAAACAATATA TGATAGTCTTACTGATATTGAAAAACAATATGTAGAAGAATTTATGCAAAGATTAAATAGTACAACCTATATTTGATG GTAAAAAATGCTTATGCCATAATGATTTTAGTTGTAATCATTTATTACTTGATGATGAAAAATAGATTATGTGGTGTA TAGATTTTGGAGATTCTGGAATTATAGATGAATACTGTGATTTTCATATATTTGCTAGAAGATAGTGAAGAAGAAATT</p>

		GGCGTGTCTTTTGGAGAAGATATATTAAGATTATACGGAAATATTGATATTTCAAAGCAAAGGAATATCAAGATGT TGTAACAATATTATCCAATAGAACTATTGTATATGGTATTAATAATAGACCTGATTTTATAGAAAAAGGTA GAAAAGAGATTTATATAAGAACTCGCAAAGATGAAAAATTAAGGAAGTGA
M26832	<i>aph(3')-III_1</i>	ATGGCTAAAATGAGAATATCACCGGAATTGAAAAAACTGATCGAAAAATACCGCTGCGTAAAAGATACGGAAGGA ATGTCTCCTGCTAAGGTATATAAGCTGGTGGGAGAAAATGAAAACCTATATTTAAAAATGACGGACAGCCGGTATA AAGGGACCACCTATGATGTGGAACGGGAAAAGGACATGATGCTATGGCTGGAAGGAAAGCTGCCTGTTCCAAAGG TCCTGCACTTTGAACGGCATGATGGCTGGAGCAATCTGCTCATGAGTGAGGCCGATGGCGTCCTTTGCTCGGAAGAG TATGAAGATGAACAAAGCCCTGAAAAGATTATCGAGCTGTATGCGGAGTGCATCAGGCTCTTTCCTCCATCGACA TATCGGATTGTCCCTATACGAATAGCTTAGACAGCCGCTTAGCCGAATTGGATTACTTACTGAATAACGATCTGGCC GATGTGGATTGCGAAAACCTGGGAAGAAGACACTCCATTTAAAGATCCGCGCGAGCTGTATGATTTTTTAAAGACGG AAAAGCCCGAAGAGGAACTTGTCTTTTCCACGGCGACCTGGGAGACAGCAACATCTTTGTGAAAGATGGCAAAGT AAGTGGCTTTATTGATCTTGGGAGAAGCGGCAGGGCGGACAAGTGGTATGACATTGCCTTCTGCGTCCGGTTCGATCA GGGAGGATATCGGGGAAGAACAGTATGTCGAGCTATTTTTTGACTTACTGGGGATCAAGCCTGATTGGGAGAAAAT AAAATATTATATTTTACTGGATGAATTGTTTTAG
JQ396378	<i>bla_{OXA-184}_1</i>	TTGAAAAAATACTTTTACTTTTTAGTCTTTTTTACTCTTTTGCTTTGGCAAATGATAAATTAAGATTTTTTTAAAG ACTACAATACAAGCGGAGTTTTTATAACTTTTGATGGAAAACATTATGCAAGTAATAATTTTAAAGAGCTAAAGA ACCTTTTTCTCCTGCTTCGACTTTTAAATTTTTAATGCTTTAATTGCGCTTGATAATGGTGTAGTTAAAGATACAAAG GAAATTTTTATCATTATAAGGGTGAAAAAGTATTTTTGCCCTCTTGGAACAAGATGCTAGTTTAAAGCTCAGCCATA AAACGCTCTCAAGTGCCTGCTTTTAAAGAATTGGCAAGAAAAATAGGACTTAAAACCATGCAAGAAAGCTTAAATA AACTTTCCTATGGAAATACAAAAATTTCAAAAATCGATACCTTTTGGTTGGATAATTCTTTACAAATTTCTGCAAAAA ATCAAGCTGATTTGCTTTTTTAACTTTACAAAAATTCTTTACCTTTTTCCAAGAAAAGTCAAGAAGAAGTTAAAAAA ATTATTCTTTTTAAAGAAGATAAAATCCAAAAATTTATGCTAAAACAGGTTTTAATGATGGTATAAATTTGGCTTG GATTGTTGGATTTATAGAGAGTAAAAACAAAATTTTATCTTTTGCTTAAATGTTGATATAAAGAACATTAAAAATC TTAAAATAAGAGAAGAATTGCTAGAAAAATATATTTATCTTTAAACTAA
