Beneficial Chromosomal Integration of the Genes for CTX-M Extended-Spectrum β-Lactamase in Klebsiella pneumoniae for Stable Propagation

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ABSTRACT The acquired CTX-M-type extended-spectrum-β-lactamase (ESBL)-producing Enterobacterales are of great concern in clinical settings because they limit therapeutic options for patients infected by the pathogens. An intriguing clonality of CTX-M ESBL-producing Klebsiella pneumoniae blood isolates was observed from a national cohort study, and comparative genomics were assessed for the 115 K. pneumoniae blood isolates carrying the blaCTX-M gene. The plasmid preference of particular clones of a sequence type (ST) was assessed by liquid mating. A quarter of the blaCTX-M gene-carrying K. pneumoniae blood isolates harbor the gene in their chromosome, and most of those with the built-in blaCTX-M gene belonged either to ST307 or ST48. Notably, all 16 K. pneumoniae ST48 isolates harbored two copies of the blaCTX-M-15 gene in the chromosome. The chromosomal integration of the blaCTX-M-15 gene was mostly derived from the ISEcp1-targeting 5-bp AT-rich locus in the chromosome. The IS26-mediated chromosomal integration occurred when the upstream ISEcp1 from the blaCTX-M gene was truncated, targeting the anchor IS26 copy in the chromosome. Higher transfer efficiency of the blaCTX-M-15 gene-carrying FIA:R plasmid was observed in ST17 than that of the blaCTX-M-14 gene-carrying FIB:FII plasmid. The transfer efficiency of the plasmid differed by isolate among the ST307 members. The K. pneumoniae clones ST307 and ST48 harboring the blaCTX-M-15 gene in the chromosome were able to disseminate stably in clinical settings regardless of the environmental pressure, and the current population of K. pneumoniae blood isolates was constructed. Further follow-up is needed for the epidemiology of this antimicrobial resistance.

IMPORTANCE Dominant F-type plasmids harboring the gene have been pointed out to be responsible for the dissemination of the CTX-M extended-spectrum-β-lactamase (ESBL)-producing K. pneumoniae. Recently, the emergence of K. pneumoniae isolates with the blaCTX-M gene in their chromosomes has been reported occasionally worldwide. Such a chromosomal location of the resistance gene could be beneficial for stable propagation, as was the Acinetobacter baumannii ST191 harboring chromosomal blaOXA-23 that is endemic to South Korea. Through the present study, particular clones were identified as having built-in resistance genes in their chromosomes, and the chromosomal integration events were tracked by assessing their genomes. The cefotaxime-resistant K. pneumoniae clones of this study were particularized as results of the fastidiousness for plasmids to acquire the blaCTX-M gene for securing the diversity and of the chromosomal addiction of the blaCTX-M gene for ensuring propagation.

KEYWORDS CTX-M, extended-spectrum β-lactamases, Klebsiella pneumoniae, chromosomal integration, ISEcp1, IS26


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The acquired CTX-M-type extended-spectrum beta-lactamases (ESBLs) belonging to the class A beta-lactamases are grouped into five groups, 1, 2, 8, 9, and 25, by amino acid sequence similarity. Members within the same group share >94% identity and the members belonging to distinct groups share ≤90% identity (1). The five groups had been shown to originate from an intrinsic beta-lactamase gene of different species of Klyvera, i.e., both groups 1 and 2 from Klyvera ascorbata (2, 3), groups 8 and 9 from Klyvera georgiana (4, 5), and group 25, which remains to be identified but probably is from another member of Klyvera. The insertion sequences (ISs), mostly ISEcp1 and, less frequently, ISCR1, hijacked blaCTX-M from the chromosome of the progenitor Klyvera spp. and recruited it into a plasmid, which is then transferred to clinically relevant Enterobacteriaceae isolates. The ISs are recognized upstream of the blaCTX-M gene and provide portable promoter sequences stronger than the natural promoter sequences (6).

After the emergence of CTX-M ESBL-producing Escherichia coli in clinical settings in 1989 (7), CTX-M ESBL-producing Enterobacterales spread rapidly in the world, and their high prevalence is a grave concern in clinical settings, as the treatment options for patients infected by these pathogens are limited (8, 9). Dominance of the blaCTX-M-14 and blaCTX-M-15 genes in Enterobacterales clinical strains is achieved by their association with the mobile transposition element ISEcp1 and its location in prevalent F-type plasmids (10, 11). Such conjugative plasmids, often carrying antimicrobial resistance genes, maintain their occupancy in bacterial populations by using plasmid addiction systems, such as the toxin-antitoxin (TA) systems that kill the plasmid-free daughter cell through a stable toxin and an unstable antitoxin (12). In addition, clonal expansion of a disseminated bacterial clone supports the successful spread of CTX-M ESBL-producing Enterobacterales. In contrast to the obvious dominance of the E. coli clone sequence type 131 (ST131) among the CTX-M ESBL producers (8), the blaCTX-M ESBL gene-carrying Klebsiella pneumoniae is known to be devoid of clonality (13, 14). The emergence of K. pneumoniae isolates carrying the blaCTX-M gene in their chromosomes, devoid of clonality, were reported rarely from the beginning of the 2010s (15–18).

