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Evidence for Recent Acquisition and Successful Transmission of *bla*$_{CTX-M-15}$ in *Salmonella enterica* in South Korea

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We identified two distinct *bla*$_{CTX-M}$-bearing and five distinct *bla*$_{CMY-2}$-bearing genetic structures located on plasmids from *Salmonella enterica* and *Escherichia coli* isolates ($n = 35$) collected from chickens in South Korea. All *Salmonella* plasmids shared a common replicon, *bla*$_{CTX-M-15}$ transposon, and core resistance phenotype, while *E. coli bla*$_{CTX-M-15}$ plasmids included four distinct replicons.

Salmonella enterica and avian pathogenic *Escherichia coli* (APEC) are the major bacterial pathogens of concern to the poultry industry (1, 2). The emergence of multidrug resistance is a major challenge in treatment of these infections, while constituting an increasing threat to public health. In particular, *S. enterica* and *E. coli* strains that are resistant to extended-spectrum cephalosporins have been isolated from chickens and other food animals (3–5). The emergence of these cephalosporin-resistant bacteria is of special concern because cephalosporins are an important class of antibiotics for both humans and animals (6–8). Resistance is conferred by extended-spectrum β-lactamases (ESBLs) and chromosomal and plasmid-mediated AmpC β-lactamases (9). In this study, we identified the presence of the *bla*$_{CTX-M}$ or *bla*$_{CMY}$ genes on plasmids of ceftiofur- or cefoxitin-resistant *S. enterica* and APEC isolates from chickens in South Korea, and the goal here was to achieve insight to the genetic context of the plasmid-carried *bla*$_{CTX-M}$ and *bla*$_{CMY}$ genes.

A total of 692 chicken clinical isolates (409 *E. coli* and 283 *S. enterica* isolates) maintained by the Avian Disease Division at the Animal, Plant and Fisheries Quarantine and Inspection Agency (QIA) in South Korea were tested for antimicrobial susceptibility as previously described (10). The isolates were collected from clinical samples of commercial layer, broiler, or breeder chickens submitted to the Avian Disease Division of the QIA for diagnosis between 2002 and 2010. Thirty-five *S. enterica* and APEC isolates were resistant to extended-spectrum cephalosporins or cephamycins and were further characterized. Isolates were screened for the presence of *bla*$_{CTX-M}$, *bla*$_{TEM}$, *bla*$_{SHV}$, or *bla*$_{CMY}$ genes using PCR (6, 11, 12). Pulsed-field gel electrophoresis (PFGE) was performed using the restriction endonuclease XbaI as described in reference13, and multilocus sequence typing (MLST) was used to further characterize APEC isolates as described in reference 14. Allelic profiles and sequence types (ST) were assigned based on the *E. coli* MLST database (http://mlst.ucc.ie/mlst/dbs/Ecoli). To determine the physical location of *bla*$_{CTX-M}$ or *bla*$_{CMY}$ genes, plasmids were transferred into *E. coli* K-12 strain J53 (azithromycin resistant [Azi^r]) by conjugation or transformed into *E. coli* DH10B cells by electroporation as described in references 4 and 15. Plasmid PCR-based replicon typing was conducted with all transconjugants and transformants as described in reference 16. All detected replicon types were confirmed by sequencing the amplicons. The genetic sequence of *bla* and flanking regions was characterized using PCR mapping and sequencing as described in references 4, 17, and 18.

The isolates resistant to ceftiofur were positive for genes encoding CTX-M-type β-lactamases (*bla*$_{CTX-M-14}$ and *bla*$_{CTX-M-15}$), and the isolates resistant to a cephamycin (cefoxitin) harbored genes encoding an AmpC β-lactamase (*bla*$_{CMY-2}$) (Table 1). The *bla*$_{CMY-2}$-positive isolates also showed reduced susceptibility to ceftiofur. Nine isolates were also positive for *bla*$_{TEM-1}$ (Table 1), while all isolates were negative for *bla*$_{SHV}$ using a published assay based on PCR and sequencing (19).

CTX-M-type or CMY-2 β-lactamase-encoding genes were located on large plasmids, ranging from 85 to 200 kb, of which the sizes were determined by plasmid profiling as described in reference4 (Fig. 1 and Table 1). As expected (10, 19), all *S. enterica* serovar Enteritidis isolates had closely related PFGE patterns (Fig. 2), differing by three to four bands (>85% similarity). Although *S.* Enteritidis isolates were highly clonal, they harbored a *bla*$_{CTX-M}$-bearing plasmid of a different size (Table 1). APEC isolates were represented by a highly diverse set of PFGE patterns (Fig. 3) and 14 different MLST types out of 18 isolates (Fig. 3). APEC isolates also harbored a *bla*$_{CTX-M}$- or *bla*$_{CMY}$-bearing plasmid of a different size (Table 1). These findings suggest that dissemination of the resistance is mediated by a combination of horizontal transfer of the resistance genes or plasmids (to new strains) and dissemination of bacteria.