JQ396379	<i>bla_{OXA-185}_1</i>	TTGAAAAAATACTTTTACTTTTTAGTCTTTTTTACTCTTTTGCTTTGGCAAATGATAAATTAAGATTTTTTTAAAG ACTACAATACAAGCGGAGTTTTTATAACTTTTGATGGAAAACATTATGCAAGTAATAATTTTAAAGAGCTAAAGA ACCTTTTTCTCCTGCTTCGACTTTTAAATTTTTAATGCTTTAATTGCGCTTGATAATGGTGTAGTTAAAGATACAAAG GAAATTTTTATCATTATAAGGGTGAAAAAGTATTTTTGCCCTCTTGGAACAAGATGCTAGTTTAAAGCTCAGCCATA AAACGCTCTCAAGTGCCTGCTTTTAAAGAATTGGCAAGAAAAATAGGACTTAAAACCATGCAAGAAAGCTTAAATA AACTTTCCTATGGAAATACAAAAATTTCAAAAATCGATACCTTTTGGTTGGATAATTCTTTACAAATTTCTGCAAAAA ATCAAGCTGATTTGCTTTTTTAACTTTACAAAAATTCTTTACCTTTTTCCAAGAAAAGTCAAGAAGAAGTTAAAAAA ATTATTCTTTTTAAAGAAGATAAAATCCAAAAATTTATGCTAAAACAGGTTTTAATGATGGTATAAATTTGGCTTG

	<p>GATTGTTGGATTTATAGAGAGTAAAAACAAAATTTTATCTTTTGCCTTAAATGTTGATATAAAGAACATTAAAAATA TTAAAATAAGAGAAGAATTGCTAGAAAAATATATTTATTCTTTAACTAA</p>
CP013032 <i>bla_{OXA-193_1}</i>	<p>ATGAAAAAATAACTTTATTTTTGCTTTTCTTAAATTTAGTGTTTGGGCAAGATAAGATATTAAATAATTGGTTTAAA GAGTATAATACAAGCGGCACCTTTTGTTTTTATGATGGAAAAACTTGGGCGAGTAACGACTTTTCAAGGGCTATGGA GACTTTCTCTCCCGCTTCCACTTTTAAAATTTTAAATGCTCTAATTGCACCTGATAGTGGTGTGATAAAAACTAAAAA AGAAATTTTTATCACTATAGAGGTGAAAAAGTATTTTTATCTTCTTGGGCGCAAGATATGAATTTAAGTTCAGCTAT AAAATATTCTAATGTTCTTGCTTTTAAAGAAGTGGCAAGAAGAATTGGTATCAAAACTATGCAAGAATATTTAAACA AGCTTCATTATGGTAATGCTAAAATTTCCAAGATCGATACTTTTTGGCTTGACAACCTCACTAAAAATAAGCGCTAAA GAACAAGCAATTTTGCTTTTATAGACTTTTACAAAATAGCTTACCTTTTTCTCAAGAAGCAATGAATAGTGTTAAGGA AATGATTTATTTAAAAAATATGGAAAATTTAGAGCTTTTTGGAAAAACAGGTTTTAATGATGAGCAAAAAAATTGCTT GGATTGTAGGTTTTGTGTATTTAAAAGATGAAAATAAATATAAGGCTTTCGCGCTAAATTTAGATATTGATAAATTTG AAGATTTATATAAAAGAGAAAAAATTTTAGAAAAATATTTAGATGAACTTGTAaaaaaaAGTTAAAAATGATGGCTA G</p>