From national antimicrobial resistance surveillance, designed as a cohort study for entire episodes of K. pneumoniae bloodstream infections occurring in a year in six general hospitals in South Korea, we were able to collect a total of 572 K. pneumoniae blood isolates, including 164 cefotaxime-nonsusceptible isolates (19). Of the cefotaxime-nonsusceptible K. pneumoniae isolates, 81.7% (134/164) harbored the blaCTX-M ESBL gene belonging either to group 1 or to group 9 (20). As shown in Fig. 1, certain STs, i.e., ST307, ST789, ST11, ST48, ST15, ST392, and ST14, have absolute high rates of cefotaxime resistance of over 78%. Particular STs also favor harboring the blaCTX-M gene. For instance, the cefotaxime-nonsusceptible ST48, ST789, ST392, and ST147, together with ST307, with one exception, harbored the group 1 blaCTX-M gene, while ST17 carried only the group 9 blaCTX-M gene. In the case of ST11 isolates, half of the cefotaxime-nonsusceptible isolates harbored the group 1 blaCTX-M gene, and the other half had the group 9 blaCTX-M gene. The phenomenon could be derived from the preferential acquisition of specific plasmids carrying a particular blaCTX-M gene or the clonal dissemination together with the expansion of the clones possessing the residential blaCTX-M gene in the chromosome. To determine how the clonality of cefotaxime resistance was achieved, blaCTX-M-ESBL gene-carrying K. pneumoniae blood isolates from the cohort study were entirely sequenced, and a comparative analysis was carried out.

RESULTS

Genomes of the K. pneumoniae blood isolates. A total of 115 K. pneumoniae blood isolates were entirely sequenced. The contigs were numbered from 1 to 19, and the circularized chromosomes had a median size of 53,115,357 bp, ranging from 4,971,228 bp to 5,532,256 bp (Fig. 2). The ST of each isolate was determined in silico, and a total of 30 STs were identified. The most prevalent was ST307, which included 25 isolates. ST48 (n = 16), ST789 (n = 15), ST15 (n = 7), ST392 (n = 6) along with the rpoB
allele of ST392-like \((n = 1)\) possessing a single-nucleotide polymorphism, ST17 \((n = 5)\), ST11 \((n = 5)\), ST395 \((n = 4)\), ST4877 \((n = 3)\), and ST463 \((n = 3)\) were detected. One or two isolates belonged to the other 19 different STs.

The intrinsic \(\text{bla}_{\text{SHV}}\) gene was extracted, and the translated sequences were used to subtype the allele. A total of 9 subtypes were identified, and one isolate lost the gene through the interruption of IS26. The subtypes of SHV \(\beta\)-lactamases 28 \((n = 36)\), 11 \((n = 34)\), and 1 \((n = 28)\) were prevalent, and SHV-28 ESBL was identified in particular clones of ST14, ST15, ST4877, and ST307 (Fig. 2; also see Fig. S1 in the supplemental material). The alleles of intrinsic SHV had fewer than 5 mismatches among 286 amino acids, with an amino acid identity of \(98.2\%\). The molecular phylogeny from the multiple alignments of SHV alleles was poor, and no clear correspondence to the phylogenetic tree of STs (Fig. S1) or to that of the core genome (Fig. 2) was observed.

A total of 29 isolates harbored CTX-M-15 coding genes in their chromosome; seven of these isolates harbored an extra \(\text{bla}_{\text{CTX-M-15}}\) gene in a plasmid, and one ST48 isolate carried a plasmid harboring the \(\text{bla}_{\text{CTX-M-14}}\) gene (Fig. 2). Characteristically, the chromosomes of all 16 ST48 isolates and the ST392-like isolate had two copies of the gene. The 16 ST48 isolates with two copies of the \(\text{bla}_{\text{CTX-M-15}}\) gene were closely related to each other, but no single strain was supported by the core genome multilocus sequence typing (cgMLST) (Fig. S2). Two isolates belonging to ST147 and ST307 carried two plasmids harboring the \(\text{bla}_{\text{CTX-M-15}}\) gene, and one ST11 isolate possessed both the \(\text{bla}_{\text{CTX-M-15}}\) gene-carrying plasmid and the \(\text{bla}_{\text{CTX-M-14}}\) gene-carrying plasmid.