All nine *bla*$_{CMY-2}$-bearing plasmids were transferred successfully by conjugation, whereas only five *bla*$_{CTX-M-15}$-bearing plasmids of all 26 *bla*$_{CTX-M}$-bearing plasmids were successfully conjugated. The replicon typing detected the presence of A/C, FII, F, I1-Iγ, K, and P replicons in the isolates tested, and three isolates were negative for all the replicons tested (Table 1). Most isolates (7/9) carrying *bla*$_{CMY-2}$-bearing plasmids and an isolate carrying the *bla*$_{CTX-M-14}$-bearing plasmid were positive for the I1-Iγ repli-

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TABLE 1 Characteristics of *S. enterica* and *E. coli* strains carrying bla_{CTX-M} or bla_{CMY-2} isolated from chickens

Strain ID	Species or *Salmonella* serotype	Yr	Resistance pattern of[a]:		β-Lactamase	*bla*-bearing plasmid size (kb)[b]	Replicon type(s)	Structure[c]
			Wild type	Transformant or transconjugant				
AD09-S19	*S. Enteritidis*	2009	AMP-APR-XNL-CEF-GEN-NAL-NEO-STR-SUL-TET	AMP-XNL-CEF-GEN-STR-SUL-TET	CTX-M-15	190	FII	B
AD09-S23	*S. Enteritidis*	2009	AMP-XNL-CEF-GEN-NAL-STR-SUL-TET	ND	CTX-M-15	200	FII	B
AD09-S25	*S. Enteritidis*	2009	AMP-XNL-CEF-GEN-NAL-STR-SUL-TET	AMP-XNL-CEF-GEN-STR-SUL-TET	CTX-M-15	120	FII	B
AD09-S26	*S. Enteritidis*	2009	AMP-XNL-CEF-GEN-NAL-STR-SUL-TET	AMP-XNL-CEF-GEN-STR-SUL-TET	CTX-M-15	120	FII	B
AD09-S29	*S. Enteritidis*	2009	AMP-XNL-CEF-GEN-NAL-STR-SUL-TET	ND	CTX-M-15	200	FII	B
AD09-S31	*S. Senftenberg*	2009	AMP-XNL-CEF-GEN-NAL-STR-SUL-TET	ND	CTX-M-15	200	FII	B
AD09-S33	*S. Enteritidis*	2009	AMP-XNL-CEF-GEN-NAL-STR-SUL-TET	AMP-XNL-CEF-GEN-STR-SUL-TET	CTX-M-15	200	FII	B
AD09-SKYH2	*S. Enteritidis*	2009	AMP-XNL-CEF-GEN-NAL-STR-SUL-TET	ND	CTX-M-15	200	FII	B
AD10-S11	*S. Enteritidis*	2010	AMP-XNL-CEF-GEN-NAL-NEO-STR-SUL-TET	AMP-XNL-CEF-GEN-NEO-STR-SUL-TET	CTX-M-15	120	FII	B
AD10-S15	*S. Enteritidis*	2010	AMP-XNL-CEF-GEN-NAL-NEO-STR-SUL-TET	AMP-XNL-CEF-GEN-NEO-STR-SUL-TET	CTX-M-15	120	FII	B
AD10-S2	*S. Enteritidis*	2010	AMP-XNL-CEF-GEN-NAL-NEO-STR-SUL-TET	AMP-XNL-CEF-GEN-STR-SUL-TET	CTX-M-15	140	FII	B
AD10-S22	*S. Enteritidis*	2010	AMP-XNL-CEF-FEP-NAL-NEO-STR-SUL-TET	AMP-XNL-CEF-STR-SUL-TET	CTX-M-15	170	FII	B
AD10-S23	*S. Enteritidis*	2010	AMP-XNL-CEF-GEN-NAL-NEO-STR-SUL-TET	AMP-XNL-CEF-GEN-STR-SUL-TET	CTX-M-15	120	FII	B
AD10-S24	*S. Enteritidis*	2010	AMP-XNL-CEF-GEN-NAL-NEO-STR-SUL-TET	AMP-XNL-CEF-GEN-STR-SUL-TET	CTX-M-15	170	FII	B