KR061500 <i>bla_{OXA-465_1}</i>	<p>TTGAAAAAATACTTTTACTTTTTAGTCTTTTTACTCTTTTGTCTTTGGCAAATGATAAATTAAAAGATTTTTTTAAAG ACTACAATACAAGCGGAGTTTTTATAACTTTTGATGGAAAACATTATGCAAGTAATGATTTTAAAAGAGCTAAAGA ACCTTTTTCTCCTGCTTCGACTTTTAAAATTTTAAATGCTTTAATTGCGCTTGATAACGGTGTAGTTAAAGATACAAAG GAAATTTTTATCATTATAAGGGTGAAAAAGTATTTTTGCCTTCTTGGAACAAGATGCTAGTTTAAAGCTCAGCCATA AAACGCTCTCAAGTGCCTGCTTTTAAAGAATTGGCAAGAAAAATAGGACTTAAAACCATGCAAGAAAGCTTAAATA AACTTTCCTATGGAAATGCAAAAATTTCAAAAATCGATACCTTTTGGTTGGATAATTCTTTACAAATTTCTGCAAAAA ATCAAGCTGATTTGCTTTTTAACTTTTCAAAAATTTCTTTACCTTTTTCCAAGAAAAGTCAAGAAGAAAGTTAAAAAA ATTATTCTTTTTAAAGAAGATAAAATCCAAAAAATTTATGCTAAAACAGGTTTTAATGATGGTATAAATTTGGCTTG GATTGTCGGATTTATAGAGAGTAAAAACAAAATTTTATCTTTTGCCTTAAATGTTGATATAAAGGACATTAAAAATA TTAAAATAAGAGAAGAATTGCTAGAAAAATATATTTATTCTTTAACTAA</p>
CP013733 <i>bla_{OXA-489_1}</i>	<p>ATGAAAAAATAACTTTATTTTTACTTTTCTTAAATTTAGTGTTTGGGCAAGATAAGATATTAAATAATTGGTTTAAA GAGTATAATACAAGCGGCACCTTTTGTTTTTATGATGGAAAAACTTGGGCGAGTAACGACTTTTCAAGGGCTATGGA GACTTTCTCTCCCGCTTCCACTTTTAAAATTTTAAATGCTCTAATTGCACCTGATAGTGGTGTGATAAAAACTAAAAA AGAAATTTTTATCACTATAGAGGTGAAAAAGTATTTTTATCTTCTTGGGCGCAAGATATGAATTTAAGTTCAGCTAT AAAATATTCTAATGTTCTTGCTTTTAAAGAAGTGGCAAGAAGAATTGGTATCAAAACTATGCAAGAATATTTAGACA AGCTTCATTATGGTAATGCTAAAATTTCCAAGATCGATACTTTTTGGCTTGACAACCTCACTAAAAATAAGCGCTAAA GAACAAGCAATTTTGCTTTTATAGACTTTTACAAAATAGCTTACCTTTTTCTCAAGAAGCAATGAATAGTGTTAAGGA AATGATTTATTTAAAAAATATGGAAAATTTAGAGCTTTTTGGAAAAACAGGTTTTAATGATGAGCAAAAAAATTGCTT GGATTGTAGGTTTTGTGTATTTAAAAGATGAAAATAAATATAAGGCTTTCGCGCTAAATTTAGATATTGATAAATTTG</p>

		AAGATTTATATAAAAGAGAAAAAATTTTAGAAAAATATTTAGATGAACTTGTAaaaaaAGTTAAAAATGATGGCTA
		G
M35190	<i>cat_2</i>	ATGCAATTCACAAAGATTGATATAAAATAATTGGACACGAAAAGAGTATTTGACCACTATTTTGGCAATACGCCCTG CACATATAGTATGACGGTAAAACCTCGATATTTCTAAGTTGAAAAAGGATGGAAAAAAGTTATACCCAACCTCTTTAT ATGGAGTTACAACGATCATCAATCGACATGAAGAGTTCAGGACCGCATTAGATGAAAACGGACAGGTAGGCGTTTT TTCAGAAATGCTGCCTTGCTACACAGTTTTTCATAAGGAAACTGAAACCTTTTCGAGTATTTGGACTGAGTTTACAGC AGACTATACTGAGTTTCTTCAGAACTATCAAAAGGATATAGACGCTTTTGGTGAACGAATGGGAATGTCCGCAAAG CCTAATCCTCCGGAaaACACTTTCCCTGTTTCTATGATACCGTGGACAAGCTTTGAAGGCTTTAACTTAAATCTAAAA AAAGGATATGACTATCTACTGCCGATATTTACGTTTGGGAAGTATTATGAGGAGGGCGGAAAAATACTATATTCCCTT ATCGATTCAAGTGCATCATGCCGTTTGTGACGGCTTTCATGTTTGCCGTTTTTTGGATGAATTACAAGACTTGCTGAAT