Plasmids carrying the \(\text{bla}_{\text{CTX-M}}\) gene. (i) Incompatibility types of the \(\text{bla}_{\text{CTX-M}}\) gene-carrying plasmids. The characteristics and gene contents of representative plasmids are schematically presented in Fig. 3 and Table 1. Among the plasmids carrying the group 1 \(\text{bla}_{\text{CTX-M}}\) genes, the dominant FIB:FII-type plasmids were observed to be diverse in terms of size and genetic components. However, the mosaic plasmids
of FIB and FII carried characteristic gene contents of those plasmids, including clustered antimicrobial genes bracketed by varied ISs and heavy-metal resistance gene clusters in the FIB plasmids and the \( \text{tra} \)-type conjugative elements in FII plasmids. The FIB:FII plasmids harboring the \( \text{bla}_{\text{CTX-M}} \) gene were observed to have more mosaicism than those carrying the \( \text{bla}_{\text{CTX-M}} \) gene, as the length was ca. 100 kb longer, and more genetic elements unrelated to FIB:FII were identified. The plasmids of infrequent incompatibility types shared only the \( \text{bla}_{\text{CTX-M}} \) gene and the vicinity with other plasmids. ISs were gathered near the genes for antimicrobial resistance, allowing the feasible mobility of the gene. The FIB:FII plasmids carrying the \( \text{bla}_{\text{CTX-M}} \) gene in ST307 and ST463 isolates possessed the GNAS-related TacTA, while those in other STs have both HigBA and STM4031 (Fig. 2).

(ii) Comparison between the \( \text{bla}_{\text{CTX-M}} \) gene-carrying plasmids. Pairwise comparison of the plasmids for the percent coverage of the sequences having >99.5% nucleic acid identity presented high percent coverage association by incompatibility type and by plasmid MLST (pMLST) of the plasmid (Fig. 4). The relatively high percent coverage of intertypes of plasmids was observed through mosaicism. For instance, the FIA:FIB plasmids carrying the \( \text{bla}_{\text{CTX-M}} \) gene in ST307 and ST463 isolates possessed the GNAS-related TacTA, while those in other STs have both HigBA and STM4031 (Fig. 2).

**FIG 2** Phylogeny of the CTX-M-type ESBL-producing \( K. \) pneumoniae blood strains based on the alignment of the core genome proteins and the characteristics associated with the \( \text{bla}_{\text{CTX-M}} \) gene carried by each strain. Blue and red indicate the presence of the group 1 and group 9 \( \text{bla}_{\text{CTX-M}} \) genes, respectively. Dark blue represents the presence of two group 1 \( \text{bla}_{\text{CTX-M}} \) genes in the chromosome or in plasmids. Chromosomal locations of the integrated \( \text{bla}_{\text{CTX-M}} \) gene are indicated in sky blue; the presence of toxin-antitoxin (TA) systems is indicated in yellow, and the incompatibility type of the plasmid carrying the \( \text{bla}_{\text{CTX-M}} \) gene is indicated in green. The numbers of contigs and IS\( \text{Ecp1} \) and IS26 insertion sequences are indicated as black and white heatmaps.
The FIB:HI1B plasmids carrying either the bla\textsubscript{CTX-M-9} or the bla\textsubscript{CTX-M-14} genes had perfect coverage except for the region upstream from the bla\textsubscript{CTX-M} gene. The plasmids belonging to the unique incompatibility types that lacked mosaicism, including I1, A/C, N, and B/O/K/Z, were incompatible with other types of plasmids presenting low percent coverage.

(iii) Conjugation efficiency differed by the plasmid and the bacterial host. The transfer efficiency of plasmids belonging to representative incompatibility types was determined by liquid mating using the ST307, ST375, and ST17 recipients. The FIA:R\textsubscript{II}H\textsubscript{9024} bla\textsubscript{CTX-M-15} plasmid transferred effectively to ST17 and one of the two ST307 isolates with transfer frequencies of $3.0 \times 10^{-5}$ to $3.4 \times 10^{-6}$ to $1.1 \times 10^{-5}$, respectively, while the FIB:FII\textsubscript{II}H\textsubscript{9024} bla\textsubscript{CTX-M-14} plasmid transferred to the other ST307 isolate with a frequency of $5.1 \times 10^{-6}$ to $5.2 \times 10^{-5}$ (Table 2). The results indicated the recipient preference of each plasmid. The differing efficiencies of plasmid transfer made a good correlation with the prevalence of CTX-M ESBLs in various STs.

by ST29 and ST1159 and those harbored by others. The FIB:HI1B plasmids carrying either the bla\textsubscript{CTX-M-9} or the bla\textsubscript{CTX-M-14} genes had perfect coverage except for the region upstream from the bla\textsubscript{CTX-M} gene. The plasmids belonging to the unique incompatibility types that lacked mosaicism, including I1, A/C, N, and B/O/K/Z, were incompatible with other types of plasmids presenting low percent coverage.

