

1 **TABLE S1** *C. jejuni* and *C. coli* isolates screened for *erm*(B) in this study

Year of isolation	2001		2007		2008			2009			2011		2012					
Province/city of isolation	Beijing		Jilin	Henan	Shandong		Ningxia	Shandong			Shandong	Shanghai	Shandong		Ningxia	Guangdong		
Host <sup>b</sup>	H		H	H	S	C	S	S	C	D	CC	H	S	D	S	C	S	C
No. of <i>C. coli</i>	5	1	3	94	18	95	133	36	27	18	66	68	89	209	17	184	94	
No. of <i>C. jejuni</i>	0	0	0	0	69	2	0	149	93	12	0	0	18	3	16	1	34	
Total No. of <i>Campylobacter</i>	5	1	3	94	87	97	133	185	120	30	66	68	107	212	33	185	128	
No. of <i>erm</i> (B)-positive isolates	0	0	1	0	1	1	1	0	1	12	9	8	1	4	0	18	1 <sup>a</sup>	
Total No. of <i>erm</i> (B)-positive <i>Campylobacter</i> in each year	0		1			2			2		21					32		

2 <sup>a</sup> This is the *C. jejuni* isolate C179b that carries *erm*(B) and all other *erm*(B)-positive isolates are *C. coli*.

3 <sup>b</sup> The abbreviations for host species represent swine (S), chicken (C), duck (D), chicken carcasses (CC), and human (H).

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5 **TABLE S2** The percentage of *erm*(B)-positive *Campylobacter* isolates in each of the sources

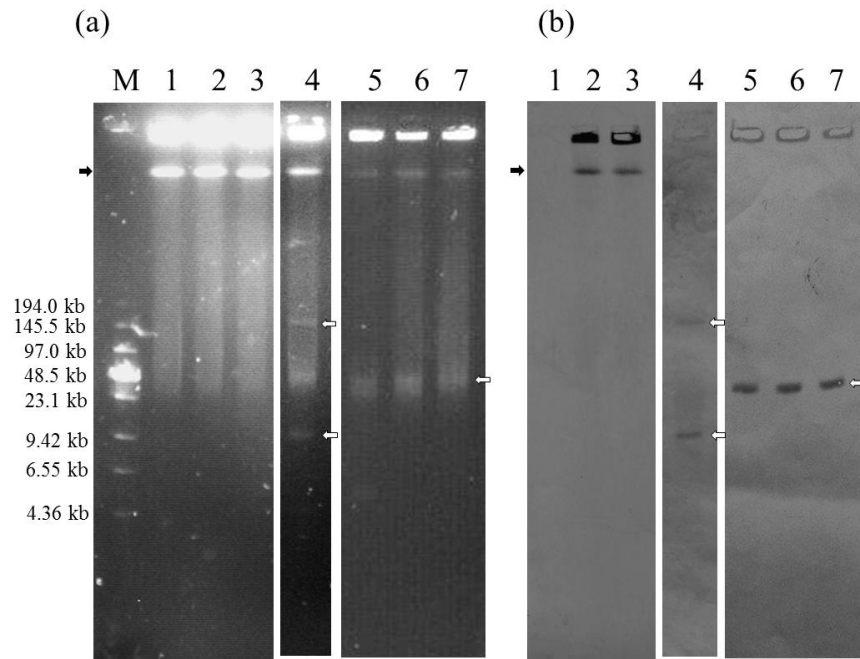
Source	Swine	Chicken	Duck	Chicken carcasses	Human
No. of <i>C. coli</i>	783	165	116	18	75
No. of <i>C. jejuni</i>	6	268	111	12	0
Total No. of <i>Campylobacter</i>	789	433	227	30	75
<i>erm</i> (B)-positive isolates	32	2	2	12	10
<i>erm</i> (B)-positive isolates/total <i>Campylobacter</i>	4.1%	0.5%	0.9%	40.0%	13.3%