AD10-S26	*S. Enteritidis*	2010	AMP-XNL-CEF-FEP-GEN-NAL-NEO-STR-SUL-TET	AMP-XNL-CEF-GEN-NEO-STR-SUL-TET	CTX-M-15	170	FII	B
AD10-S7	*S. Enteritidis*	2010	AMP-XNL-CEF-GEN-NAL-NEO-STR-SUL-TET	AMP-XNL-CEF-GEN-NEO-STR-SUL-TET	CTX-M-15	120	FII	B
AD10-S9	*S. Enteritidis*	2010	AMP-XNL-CEF-GEN-NAL-NEO-STR-SUL-TET	AMP-XNL-CEF-GEN-STR-SUL-TET	CTX-M-15	120	FII	B
AD09-EC2[d]	*E. coli*	2009	AMP-XNL-CEF-NAL-STR-SUL-TET	AMP-XNL-CEF-STR-SUL-TET	CTX-M-15	190	P	B
AD09-EC3	*E. coli*	2009	AMC-AMP-CEF-CHL-FFN-FOX-GEN-STR-SUL-TET	AMC-AMP-CEF-CHL-FFN-FOX-GEN-STR-SUL-TET	CMY-2	160	A/C	C
AD09-EC6	*E. coli*	2009	AMC-AMP-CEF-FOX-NAL	AMC-AMP-CEF-FOX-STR	CMY-2	100	I1-Iγ	E
AD09-EC7[d]	*E. coli*	2009	AMC-AMP-CEF-CIP-ENO-FOX-NAL-STR-TET	AMC-AMP-CEF-FOX-STR	CMY-2	100	I1-Iγ	E
AD09-EC17[d]	*E. coli*	2009	AMP-XNL-CEF-CIP-ENO-GEN-NAL-NEO-STR-SUL-TET	AMP-XNL-CEF-GEN-STR-SUL-TET	CTX-M-15	190	P	B
AD09-EC25	*E. coli*	2009	AMP-XNL-CEF-CHL-FFN-NAL-STR-SUL-TET	AMP-XNL-CEF-STR-SUL-TET	CTX-M-15	160	Negative	B
AD09-EC36[d]	*E. coli*	2009	AMP-XNL-CEF-GEN-NAL-STR-SUL-TET	AMP-XNL-CEF-GEN-STR-SUL-TET	CTX-M-15	180	Negative	B
AD09-EC38	*E. coli*	2009	AMP-XNL-CEF-GEN-NAL-NEO-STR-SUL-TET	AMP-XNL-CEF-GEN-STR-SUL-TET	CTX-M-15	180	Negative	B
AD09-EC44[d]	*E. coli*	2009	AMP-XNL-CEF-CIP-ENO-GEN-NAL-STR-SUL-TET	AMP-XNL-CEF-GEN-STR-SUL-TET	CTX-M-15	85	F	B
AD10-EC11	*E. coli*	2009	AMC-AMP-CEF-FOX-NAL-SUL-SXT-TET	AMC-AMP-CEF-FOX	CMY-2	100	K	F
DDC10-15	*E. coli*	2010	AMP-XNL-CEF-GEN-NAL-STR-SUL-TET	AMP-XNL-CEF-GEN-STR-SUL-TET	CTX-M-15	160	FIV	B
DDC10-30	*E. coli*	2010	AMC-AMP-CEF-FOX-NAL-NEO-SXT-TET	AMC-AMP-CEF-FOX	CMY-2	100	I1-Iγ	E
DDC10-52[d]	*E. coli*	2010	AMP-XNL-CEF-CHL-CIP-ENO-FFN-GEN-NAL-NEO-STR-SUL-SXT-TET	AMP-XNL-CEF-CHL-FFN-GEN-NEO-STR-SUL-SXT-TET	CTX-M-15	160	FIV	B
EC02384[d]	*E. coli*	2002	AMC-AMP-CEF-CIP-ENO-FOX-NAL-STR-SUL-SXT-TET	AMC-AMP-CEF-FOX-STR	CMY-2	95	I1-Iγ, P	C
EC02502[d]	*E. coli*	2002	AMC-AMP-CEF-CHL-FFN-FOX-GEN-NEO-STR-SUL-SXT-TET	AMC-AMP-CEF-CHL-FFN-FOX-NEO-STR-SUL-SXT-TET	CMY-2	160	I1-Iγ, P	D
EC06036L1	*E. coli*	2006	AMC-AMP-CEF-CIP-ENO-FOX-GEN-NAL-STR-SUL-TET	AMC-AMP-CEF-FOX-STR	CMY-2	95	I1-Iγ	G
EC06D097	*E. coli*	2006	AMP-APR-XNL-CEF-CIP-ENO-GEN-NAL-NEO-STR-SUL-SXT-TET	AMP-XNL-CEF-STR	CTX-M-14	100	I1-Iγ	A
EC07Q066L2[d]	*E. coli*	2007	AMC-AMP-CEF-CIP-ENO-FOX-GEN-NAL-STR-TET	AMC-AMP-CEF-FOX-STR	CMY-2	100	I1-Iγ	E