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**The bla\textsubscript{CTX-M-15} gene integrated into chromosomes.** (i) Bacterial clones carrying the bla\textsubscript{CTX-M} gene in chromosomes. The chromosomal location of the bla\textsubscript{CTX-M} gene was observed for the bla\textsubscript{CTX-M-15} gene in 29 K. pneumoniae isolates: 16 ST48, 8 ST307, and 1 each of ST14, ST15, ST101, ST392, and ST392-like, with one nucleotide difference at the rpoB allele (Fig. 2). Two copies of the bla\textsubscript{CTX-M-15} gene were found on 17 chromosomes of all 16 ST48 isolates and 1 ST392-like isolate. Nine of the 29 K. pneumoniae isolates possessed a plasmid harboring the bla\textsubscript{CTX-M} gene: the ST392-like isolate, one ST101 isolate, and two ST307 isolates possessed an FIB:FII\textsubscript{II}bla\textsubscript{CTX-M-15} plasmid; one ST15 isolate and two ST307 isolates had an FIA\textsubscript{II}bla\textsubscript{CTX-M-15} plasmid; one ST48 isolate had an FIA\textsubscript{II}bla\textsubscript{CTX-M-15} plasmid; and one ST48 isolate had an A/C\textsubscript{II}bla\textsubscript{CTX-M-14} plasmid. A K. pneumoniae ST392 isolate had FIB and FII replication origins in the chromosome, and the plasmid-like 196,572-bp portion included the bla\textsubscript{CTX-M-15} gene. The integration unit was bracketed by IS26 copies in the same direction, and the possibility of any assembly error was rejected by direct repeats at

**FIG 3** Schematic structure of the representative plasmids harboring the group 1 (A) or group 9 (B) bla\textsubscript{CTX-M} genes.
both ends of the integration unit (Table S1). Intriguingly, the chromosomal sequences were similar to the 193,678-bp FIB:FII plasmid in the ST392-like isolate. The integration units associated with the \textit{bla}\_CTX-M gene and the targeting locus. The integration was mediated either by IS\_Ecp1 (\textit{n} = 42) or by IS\_26 (\textit{n} = 3). Two integration events per chromosome, both mediated by IS\_Ecp1, were observed in all 16 ST48 isolates, and single integration by IS\_Ecp1 was observed in seven of the eight ST307 isolates and one each of the ST101, ST14, and ST15 isolates. Chromosomal integration by IS\_26 was found in one of the eight ST307 isolates and one each of the ST392 and ST392-like isolates. All of the targeted sites of integration were in the so-called core genome of \textit{K. pneumoniae}, including the 16S rRNA and the coding sequences of OmpK35; except for the case found in ST15, the IS\_Ecp1-\textit{bla}\_CTX-M-15-\textit{orf477} unit transposon was integrated into a 42,544-bp prophage bracketed by a complete 64-bp \textit{attL}-\textit{attR} sequence. The sequential order and the integration of the prophage carrying the \textit{bla}\_CTX-M-15 unit transposon or that of the \textit{bla}\_CTX-M-15 unit transposon into the preintegrated prophage were debatable. The integrations by IS\_Ecp1 generated 5-bp direct repeats and were 2,971 to 29,048 bp in length, and those by IS\_26 were bracketed by 8-bp direct repeats and were 16,570 to 196,572 bp in length (Table S1). Comparison of the chromosomal integration units with plasmids for percent coverage of sequences having a nucleic acid identity of >99.5%, except for the IS\_Ecp1-\textit{bla}\_CTX-M-15-\textit{orf477} unit transposon, showed that the integration units were more covered by the FIB (F-:A-:B-) and FIB:FII (K7:A-:B-) plasmids hosted by ST307 (Fig. 5).