		AAATAA
X66468	<i>erm(B)_18</i>	ATGTATCACTTCAGGAGTGATTACATGAACAAAAATATAAAATATTCTCAAAACTTTTTAACGAATGAAAAGGTACT CAACCAAATAAATAAAACAATTGAATTTAAAAGAAACCGATACCGTTTACGAAATTGGAACAGGTAAAGGGCATTT AACGACGAAACTGGCTAAAATAAGTAAACAGGTAACGTCTATTGAATTAGACAGTCATCTATTCAACTTATCGTCA GAAAAATTAAACTGAACATTCGTGTCACTTTAATTCACCAAGATATTCTACAGTTTCAATTCCTAACAAACAGAG GTATAAAATTGTTGGGAATATTCCTTACCATTTAAGCACACAAATTATTAaaaaaAGTGGTTTTTGAAAGCCATGCCGT CTGACATCTATCTGATTGTTGAAGAAGGATTCTACAAGCGTACCTTGGATATTCACCGAACACTAGGGTTGCTCTTG CACACTCAAGTCTCGATTGAGCAATTGCTTAAGCTGCCAGCGGAATGCTTTCATCCTAAACCAAAAGTAAACAGTGT CTTAATAAAACTTACCCGCCATACCACAGATGTTCCAGATAAATATTGGAAGCTATATACGTACTTTGTTTCAAAT GGGTCAATCGAGAATATCGTCAACTGTTTACTAAAAATCAGTTTCATCAAGCAATGAAACACGCCAAAGTAAACAA TTTAAGTACCGTTACTTATGAGCAAGTATTGTCTATTTTAAATAGTTATCTATTATTTAACGGGAGGAAATAA
AJ549214	<i>fexA_1</i>	AATGAAAAAGGATAGTAAATCTAAAGAAATGATTCAATCTGAAAAAAGGGGTCTACTAGGCTTTTAATGATGGTA CTCTCCCTATCTGTACTTGTAGGTGCAATTACGGCTGATTTAGTCAATCCCGTACTTCCACTAATAAGCAAAGATTTA GAAGCTTCGAAATCTCAAGTGAGTTGGATAGTTAGTGGTATTGCACATTGTTCTTGCGATTGGAGTCCGATTTATGGT CGAATCTCAGACTTTTTTGAGTTACGAAAGCTATATATCTTTGCCATTATGATTCTGGCAAGTGGTAGTCTTTTATGTG CAATTGCCCCGAACCTCCCATTGTTGGTTTTGGGAAGAATGGTTCAGGGTGCTGGGATGTCCGCAATTCCAGTTCTAT CAATCATTGCAATTTTCGAAGGTTTTCCACAAAGGAAAACGTGGGGGAGCTTTGGGAATTATCGCAGGAAGTATTGGT GTTGGAACTGCTGCTGGTCCAATATTTGGTGGAGTAGTTGGTCAATATTTAGGGTGGAATGCCTTGTTTTGGTTCACA TTTTTGTTAGCCATTATGATTGTTATTGGTGCCTACTACGCGTTACCGACAATTAAACCGGCAGAATCCGTAGGAAGC AATAAGAACTTTGATTTCAATTGGTGGTTTATTCTCGGCCTCACAGTAGGATTACTCCTTTTTGGCATCACTCAAGGA GAAACTTCTGGTTTTTCTTCGTTCTCATCGTTAACTAGCCTAATTGGTTCGTGTGTAGCTTTGGTGGGATTTATTTGGAG AATTGTTACCGCAGAAAATCCATTTGTACCACCTGTCCTGTTCAATAACAAGGATTATGTCAATACGGTCATAATTG CATTTTTTTCGATGTTTGCTTATTTTCGCTGTTCTTGTGTTTCGTCCTTACTAGTCGTTGAGGTGAATGGACTCTCTCT