[a] Resistance patterns were determined by the Kirby-Bauer disk diffusion assay on Mueller-Hinton agar for 18 antimicrobials, including ampicillin (AMP), amoxicillin-clavulanic acid (AMC), apramycin (APR), cefepime (FEP), cefoxitin (FOX), ceftiofur (XNL), cephalothin (CEF), chloramphenicol (CHL), ciprofloxacin (CIP), enrofloxacin (ENO), florfenicol (FFN), gentamicin (GEN), nalidixic acid (NAL), neomycin (NEO), streptomycin (STR), sulfisoxazole (SUL), tetracycline (TET), and trimethoprim-sulfamethoxazole (SXT). ND, not determined.

[b] Each DH10B transformant or J53 transconjugant carried only one large plasmid, ranging in size from approximately 85 to 200 kb. Plasmid sizes were estimated by comparison with a supercoiled DNA ladder containing DNA bands of 8 to 165 kb (BAC-Tracker supercoiled DNA ladder; Epicentre, Madison, WI).

[c] Structures indicate the genetic context of bla_{CMY-2} regions as shown in Fig. 4.

[d] Nine strains also had bla_{TEM-1}, which was harbored by *bla*-bearing large plasmids in five of the strains (AD09-EC2, AD09-EC17, AD09-EC44, DDC10-52, and EC02384).

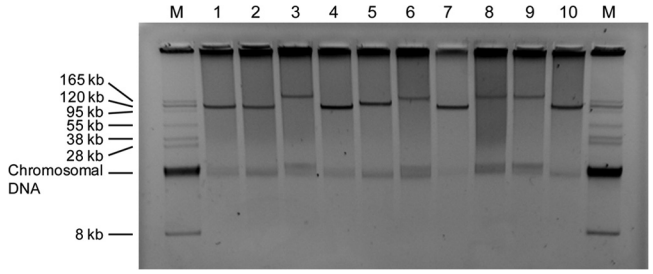

FIG 1 Plasmid profiles of representative transformants. Plasmids from *E. coli* transformants of strains AD10-S9 (lane 1), AD10-S15 (lane 2), AD09-EC2 (lane 3), AD10-S11 (lane 4), AD10-S2 (lane 5), AD10-S22 (lane 6), AD10-S23 (lane 7), AD10-S24 (lane 8), AD10-S26 (lane 9), and AD10-S7 (lane 10) were analyzed on 1% agarose gel. Plasmid sizes were estimated by comparison with a supercoiled DNA ladder containing DNA bands of 8 to 165 kb, as shown in lane M (BAC-Tracker supercoiled DNA ladder; Epicentre).

con plasmid, and bla_{CMY-2}-bearing plasmids of two isolates (EC02384 and ECEC02502) possessed two replicons, I1-Iγ and P (Table 1). An A/C replicon plasmid was detected in an isolate (AD09-EC3) carrying the bla_{CMY-2}-bearing plasmid with a different reverse primer (5′-ACGACAAACCTGGATTGCTTCCTT-3′) designed based on the sequence of a bla_{CMY-2}-positive A/C plasmid (peH4H) (20). Most isolates (17/25) carrying $bla_{CTX-M-15}$-bearing plasmids were positive for the FII replicon (Table 1). FII replicon plasmids bearing bla_{CMY-2} or bla_{CTX-M} have been reported in other countries (21), confirming the global distribution of bla_{CMY-2}- or bla_{CTX-M}-bearing plasmids.

Two types of bla_{CTX-M}-bearing genetic "structures" (5-kb and 3-kb fragments) were identified in 26 isolates of *S. enterica* and APEC containing bla_{CTX-M}-bearing plasmids, of which 25 isolates carried $bla_{CTX-M-15}$ (Fig. 4 and Table 1). Only one APEC isolate, which was isolated in 2006, harbored $bla_{CTX-M-14}$ (Table 1). Also, five types of bla_{CMY-2}-bearing genetic structures (11-kb, 15-kb, 12-kb, 5-kb, and 8-kb fragments) were identified from nine APEC isolates containing bla_{CMY-2}-bearing plasmids (Fig. 4 and Table 1). The most predominant 3-kb fragment (structure B) bearing $bla_{CTX-M-15}$ and the 5-kb fragment (structure A) were related to the genetic structures previously described (17). The first two genetic structures (C and D) bearing one or two copies of bla_{CMY-2} have been previously identified in *S. enterica* and *E. coli* isolates in the United States and Europe (4, 18, 20). The 12-kb sequence (structure E) shared almost 100% sequence identity with a 12-kb region of the plasmid of *S. enterica* serovar Kentucky strain CVM29188 (22). Two other structures (F and G) identified in this study were unique from any reported sequences (Fig. 4).

Several plasmids of different replicons had an identical genetic structure (Table 1), indicating probable interplasmid transmission of the resistance genes. In addition, the $bla_{CTX-M-15}$ gene was only detected from 2009 to 2010, whereas $bla_{CTX-M-14}$ and bla_{CMY-2} genes were detected from earlier years (Table 1). All isolates of *S. enterica*, including serovars Enteritidis and Senftenberg, shared the same plasmid replicon, $bla_{CTX-M-15}$-bearing genetic structure, and core resistance trait. In contrast, $bla_{CTX-M-15}$-bearing plasmids from *E. coli* included three distinct replicons and one unidentified replicon. This pattern is consistent with either the recent acquisition of a $bla_{CTX-M-15}$-bearing plasmid by *S. enterica* in South Korea or repeated acquisition of a FII replicon plasmid by these strains. We documented some size variation in these plasmids, but this type of variation can arise in a relatively short number of generations (23). The only other way that this pattern of limited diversity could arise is if there was bias in isolate collection. We have no means to assess this variable, but $bla_{CTX-M-15}$-positive isolates from this study were collected from independent submis-