### Table 1: Completeness of IS\_Ecp1 upstream from the \textit{bla}\_CTX-M gene

<table>
<thead>
<tr>
<th>Plasmid</th>
<th>Complete copy of IS_Ecp1</th>
<th>Truncated IS_Ecp1</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total (\textit{n} = 78)</td>
<td>36 (46.2%)</td>
<td>42 (53.8%)</td>
</tr>
<tr>
<td>FIA [K2:A21:B-] (\textit{n} = 5)</td>
<td>5</td>
<td>0</td>
</tr>
<tr>
<td>FIAF [F-A13:B-] (\textit{n} = 15)</td>
<td>0</td>
<td>15</td>
</tr>
<tr>
<td>FIB [F-A-B-] (\textit{n} = 16)</td>
<td>5</td>
<td>11</td>
</tr>
<tr>
<td>FIB:FII total (\textit{n} = 29)</td>
<td>21</td>
<td>8</td>
</tr>
<tr>
<td>[K9:A-B-] (\textit{n} = 3)</td>
<td>3</td>
<td>0</td>
</tr>
<tr>
<td>[K2:A-B-] (\textit{n} = 8)</td>
<td>7</td>
<td>1</td>
</tr>
<tr>
<td>[K7:A-B-] (\textit{n} = 16)</td>
<td>10</td>
<td>6</td>
</tr>
<tr>
<td>[F-A-B-] (\textit{n} = 1)</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>[F21:A-B-] (\textit{n} = 1)</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>FIA:FIB [K2:A21:B-] (\textit{n} = 1)</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>FIB [K7:A-B-] (\textit{n} = 1)</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>FIBR [F-A-B-] (\textit{n} = 1)</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>R (\textit{n} = 6)</td>
<td>1</td>
<td>5</td>
</tr>
<tr>
<td>I1 [16] (\textit{n} = 1)</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>— (\textit{n} = 3)</td>
<td>1</td>
<td>2</td>
</tr>
</tbody>
</table>

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**a**Truncation of IS\_Ecp1 was associated with one of the ISs, IS\_6100 (four FIB:FII [K7:A-B-] plasmids in ST392), IS\_Kpn17 (three FIB [K7:A-B-] plasmids in ST307), IS\_Kpn14 (four FIB [K7:A-B-] plasmids in two of each ST15 and ST4877 strain), and IS\_26 (the rest).

**b**Two cases had uncirculated contigs. One \textit{bla}\_CTX-M-9 gene carried by the FIB:HI1B [K-A-B-] plasmids was associated with IS\_CR1.
unit transposon from the primary integration unit found in ST48. For the second group, the primary integration identically targeted KPHS_45800 of the reference genome, and the ensuing integration was directed to KPHS_51830 or to KPHS_41460. The primary integration units interrupting KPHS_45800 had diverse structures, indicating indepen-

**FIG 4** Heatmap of the pairwise coverage comparison of the group 1 (A) and group 9 (B) bla<sub>CTX-M</sub> gene-carrying plasmids. The plasmids are ordered by incompatibility type, pMLST, and MLST of the bacterial host carrying the plasmid, and the plasmids are grouped based on the bla<sub>CTX-M</sub> gene with white lines.

**TABLE 2** Conjugation efficiency

<table>
<thead>
<tr>
<th>Recipient</th>
<th>ST</th>
<th>C17KP0019 (ST789)/FIA:RΩbla&lt;sub&gt;CTX-M-15&lt;/sub&gt;</th>
<th>E16KP0235 (ST432)/FIB:FILΩbla&lt;sub&gt;CTX-M-14&lt;/sub&gt;</th>
</tr>
</thead>
<tbody>
<tr>
<td>B16KP0003</td>
<td>ST17</td>
<td>3.0 × 10&lt;sup&gt;-5&lt;/sup&gt; to 1.3 × 10&lt;sup&gt;-6&lt;/sup&gt;</td>
<td>&lt;1.0 × 10&lt;sup&gt;-9&lt;/sup&gt;</td>
</tr>
<tr>
<td>F16KP0005</td>
<td>ST375</td>
<td>&lt;1.0 × 10&lt;sup&gt;-9&lt;/sup&gt;</td>
<td>&lt;1.0 × 10&lt;sup&gt;-9&lt;/sup&gt;</td>
</tr>
<tr>
<td>E16KP0152</td>
<td>ST307</td>
<td>&lt;1.0 × 10&lt;sup&gt;-9&lt;/sup&gt;</td>
<td>5.1 × 10&lt;sup&gt;-6&lt;/sup&gt; to 5.2 × 10&lt;sup&gt;-5&lt;/sup&gt;</td>
</tr>
</tbody>
</table>

<sup>a</sup>The experiments were performed in duplicate and repeated at least three times.
dent events of each isolate. The second integration presumably had preferential sequences of the IS\textsuperscript{Ecp1}-\text{bla}\textsuperscript{CTX-M-15}-orf477 unit transposon, and the sequence logo from the upstream and downstream sequences of the IS\textsuperscript{Ecp1}-mediated integration sites presented a consensus of the 5-bp AT-rich sequences upstream from the direct repeats, while the sequences further upstream and downstream did not (Fig. 6B) (21).