6 **TABLE S3** Annotation of ORFs in the MDRGIs

Gene	Size (bp)	G+C content (%)	Length (aa) <sup>a</sup>	Length (aa) <sup>b</sup>	%Identity/%positive (no. of aa)	Annotation and accession no.
<i>aac</i>	366	24.9	121	121	100/100 (121)	Acetyltransferase, <i>Enterococcus faecalis</i> T2; ZP_05426921
<i>aacA-aphD</i>	1440	24.6-24.7	479	479	99-100/99-100 (479)	Bifunctional aminoglycoside modifying enzyme AacA-AphD, <i>Staphylococcus aureus</i> ; NP_863643
<i>orf1</i>	117	19.7	41	38	100/100 (38)	Hypothetical protein HMPREF1327_01382, partial, <i>Enterococcus faecalis</i> 599; AFJ97256
<i>aadE</i>	702	37.6	233	233	100/100 (233)	Streptomycin aminoglycoside 6-adenyltransferase, <i>Enterococcus faecalis</i> D6; ZP_05581297
<i>sat4</i>	531	37.9	176	176	100/100 (176)	Streptothricin acetyltransferase, <i>Enterococcus faecium</i> ; ZP_05674679
<i>aphA-3</i>	795	44.9	264	264	100/100 (264)	Aminoglycoside phosphotransferase type III, <i>Enterococcus faecalis</i> ; YP_783930
<i>orf2</i>	675	44.1	224	224	99/100 (224)	Hypothetical protein BSEG_01714, <i>Bacteroides dorei</i> 5_1_36, D4; ZP_08793206
<i>orf3</i>	453	41.3	150	150	99/99 (150)	Hypothetical protein BSEG_01714, <i>Bacteroides dorei</i> 5_1_36, D4; ZP_08793207
<i>Δpcp</i>	303	51.2	139	100	100/100 (100)	Pyrrolidone carboxylate peptidase, <i>Bacteroides</i> sp. 9_1_42FAA; ZP_04541315
<i>orf4</i>	429	31.7	132	142	95/97 (120)	Hypothetical protein, <i>Streptococcus suis</i> ; CBZ42064
<i>orf7</i>	420	39.6-39.8	139	139	96-97/99-100 (139)	Conserved hypothetical protein, <i>Clostridium difficile</i> NAP08; ZP_06892641
<i>erm(B)</i>	738	33.1	245	245	100/100 (245)	rRNA adenine N-6-methyltransferase, <i>Streptococcus suis</i> BM407; YP_003028697
<i>Ω</i>	216	36.1	71	71	97/100 (71)	Omega, transcriptional repressor, <i>Streptococcus agalactiae</i> MRI Z1-211; ZP_22245542
<i>ε</i>	288	28.5	90	95	99/100 (90)	Antidote of epsilon-zeta postsegregational killing system, <i>Streptococcus pyogenes</i> ; YP_232758
<i>aadE</i>	867	35.3-35.5	288	288	99-100/99-100 (288)	Putative adenylyltransferase, <i>Pediococcus acidilactici</i> ; YP_001965484
<i>orf6</i>	516	58.9	166	171	92/93(171)	Hypothetical protein HMPREF9453_00882, <i>Dialister succinatiphilus</i> YIT 11850; ZP_09546713
<i>Δtet(O)</i>	1362	39.4-39.7	639	453	97-99/98-99 (449)	Tetracycline resistant protein, <i>Campylobacter jejuni</i> subsp. <i>jejuni</i> HB93-13; ZP_01072284
<i>orf8</i>	375	33.9	178	119	55/70 (119)	Acetyltransferase, <i>Enterococcus casseliflavus</i> EC30; ZP_05646091
<i>orf9</i>	426	31.2	133	141	65/81(133)	Fosfomycin resistance protein FosX, <i>Listeria monocytogenes</i> 10403S; YP_005962817
<i>orf10</i>	255	49.8	144	84	100/100 (84)	Unknown, <i>Trueperella pyogenes</i> ; ABF72143
<i>orf11</i>	546	39.2	181	181	99/99 (181)	Hypothetical protein, <i>Pediococcus acidilactici</i> ; YP_001965499
<i>tet(O)</i>	1920	40.4	639	639	99/99 (639)	Tetracycline resistance protein, <i>Campylobacter coli</i> ; YP_063396
<i>cpp2</i>	174	36.8	57	57	100/100 (57)	Unknown of pTet plasmid, <i>Campylobacter jejuni</i> subsp. <i>jejuni</i> 81-176; YP_063447
<i>Δpnp</i>	225	40.4	256	74	100/100 (74)	Phosphorylase Pnp/Udp family protein, <i>Bacteroides</i> sp. 3_1_33FAA; ZP_06089331
<i>aad9</i>	777	35.8	258	258	100/100 (258)	Streptomycin 3'-adenylyltransferase, <i>Clostridium difficile</i> NAP08; ZP_06893323
<i>aspR</i>	312	37.2	72	103	100/100 (72)	Aspartate racemase, <i>Bacteroides</i> sp. 9_1_42FAA; ZP_04541310
<i>orf12</i>	306	57.2	157	101	97/97(91)	Conserved hypothetical protein, <i>Bacteroides</i> sp. 1_1_14; ZP_06994823
<i>orf13</i>	273	53.1	267	90	100/100 (90)	Hypothetical protein HMPREF0490_02053, <i>Lachnospiraceae</i> bacterium 4_1_37FAA; ZP_08151313
<i>cpp3</i>	549	46.1	182	182	100/100 (182)	Cpp3, recombination and DNA strand exchange inhibitor, <i>Campylobacter coli</i> LMG 9854; ZP_14129369

7 <sup>a</sup> Size of the ortholog protein. aa, amino acids.8 <sup>b</sup> Length of the peptides from the six types of MDRGIs.

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11 **FIG S1** Localization of *erm(B)* in *C. coli* by PFGE (a) and Southern hybridization (b).

12 *C. coli* ATCC33559 (lane 1), transformant g113 (lane 2), and representative *C. coli*

13 isolates including SH-CCD11C073 (Shanghai), 10-5-18 (Guangdong), JW16

14 (Ningxia), TH45 (Guangdong), DZB41 (Shandong) (lanes 3-7) are included in the

15 figure. Lane M contains Low Range PFG Marker (New England Biolabs, Beverly,

16 MA, USA). An *erm(B)*-specific probe was used for hybridization. ATCC33559 and

17 g113 are used as negative and positive controls, respectively. The figure is composed

18 of three different gels to show the chromosomal DNA and plasmids of various sizes

19 that hybridized to the *erm(B)* probe. The location of chromosomal DNA is indicated

20 by black arrows, while the locations of plasmids are indicated by white arrows.

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