M29725	<i>tet(L)_2</i>	<p>GGACAGGCTGGAATGATATTGTTGCCAGGTGGTGTGGCTGTTGCAATCTTATCTCCCTTCGTTGGCCGTCTTTCTGAT CGATTTGGGGATAAACGTCTGATAATTACTGGGATGACTCTGATGGGGCTGTCTACCTTATTCTTGTCCACCTATGCA TCTGGTGCCTTACCTCTGTTAGTTTCCGTGGGGGTCCTCGGAGTAGGGATTGCTTTTGCATTACGAATTCTCCCGCA AATAACGCCGCAGTAAGTGCACCTCGATGCAGACAAGGTTGGTGTCCGAATGGGGATTTTCCAAGGTGCTTTGTACCT TGGAGCAGGAAGTGGAGCAGGTATGATTGGAGCATTATTATCCGCTCGACGTGATGCTACTGAGCCGATAAATCCA TTATATATATTGGACGCTATGTCCTACTCAGATGCGTTCCTTGCAGCTACAGGGGCAATACTCATTGCCTTAATAGCT GGATTAGGTTTAAAAAAGCGTGGGTAA</p>
M29725	<i>tet(L)_2</i>	<p>GTGAATACATCCTATTCACAATCGAATTTACGACACAACCAAATTTTAATTTGGCTTTGCATTTTATCTTTTTTTAGCG TATTAAATGAAATGGTTTTGAACGTCTCATTACCTGATATTGCAAATGATTTTAATAAACCACCTGCGAGTACAAAC TGGGTGAACACAGCCTTTATGTTAACCTTTTCCATTGGAACAGCTGTATATGGAAAGCTATCTGATCAATTAGGCATC AAAAGTTACTCCTATTTGGAATTATAATAAATTGTTTCGGGTCGGTAATTGGGTTTGTGGCCATTCTTTCTTTTCT TACTTATTATGGCTCGTTTTATTCAAGGGGCTGGTGCAGCTGCATTTCCAGCACTCGTAATGGTTGTAGTTGCGCGCT ATATTCCAAAGGAAAATAGGGGTAAAGCATTGGTCTTATTGGATCGATAGTAGCCATGGGAGAAGGAGTCGGTCC AGCGATTGGTGAATGATAGCCATTATATTCAATTGGTCCTATCTTCTACTCATTCCCTATGATAACAATTATCACTGTT CCGTTTCTTATGAAATTATTAAAGAAAGAAGTAAGGATAAAAGGTCATTTTGATATCAAAGGAATTATACTAATGTC TGTAGGCATTGTATTTTTTATGTTGTTTACAACATCATATAGCATTTCCTTTCTTATCGTTAGCGTGCTGTCATTCCCTGA TATTTGTAAAACATATCAGGAAAGTAACAGATCCTTTTGTTGATCCCGGATTAGGGAAAAATATACCTTTTATGATT GGAGTTCTTTGTGGGGGAATTATATTTGGAACAGTAGCAGGGTTTGCTCTATGGTTCCTTATATGATGAAAGATGTT CACCAGCTAAGTACTGCCGAAATCGGAAGTGTAATTATTTCCCTGGAACAATGAGTGTCAATTATTTCCGGCTACATT GGTGGGATACTTGTTGATAGAAGAGGTCCTTTATACGTGTTAAACATCGGAGTTACATTTCTTCTGTTAGCTTTTTAA CTGCTTCCTTTCTTTTAGAAACAACATCATGGTTCATGACAATTATAATCGTATTTGTTTTAGGTGGGCTTTCGTTTAC CAAAACAGTTATATCAACAATTGTTTCAAGTAGCTTGAAACAGCAGGAAGCTGGTGCTGGAATGAGTTTGCTTAAC TTACCAGCTTTTTATCAGAGGGAACAGGTATTGCAATTGTAGGTGGTTTATTATCCATACCCTTACTTGATCAAAGGT TGTTACCTATGGAAGTTGATCAGTCAACTTATCTGTATAGTAATTTGTTATTACTTTTTTCAGGAATCATTGTCATTAG TTGGCTGGTTACCTTGAATGTATATAAACATTCTCAAAGGGATTCTAA</p>