**Promoter sequences of the \textit{bla}_{\text{CTX-M}} gene.** Promoter sequences of the \textit{bla}_{\text{CTX-M}} gene were provided from the upstream ISs (Fig. S3). All group 1 \textit{bla}_{\text{CTX-M}} genes had an \textit{ISEcp1} copy 48 bp upstream from the gene except for the \textit{bla}_{\text{CTX-M-3}} gene of the longest region, 124 bp. The 76-bp elongated region indicates that the \textit{bla}_{\text{CTX-M-3}} gene-capturing event was independent from those of the other group 1 \textit{bla}_{\text{CTX-M}} genes. In the case of the group 9 \textit{bla}_{\text{CTX-M}} gene, the \textit{ISEcp1} copy was located 45 bp upstream from the \textit{bla}_{\text{CTX-M-9}} gene, and \textit{ISCR1} was found 115 bp upstream from the \textit{bla}_{\text{CTX-M-9}} gene. The promoter sequences were identical if they were given by the upstream \textit{IS\textsuperscript{Ecp1}} copy.

**DISCUSSION**

Third-generation cephalosporins are widely used in clinical settings to treat patients with \textit{K. pneumoniae} bloodstream infections, and the increasing rate of cephalosporin resistance leads to increased use of carbapenems, encouraging the emerging carba-
penem-resistant Enterobacterales. Currently, resistance to third-generation cephalosporins is mainly due to the acquisition of ESBL genes, and the genes mainly belong to the bla\textsubscript{CTX-M} type. The dissemination of the gene has mostly been favored due to its location in incompatibility F-type plasmids, which are widely distributed in E. coli and K. pneumoniae (8) and are freely acquired and lost by the bacterial host as the antimicrobial environment changes. The chromosomal location of the resistance determinants has taken the situation to a new level of steady spread of resistance regardless of the habitat of the bacterial host, and particular attention needs to be paid to the widespread clinical isolates harboring the chromosomal bla\textsubscript{CTX-M} gene.

The study was conceived through the observation of the resistance isolates belonging to some STs and the almost absolute prevalence of CTX-M-15 and CTX-M-14. Antimicrobial resistance in the dominant clone ST25 is indeed meager, and the ST307, ST789, ST11, and ST48 clones that make up no more than 4.5% of total K. pneumoniae blood isolates presented high rates of cefotaxime resistance between 78% and 100% (20). Even though an extra consideration for the presence of clonally related isolates is needed, the disproportional groups of the bla\textsubscript{CTX-M} gene carried by each ST isolate were caused by, at least partially, the preferred plasmid type carrying the gene. It was likely that the particular clone has a preferential plasmid type and vice versa.

The base pair distance between the right end of the inverted repeat for IS\textsubscript{Ecp1} and
the start codon of the \( \text{bla}_{\text{CTX-M}} \) gene could give a brief point of comparison for the international genetic contexts. The 48-bp distance for the group 1 \( \text{bla}_{\text{CTX-M}} \) genes found in the present study was frequently identified in other parts of the world, i.e., France, India, and China (22–24). However, the 124-bp distance for the \( \text{bla}_{\text{CTX-M-14}} \) gene and the 45-bp distance for the \( \text{bla}_{\text{CTX-M-14}} \) gene seemed unique to this study, and no identical sequence was found even from the nucleotide collection of the GenBank database.

The plasmids carrying the \( \text{bla}_{\text{CTX-M}} \) gene mostly belonged to the incompatibility F-type as a mosaic FIB:FII. Among the FIB:FII plasmids, those in the isolates belonging to the most prevalent CTX-M ESBL-producing ST307 seemed discrete in terms of its TA systems. The GNAT-related toxin, first identified in *Salmonella*, is known to inhibit translation and arrest further growth of the bacterial host (25). The rare incompatibility types were R, which is also famous as an antimicrobial resistance-associated plasmid, I1, carrying the group 1 \( \text{bla}_{\text{CTX-M}} \) type, and the N, A/C2, and B/O/K/Z types, harboring the group 9 \( \text{bla}_{\text{CTX-M}} \) gene. Compared to the previous reports (10, 13), the plasmid types became more disproportionate. Among the 115 CTX-M ESBL-producing *K. pneumoniae* blood isolates in this study, more than a quarter of the isolates harbored the \( \text{bla}_{\text{CTX-M}} \) gene in their chromosomes. All of the chromosomal \( \text{bla}_{\text{CTX-M}} \) genes were subtype 15 and were harbored by *K. pneumoniae* hosts mostly belonging to ST48 and ST307, although the disproportionate distribution of \( \text{bla}_{\text{CTX-M}} \) gene-harboring clones was considered. ST307 and, less dominantly, ST48 are globally notorious *K. pneumoniae* carbapenemase (KPC)-producing clones, and both have been reported as KPC producers in South Korea (26).