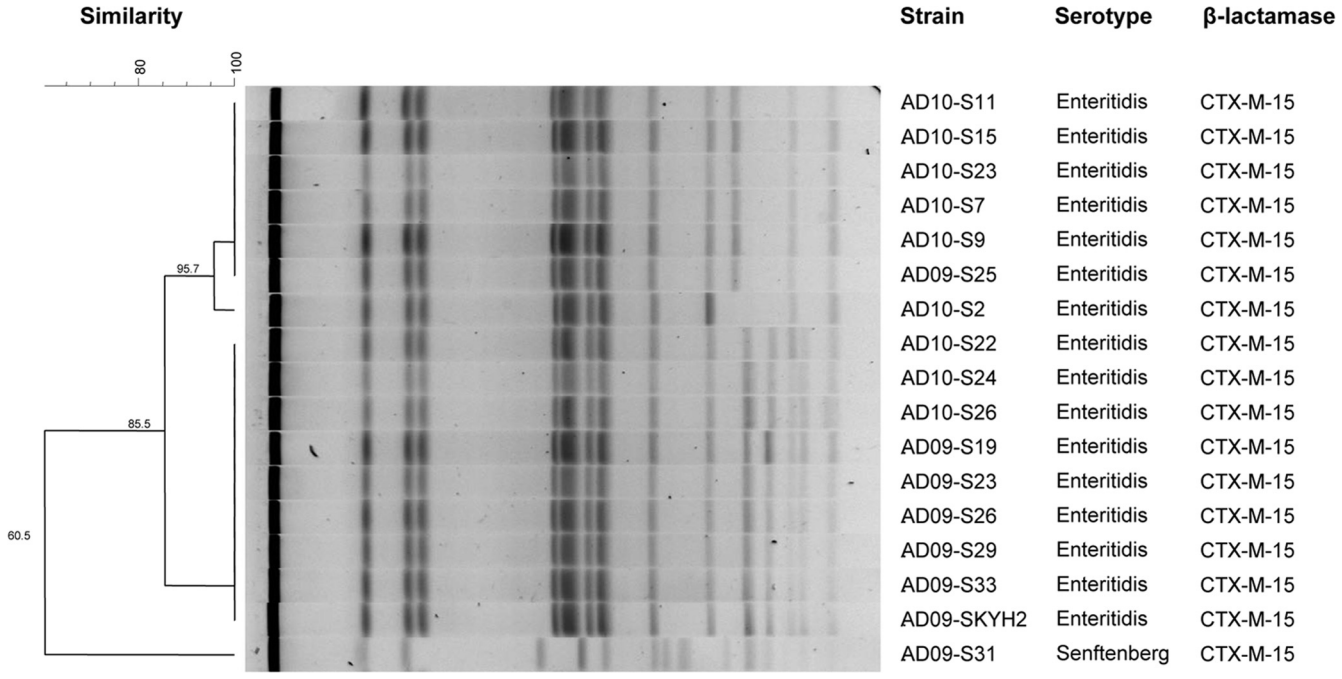

FIG 2 Pulsed-field gel electrophoresis patterns for *S. enterica* isolates based on XbaI digestion. All *S.* Enteritidis isolates had closely related patterns, differing by three to four bands (>85% similarity). The *S. enterica* serovar Senftenberg isolate had a distinct PFGE pattern.