M18896	<i>tet(O)_1</i>	<p>ATGAAAATAATTAACCTTAGGCATTCTGGCTCACGTTGACGCAGGAAAGACAACATTAACGGAAAGTTTATTGTATA CCAGTGGTGCAATTGCAGAACTAGGGAGCGTAGATGAAGGCACAACAAGGACAGATACAATGAATTTGGAGCGTC AAAGGGGAATCACTATCCAGACAGCAGTGACATCTTTTCACTGGGAGGATGTAAAAGTCAACATTATAGATACGCC AGGCCATATGGATTTTTTGGCGGAAGTATACCGTCTTTATCCGTATTAGACGGAGCAGTATTATTAGTTTCTGCAAA GGATGGCATAACAGGCACAGACCCGTATACTGTTTCATGCACTACAGATAATGAAGATTCCGACAATTTTTTTCATCA ATAAAATTGACCAAGAGGGGATTGATTTGCCAATGGTATATCGGGAAATGAAAGCAAAGCTTTCTTCGGAAATTAT AGTGAAGCAAAGGTTGGGCAGCATCCCCATATAAATGTAACGGACAATGACGATATGGAACAGTGGGATGCGGT AATTATGGGAAACGATGAACATTAGAGAAATATATGTCAGGGAAACCGTTTAAAATGTCAGAACTGGAACAGGA</p>

AGAAAACAGGAGATTCCAAAACGGAACGTTATTTCCCGTTTATCACGGAAGCGCTAAAAACAATCTGGGGACTCGG
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CGATACAGCCTGCTCTGGTGATATTGTAATTTTACCAAATGATGTTTTGCAGCTAAACAGTATTTTGGGGAACGAAA
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ACAGCGGGAATATTGCTTGGGGCACTTACAGAAATTCAGATTGCGACCCTCTTTTAAAAATATTATGTGGATACTA
CAACGCATGAGATTATACTTTCTTTTTTGGGGAATGTGCAGATGGAAGTCATTTGTGCCATCCTTGAGGAAAAATAT
CATGTGGAGGCAGAAATAAAAAGAGCCTACTGTTATATATATGGAAAGACCGCTTAGAAAAGCAGAATATACCATC
CACATAGAAGTCCCGCCAAATCCTTTCTGGGCTTCTGTGCGGTTGTCCATAGAGCCGCTCCCTATTGGAAGCGGAGT
GCAGTATGAAAGCAGAGTTTCACTTGGATATTTAAATCAATCGTTCCAAAATGCGGTTATGGAGGGGGTTCTTTATG
CCTGCGAGCAGGGGCTGTATGGATGGAAAAGTGACAGACTGTAAAATCTGTTTTGAATATGGATTGTATTATAGTCTT
GTAAGTACCCCCGCAGACTTTTCGGCTGCTTTCCCTATCGTATTGGAGCAGGCTTTAAAAAAGCAGGGACAGAAC
TATTAGAGCCATATCTCCACTTTGAAATTTATGCACCGCAGGAATATCTCTCACGGGCGTATCATGATGCTCCAAGG
TATTGTGCAGATATTGTAAGTACTCAGATAAAGAATGACGAGGTCAATCTGAAAGGAGAAAATCCCTGCTAGATGTA
TTCAAGAATACAGGAACGATTAACTTATTTACAAAATGGGCAGGGAGTCTGCTTGACAGAGTTAAAAGGATACCA
GCCAGCTATTGGTAAATTTATTTGCCAACCCCGCGCCCGAATAGCCGTATAGATAAGGTTCCGCATATGTTCCACA
AGTTAGCTTAA

M20925 *tet(O)_2*

ATGAAAATAATTAACCTTAGGCATTCTGGCTCACGTTGACGCAGGAAAAGACAACATTAACGGAGAGTTTATTGTATA
CCAGTGGTGCAATTGCAGAACCAGGGAGCGTAGATAAAGGCACAACAAGGACAGATACAATGAATTTGGAGCGTC
AAAGGGGAATCACTATCCAGACAGCAGTGACATCTTTTCAGTGGGAGGATGTAAAAGTCAACATTATAGATACGCC
AGGCCATATGGATTTTTTGGCGGAAGTATACCGTCTTTATCCGTATTAGACGGAGCAGTATTATTAGTTTCTGCAA