More than a quarter of the ST307 isolates harbored the chromosomal \( \text{bla}_{\text{CTX-M-15}} \) gene. The gene was included in varied integration units in terms of length, which differed by the 3′ region of the unit transposon of IS\( \text{Ecp1-bla}_{\text{CTX-M-15}} \)-orf477. The integration units found in ST307 targeted diverse loci in the chromosome, emphasizing the genome plasticity of the notorious clone. One of the isolates harbored the gene in an integration unit bracketed by a pair of IS26 elements of a direction of the KHPS_51550 K\(^{+}\)-transporting ATPase-coding sequence. Interestingly, the other seven ST307 isolates had one copy of IS26 interrupting KHPS_51550, disclosing the IS26-anchored chromosomal integration of the \( \text{bla}_{\text{CTX-M-15}} \) gene-including segment in a plasmid. In this case, the IS\( \text{Ecp1} \) copy upstream from the \( \text{bla}_{\text{CTX-M-15}} \) gene was truncated, and the lost mobility was replaced with the IS26 copy. Two other IS26-mediated integration cases in ST392 and ST392-like clones also included the truncated IS\( \text{Ecp1} \) copy upstream from the \( \text{bla}_{\text{CTX-M-15}} \) gene. Integration of the entire FIB:FII plasmid in the ST392 chromosome and that of the duplicated composite transposon in the ST392-like chromosome was bracketed by a pair of IS26 elements in a particular direction. In the latter case, a supposed rolling-circle tandem amplification by IS26 resulted in the double copy of the \( \text{bla}_{\text{CTX-M-15}} \) gene in a chromosome.

More than half of the isolates harboring the residential \( \text{bla}_{\text{CTX-M}} \) gene belonged to ST48, which had two copies of the gene at a distant locus in the chromosome. The ST48 isolates were clonally distinct, and the chromosomal integration events seemed to be independent. The integration was always mediated by IS\( \text{Ecp1} \), and the integration hot spots were the zinc transporter \( \text{zupT} \) gene and the genes encoding phosphoenolpyruvate-dependent phosphotransferase II and putative glycoside hydrolase. The \( \text{zupT} \) gene was presumed to be a primary integration site for an IS\( \text{Ecp1} \) unit transposon from an R plasmid, because the unit size is longer than 9 kb and the genetic contexts included plasmid-associated components. At the other hot spot, the identical 2,971-bp unit transposon of IS\( \text{Ecp1-bla}_{\text{CTX-M-15}} \)-orf477 was identified as prevailing in the second integration, probably from the primary integration unit. In one exceptional ST48 case, secondary integration was observed at the other gene as a 3′-terminal truncated form of the unit transposon of IS\( \text{Ecp1-bla}_{\text{CTX-M-15}} \)-orf477.

The targeted integration locus had a peculiar consensus AT-rich sequence 5 bp upstream from the direct repeats. This integration site was preferred not only by the major clones but also by the minor ST101, ST14, and ST15 clones. An ST15 isolate was infected by a prophage, and the chromosomal integration of the unit transposon
ISep1-ctx-M-15-orf477 targeted the AT-rich region within the prophage. Based on the
rareness of integration mediated by IS26, complex contexts of the IS26-associated
integration unit and identified truncated ISep1 copy made it possible to form a
reasonable hypothesis: IS26 would be the second-best choice, following ISep1, for the
chromosomal integration of the ctx-M gene.

The cefotaxime-resistant <i>K. pneumoniae</i> clones of this study were particularized
because of the fastidiousness for plasmids to acquire the ctx-M gene and of the
chromosomal accumulation of the ctx-M gene. The fit clones in clinical settings may
have performed a consequent dissemination through acquired resistance, during which
the present population of <i>K. pneumoniae</i> blood isolates was likely being made. The
diverse genetic contexts bracketing the ctx-M gene, chromosomal locus of inte-
gration, and the hospitals from which the isolates were recovered provided enough
evidence to make an assumption. Thus far, to the best of our knowledge, nationwide
dissemination of <i>K. pneumoniae</i> clones with the residential ctx-M gene has never
been reported, and we consider it important to keep a close watch on its status.