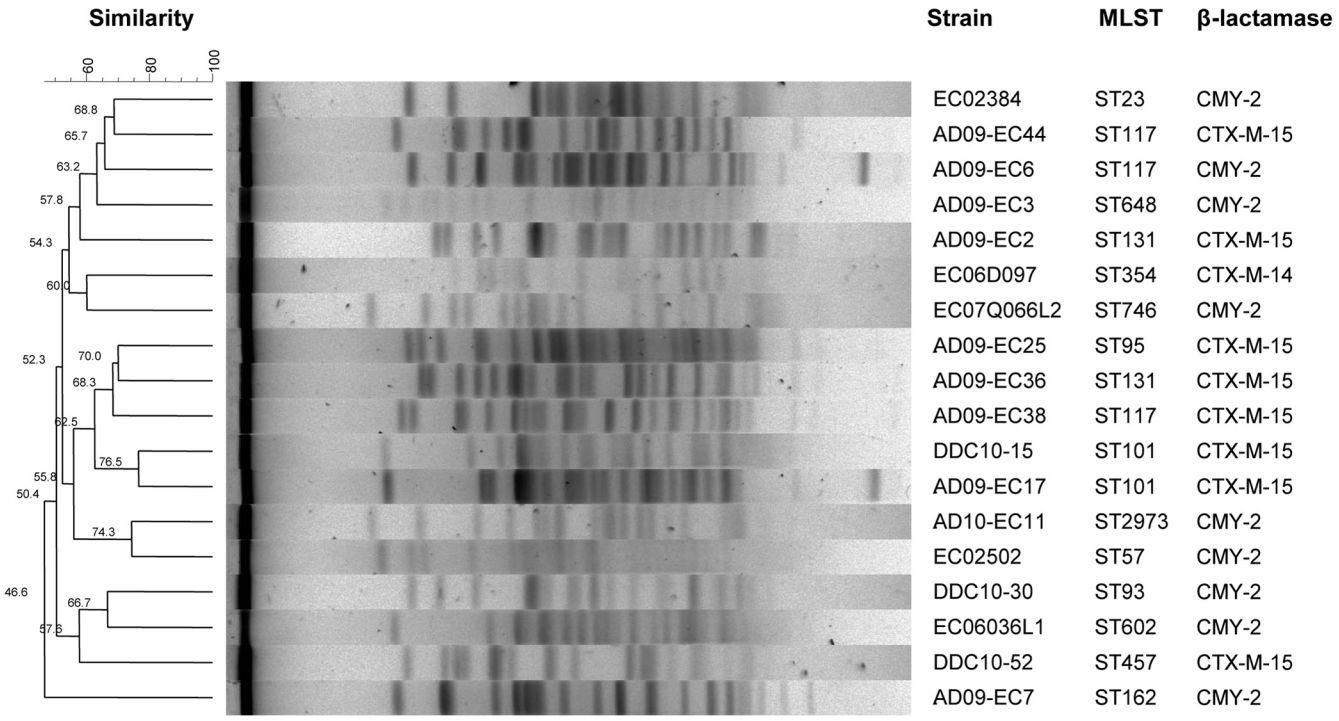

FIG 3 Pulsed-field gel electrophoresis patterns (XbaI digestion) and MLST types of APEC isolates. Sequence types (STs) were assigned based on the *E. coli* MLST database (http://mlst.ucc.ie/mlst/dbs/Ecoli). APEC isolates had diverse restriction patterns and MLST types.

sions from 25 different facilities, and no two isolates were included from a single collection event; therefore, these represent biologically independent samples.

Ceftiofur, which was developed strictly for veterinary use, is used worldwide for the treatment of diseased livestock (7), including in South Korea (24). The $bla_{\text{CTX-M-14}}$, $bla_{\text{CTX-M-15}}$, and $bla_{\text{DHA-1}}$ genes have been identified in *E. coli* isolates from sick animals, including cows, dogs, and pigs (24, 25), and $bla_{\text{CTX-M-15}}$ and $bla_{\text{DHA-1}}$ were also found in *S. enterica* isolates from chickens (15, 25, 26). The present study, which was conducted with ceftiofur- or cefoxitin-resistant *S. enterica* and APEC isolates from chickens in South Korea, revealed $bla_{\text{CTX-M-14}}$ and $bla_{\text{CMY-2}}$ in APEC isolates and $bla_{\text{CTX-M-15}}$ in both *S. enterica* and APEC isolates. This study also showed that all of the $bla_{\text{CTX-M}}$ and $bla_{\text{CMY-2}}$

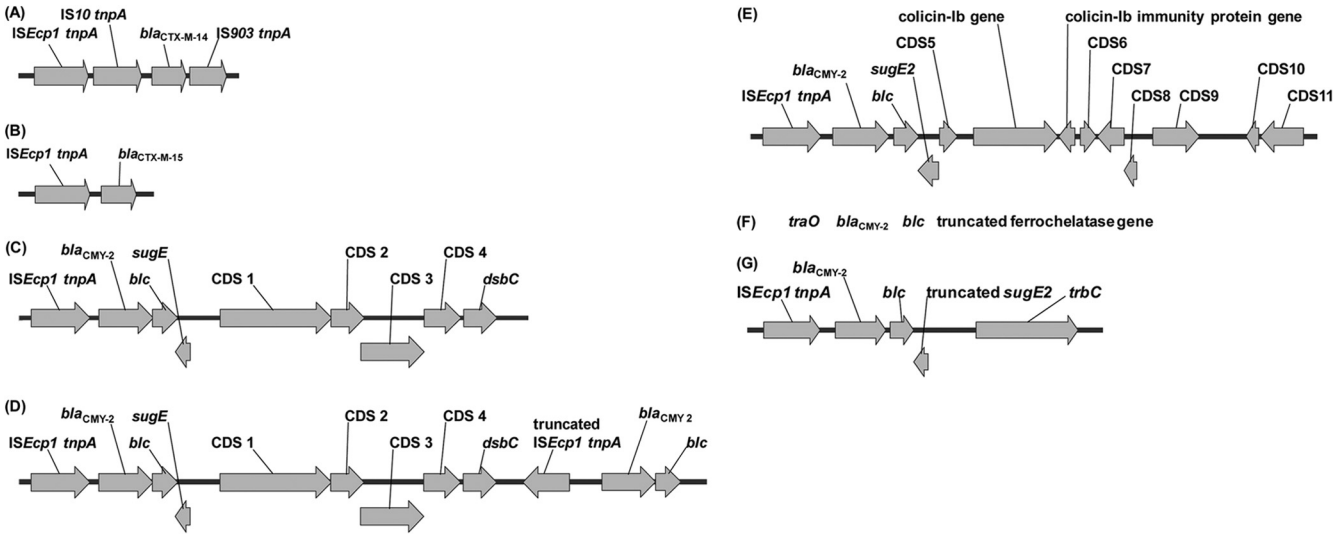

FIG 4 Genetic context of 5-kb (A), 3-kb (B), 11-kb (C), 13-kb (D), 12-kb (E), 5-kb (F), and 8-kb (G) fragments bearing $bla_{\text{CTX-M-14}}$, $bla_{\text{CTX-M-15}}$, or $bla_{\text{CMY-2}}$ identified in extended-spectrum cephalosporin-resistant *S. enterica* and *E. coli* strains. The genes *tnpA*, $bla_{\text{CTX-M-14}}$, $bla_{\text{CTX-M-15}}$, $bla_{\text{CMY-2}}$, *blc*, *sugE(2)*, *ecnR*, *dsbC*, *traC*, *traO*, and *trbC* encode a transposase, a CTX-M-14 ESBL, a CTX-M-15 ESBL, a CMY-2 AmpC β-lactamase, an outer membrane lipoprotein (lipocalin), a small multidrug resistance protein, a transcriptional regulatory protein (entericidin R), a disulfide bond isomerase, and three sex pilus assembly/synthesis proteins, respectively.