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AGAAAACAGGAGATTCCAAAACGGAACGTTATTTCCCGTTTATCACGGAAGCGCTAAAAACAATCTGGGGATTCCG
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TAAGATTGAATATTCAGAGAAAAGGCGGCGTTTTGTTTATGTGCGTATATATAGCGGAACATTGCATTTGAGGGATG
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CGATACAGCCTGCTCTGGTGATATTGTAATTTTACCAAATGATGTTTTGCAGCTAAACAGTATTTTGGGGAACGAAA
TACTGTTGCCGCAGAGAAAATTTATTGAAAATCCTCTCCCTATGCTCCAAACAACGATTGCAGTAAAGAAATCTGAA
CAGCGGGAATATTGCTTGGGGCACTTACAGAAATTCAGATGGCGACCCTCTTTTAAAAATATTATGTGGATACTAC
AACGCATGAGATTATACTTTCTTTTTTGGGGAATGTGCAGATGGAAGTCATTTGTGCCATCCTTGAGGAAAAATATC

ATGTGGAGGCAGAAATAAAAGAGCCTACTGTTATATATATGGAAAGACCGCTTAGAAAAGCAGAATATACCATCC
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CAGTATGAAAGCAGAGTTTCACTTGGATATTTAAATCAATCGTTCCAAAATGCGGTTATGGAGGGGGTTCTTTATGG
CTGCGAGCAGGGGCTGTATGGATGGAAAGTGACAGACTGTAAAATCTGTTTTGAATATGGATTGTATTATAGTCCTG
TAAGTACCCCCGCAGACTTTTCGGCTGCTTTCCCCTATCGTATTGGAGCAGGCTTTAAAAAAGCAGGGACAGAACT
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ATTGTGCAGATATTGTAAGTACTCAGATAAAGAATGACGAGGTCATTCTGAAAGGAGAAATCCCTGCTAGATGTAT
TCAAGAATACAGGAACGATTAACTTATTTACAAATGGGCAGGGAGTCTGCTTGACAGAGTTAAAAGGATACCAG
CCAGCTATTGGTAAATTTATTTGCCAACCCCGCCGCCGAATAGCCGTATAGATAAGGTTCCGCATATGTTCCACAA
GTTAGCTTAA

All reference sequences were extracted from resfinder database on webpage https://bitbucket.org/genomicepidemiology/resfinder_db (updated before May 27 2024).

Table S6. The interpretative standards for antibiotic resistance used in this study.

Antibiotics	<i>C.jejuni/C. coli</i>		
	Susceptible	Intermediate	Resistant
Ciprofloxacin ^a	≤1	2	≥4
Erythromycin ^a	≤8	16	≥32
Doxycycline ^a	≤2	4	≥8
Tetracycline ^a	≤4	8	≥16
Chloramphenicol ^b	≤16	-	≥32
Gentamicin ^b	≤2	-	≥4

^a From Clinical and Laboratory Standard Institute (CLSI, M45-A3) ^b From EUCAST epidemiological cut-off values (ECOFFs), with wild type as susceptible and non-wild type as resistant. (https://www.eucast.org/mic_and_zone_distributions_and_ecoffs, accessed on 27 May 2024).