This study showed an evolutionary path for antimicrobial resistance in clinical
isolates to sustain their life while surrounded by an abundance of antimicrobials. The
evolutionary strategy could be summed up in two parts, securing diversity and ensur-
ing propagation. For diversification, different types of plasmids were equipped for
enough trials of the bacterial host, and various accessible mobile genetic elements
were used to acquire the gene. Such a plan is important for the bacterial host to avoid
being at a standstill. To ensure stable propagation, the antimicrobial resistance deter-
minant was appointed as a residential gene in the chromosome. The bacterial host then
could better deal with encountering the life-threatening antimicrobials.

MATERIALS AND METHODS

Isolates used in the study. Among the 134 isolates collected from the cohort study, a total of 115
isolates harboring the ctx-M genes were recoverable in good shape, and those 115 isolates were used
for the study.

Whole-genome sequencing. From the 115 <i>K. pneumoniae</i> isolates, genomic DNA was extracted with the
GenElute bacterial genomic DNA kit (Sigma-Aldrich, St. Louis, MO). The entire genomes were
sequenced using both Illumina and Nanopore technologies. Libraries were prepared for Illumina using
both the Swift 25 Turbo DNA library kit (Swift Biosciences, Ann Arbor, MI) and Swift 25 Turbo combi-
natorial dual indexing primer kit (Swift Biosciences) and for Nanopore using the ligation sequencing kit
(Oxford Nanopore, Oxford, UK). Reads were assembled using Spades (ver. 3.11.1) (27). Annotation of the
complete sequences was carried out using prokka 1.13.7 (https://github.com/tseemann/prokka) (28).

Phylogenetic analysis. A total of 16 housekeeping proteins of the 115 <i>K. pneumoniae</i> core genomes
were used to produce a multiple alignment with muscle v3.8 (29). The phylogeny was analyzed using
PhyML v3.0 with the Whelan and Goldman matrix, and a gamma correction was made. To ensure the
robustness of the topology, 100 bootstraps were calculated for the concatenated sequences. To root the
phylogenetic tree, the genome of Klebsiella oxytoca CAV1374 (NZ_CP011636.1) was used.

In silico molecular epidemiology study using the whole genome. For multilocus sequence typing
(MLST), allele numbers of seven housekeeping genes, gapA, infB, mdh, pgi, phoE, rpoB, and tonB, of <i>K.
K. pneumoniae</i> were extracted by using MLST 2.0 (https://cge.cbs.dtu.dk/services/MLST/), and the corre-
sponding ST was obtained through the procedures of Diancourt et al. (30). For six dominant STs, cgMLST,
which is implemented in BIGSdb-Ki (https://bigbdbpasteur.fr/), was further carried out using a total of
2,537 loci (31). The relatedness of each isolate was inferred through constructing minimum spanning
trees using PHYLOViZ (32). The identification of resistance determinants was assessed by using ResFinder
(https://cge.cbs.dtu.dk/services/ResFinder/) (33). The incompatibility type of the ctx-M gene-harboring
plasmid and the plasmid MLST (pMLST) were determined by plasmid finder (https://cge.cbs.dtu.dk//
services/PlasmidFinder/) and pMLST (https://cge.cbs.dtu.dk/services/pMLST/), respectively (34). Type II
toxin/antitoxin systems were searched against the database of TADB 2.0 (35), and subtyping of SHV
and CTX-M was conducted using a laboratory-made database.

Plasmid transfer by bacterial conjugation. For bacterial conjugation, spontaneous mutants resis-
tant to both nalidixic acid and sodium azide were generated from drug-susceptible <i>K. pneumoniae</i>
clinical isolates B16KP0003 of ST17, F16KP0005 of ST375, and E16KP0152 and C16KP0223 of ST307, which
are devoid of any obvious plasmid by electrophoresis, for recipients. <i>K. pneumoniae</i> ST7789 C17KP0019/
FIAaR115-aCTX-M-15 and ST432 E16KP0235/FIB.F115-aCTX-M-14 were selected as donors. Equal amounts of
exponential cultures of the donor and recipient isolates were mixed, incubated in Mueller-Hinton broth
devoid of any drug for 12 h, and spread on brain heart infusion agar (Difco Laboratories) containing
nalidixic acid (30 mg/liter), sodium azide (100 mg/liter), and cefotaxime (10 mg/liter). Each colony was
confirmed by PCR, and the plasmid transfer frequency was calculated as the number of transconjugants
per donor. The experiments were performed in duplicate and repeated at least three times.
SUPPLEMENTAL MATERIAL

Supplemental material is available online only.

FIG S1, TIF file, 2.4 MB.

FIG S2, TIF file, 2.6 MB.

FIG S3, TIF file, 2.7 MB.

TABLE S1, DOCX file, 0.02 MB.

TABLE S2, DOCX file, 0.03 MB.

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REFERENCES