genes were located on large plasmids, consistent with previous reports (15, 24, 26). We used PCR assays to detect plasmid-mediated quinonole resistance (PMQR) genes [*qnrA*, *qnrB*, *qnrC*, *qnrS*, *qepA*, and *aac(6′)-Ib-cr*], which may coexist with β-lactamase genes (27), but amplification for these resistance determinants was negative.

Plasmid-mediated ESBLs and AmpC β-lactamases have been also reported frequently from human isolates of *S. enterica* and *E. coli* in South Korea (8, 26, 28). This is consistent with poultry being a reservoir for transmission of resistance. Putative transposable genetic elements bearing bla_{CTX-M} or bla_{CMY-2} may be directly implicated in horizontal dissemination of the resistance genes among different bacterial hosts. Therefore, appropriate intervention strategies to reduce antimicrobial selection pressure are needed to limit risks from ESBL or AmpC β-lactamase-producing *S. enterica* and *E. coli* in chickens.

Nucleotide sequence accession numbers. The GenBank accession numbers for the sequences of structures A, B, E, F and G shown in Fig. 4 are JQ318854 to JQ318858, respectively. Structures C and D were determined based on the regions identified by PCR, as previously described (4).

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REFERENCES

1. **Barnes HJ, Vaillancourt J-P, Gross WB.** 2008. Colibacillosis, p 631–656. *In* Siaf YM (ed), Diseases of poultry, 11th ed. Iowa State University Press, Ames, IA.
2. **Gast RK, Shivaprasad HL.** 2008. *Salmonella* infections, p 567–613. *In* Siaf YM (ed), Diseases of poultry, 11th ed. Iowa State University Press, Ames, IA.
3. **Brinas L, Moreno MA, Zarazaga M, Porrero C, Saenz Y, Garcia M, Dominguez L, Torres C.** 2003. Detection of CMY-2, CTX-M-14, and SHV-12 β-lactamases in *Escherichia coli* fecal-sample isolates from healthy chickens. Antimicrob. Agents Chemother. **47**:2056–2058.
4. **Kang MS, Besser TE, Call DR.** 2006. Variability in the region downstream of the bla_{CMY-2} β-lactamase gene in *Escherichia coli* and *Salmonella enterica* plasmids. Antimicrob. Agents Chemother. **50**:1590–1593.
5. **Smet A, Martel A, Persoons D, Dewulf J, Heyndrickx M, Catry B, Herman L, Haesebrouck F, Butaye P.** 2008. Diversity of extended-spectrum β-lactamases and class C β-lactamases among cloacal *Escherichia coli* isolates in Belgian broiler farms. Antimicrob. Agents Chemother. **52**:1238–1243.
6. **Batchelor M, Hopkins K, Threlfall EJ, Clifton-Hadley FA, Stallwood AD, Davies RH, Liebana E.** 2005. bla_{CTX-M} genes in clinical *Salmonella* isolates recovered from humans in England and Wales from 1992 to 2003. Antimicrob. Agents Chemother. **49**:1319–1322.
7. **Hornish RE, Kotarski SF.** 2002. Cephalosporins in veterinary medicine—ceftiofur use in food animals. Curr. Top. Med. Chem. **2**:717–731.
8. **Yoo JS, Byeon J, Yang J, Yoo JI, Chung GT, Lee YS.** 2010. High prevalence of extended-spectrum β-lactamases and plasmid-mediated AmpC β-lactamases in *Enterobacteriaceae* isolated from long-term care facilities in Korea. Diagn. Microbiol. Infect. Dis. **67**:261–265.
9. **Thomson KS.** 2010. Extended-spectrum-β-lactamase, AmpC, and carbapenemase issues. J. Clin. Microbiol. **48**:1019–1025.
10. **Oh JY, Kang MS, An BK, Song EA, Kwon JH, Kwon YK.** 2010. Occurrence of purulent arthritis broilers vertically infected with *Salmonella enterica* serovar Enteritidis in Korea. Poult. Sci. **89**:2116–2122.
11. **Branger C, Zamfir O, Geoffroy S, Laurans G, Arlet G, Thien HV, Gouriou S, Picard B, Denamur E.** 2005. Genetic background of *Escherichia coli* and extended-spectrum β-lactamase type. Emerg. Infect. Dis. **11**:54–61.
12. **Zhao S, White DG, McDermott PF, Friedman S, English L, Ayers S, Meng J, Maurer JJ, Holland R, Walker RD.** 2001. Identification and expression of cephamycinase bla_{CMY} genes in *Escherichia coli* and *Salmonella* isolates from food animals and ground meat. Antimicrob. Agents Chemother. **45**:3647–3650.
13. **Ribot EM, Fair MA, Gautom R, Cameron DN, Hunter SB, Swaminathan B, Barrett TJ.** 2006. Standardization of pulsed-field gel electrophoresis protocols for the subtyping of *Escherichia coli* O157:H7, *Salmonella*, and *Shigella* for PulseNet. Foodborne Pathog. Dis. **3**:59–67.
14. **Wirth T, Falush D, Lan R, Colles F, Mensa P, Wieler LH, Karch H, Reeves PR, Maiden MC, Ochman H, Achtman M.** 2006. Sex and virulence in *Escherichia coli*: an evolutionary perspective. Mol. Microbiol. **60**:1136–1151.
15. **Rayamajhi N, Jung BY, Cha SB, Shin MK, Kim A, Kang MS, Lee KM, Yoo HS.** 2010. Antibiotic resistance patterns and detection of bla_{DHA-1} in *Salmonella* species isolates from chicken farms in South Korea. Appl. Environ. Microbiol. **76**:4760–4764.
16. **Carattoli A, Bertini A, Villa L, Falbo V, Hopkins KL, Threlfall EJ.** 2005. Identification of plasmids by PCR-based replicon typing. J. Microbiol. Methods **63**:219–228.
17. **Diestra K, Juan C, Curiao T, Moya B, Miro E, Oteo J, Coque TM, Perez-Vazquez M, Campos J, Canton R, Oliver A, Navarro F.** 2009. Characterization of plasmids encoding bla_{ESBL} and surrounding genes in Spanish clinical isolates of *Escherichia coli* and *Klebsiella pneumoniae*. J. Antimicrob. Chemother. **63**:60–66.
18. **Verdet C, Gautier V, Chachaty E, Ronco E, Hidri N, Decre D, Arlet G.** 2009. Genetic context of plasmid-carried bla_{CMY-2}-like genes in *Enterobacteriaceae*. Antimicrob. Agents Chemother. **53**:4002–4006.
19. **Monstein HJ, Ostholm-Balkhed A, Nilsson MV, Nilsson M, Dornbusch K, Nilsson LE.** 2007. Multiplex PCR amplification assay for the detection of bla_{SHV}, bla_{TEM} and bla_{CTX-M} genes in *Enterobacteriaceae*. APMIS **115**:1400–1408.
20. **Call DR, Singer RS, Meng D, Broschat SL, Orfe LH, Anderson JM, Herndon DR, Kappmeyer LS, Daniels JB, Besser TE.** 2010. bla_{CMY-2}-positive IncA/C plasmids from *Escherichia coli* and *Salmonella enterica* are a distinct component of a larger lineage of plasmids. Antimicrob. agents chemother. **54**:590–596.
21. **Carattoli A.** 2009. Resistance plasmid families in *Enterobacteriaceae*. Antimicrob. Agents Chemother. **53**:2227–2238.
22. **Fricke WF, McDermott PF, Mammel MK, Zhao S, Johnson TJ, Rasko DA, Fedorka-Cray PJ, Pedroso A, Whichard JM, Leclerc JE, White DG, Cebula TA, Ravel J.** 2009. Antimicrobial resistance-conferring plasmids with similarity to virulence plasmids from avian pathogenic *Escherichia coli* strains in *Salmonella enterica* serovar Kentucky isolates from poultry. Appl. Environ. Microbiol. **75**:5963–5971.
23. **Subbiah M, Top EM, Shah DH, Call DR.** 2011. Selection pressure required for long-term persistence of bla_{CMY-2}-positive IncA/C plasmids. Appl. Environ. Microbiol. **77**:4486–4493.
24. **Lim SK, Lee HS, Nam HM, Jung SC, Bae YC.** 2009. CTX-M-type β-lactamase in *Escherichia coli* isolated from sick animals in Korea. Microb. Drug Resist. **15**:139–142.
25. **Rayamajhi N, Cha SB, Shin SW, Jung BY, Lim SK, Yoo HS.** 2011. Plasmid typing and resistance profiling of *Escherichia fergusonii* and other *Enterobacteriaceae* isolates from South Korean farm animals. Appl. Environ. Microbiol. **77**:3163–3166.
26. **Tamang MD, Nam HM, Kim TS, Jang GC, Jung SC, Lim SK.** 2011. Emergence of extended-spectrum β-lactamase (CTX-M-15 and CTX-M-14)-producing nontyphoid *Salmonella* with reduced susceptibility to ciprofloxacin among food animals and humans in Korea. J. Clin. Microbiol. **49**:2671–2675.
27. **Jacoby GA, Gacharna N, Black TA, Miller GH, Hooper DC.** 2009. Temporal appearance of plasmid-mediated quinolone resistance genes. Antimicrob. Agents Chemother. **53**:1665–1666.
28. **Song W, Lee H, Lee K, Jeong SH, Bae IK, Kim JS, Kwak HS.** 2009. CTX-M-14 and CTX-M-15 enzymes are the dominant type of extended-spectrum β-lactamase in clinical isolates of *Escherichia coli* from Korea. J. Med. Microbiol. **58**:261–266.