CTX-M β-Lactamase–producing Klebsiella pneumoniae in Suburban New York, New York, USA

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CTX-M extended-spectrum β-lactamase (ESBL)–producing Klebsiella pneumoniae isolates are infrequently reported in the United States. In this study, we analyzed non-duplicate ESBL-producing K. pneumoniae and Escherichia coli clinical isolates collected during 2005–2012 at a tertiary care medical center in suburban New York City, USA, for the presence of blaCTX-M, blaSHV, blaTEM, and blaKPC genes. Despite a high prevalence of blaCTX-M genes in ESBL-producing E. coli since 2005, blaCTX-M genes were not detected in K. pneumoniae until 2009. The prevalence of CTX-M–producing K. pneumoniae increased significantly over time from 1.7% during 2005–2009 to 26.4% during 2010–2012 (p<0.0001). CTX-M-15 was the dominant CTX-M genotype. Pulsed-field gel electrophoresis and multilocus sequence typing revealed high genetic heterogeneities in CTX-M–producing K. pneumoniae isolates. This study demonstrates the recent emergence and polyclonal spread of multidrug resistant CTX-M–producing K. pneumoniae isolates among patients in a hospital setting in the United States.

CTX-M enzymes are a group of class A extended-spectrum β-lactamases (ESBLs) that are rapidly spreading among Enterobacteriaceae worldwide (1). Since the initial isolation of CTX-M-1 from a European patient in the late 1980s (2), >130 CTX-M allelic variants have been described (http://www.lahey.org/Studies/other.asp#table1). These CTX-M variants have been divided into 5 major phylogenetic groups, CTX-M-1, CTX-M-2, CTX-M-8, CTX-M-9, or CTX-M-25 on the basis of their amino acid sequences (1,2).

During the past decade, CTX-M enzymes have become the most prevalent ESBL enzymes in clinical Enterobacteriaceae isolates, especially in ESBL-producing Escherichia coli in Europe, Asia, and South America (1,3). By contrast, SHV- and TEM-type ESBL enzymes are primarily found in ESBL-producing K. pneumoniae and E. coli clinical isolates in North America (3). In the United States, CTX-M–like ESBL-producing Enterobacteriaceae was first reported in 2003, when CTX-M enzymes were detected in 9 E. coli clinical isolates from 5 US states (4). The spread of CTX-M type ESBL in Enterobacteriaceae, however, was not appreciated until 2007 when a Texas study showed a high prevalence of CTX-M ESBL in E. coli clinical isolates recovered during 2000–2005 (5). Since then, CTX-M–producing E. coli isolates have been documented in dispersed US geographic regions (3,6,7). CTX-M enzymes are now the predominant ESBL type in E. coli clinical isolates in Texas (5), Pennsylvania (6), Illinois (8), and New York (9,10).

CTX-M–type ESBL enzymes have also been reported in the United States in some non-E. coli Enterobacteriaceae species, such as Klebsiella spp. (5,11,12), Proteus mirabilis (5,11), Enterobacter spp. (5), Salmonella spp. (13), Shigella spp. (14), and Morganella morganii (5). Nevertheless, CTX-M–type ESBL have been principally detected and reported in E. coli clinical isolates. To date, <50 CTX-M–producing K. pneumoniae isolates have been described in the United States, and the epidemiologic and microbiological data provided have been limited (5,11,12,15–18). The implications of CTX-M–producing K. pneumoniae for laboratory detection, patient care, and public health in the United States remain to be elucidated.

In this study, we investigated the prevalence of SHV-, TEM-, and CTX-M–encoding genes in a large collection of ESBL-producing K. pneumoniae and E. coli clinical isolates from a tertiary care medical center in suburban New York City in Westchester County, New York, over an

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8-year period (2005–2012). Microbiological characteristics of CTX-M ESBL-producing K. pneumoniae isolates were examined, and certain clinical/epidemiologic features of patients with these isolates were analyzed.

Materials and Methods

Bacterial Isolates and Phenotypic Detection of ESBLs

Nonduplicate K. pneumoniae clinical isolates were recovered from patient specimens during January 2005–July 2012 at the clinical microbiology laboratory of Westchester Medical Center. These included 208 blaKPC-negative non-K. pneumoniae carbapenemase (non-KPC) ESBL-producing or third-generation cephalosporin-resistant K. pneumoniae isolates and 228 KPC (blaKPC-positive)–producing K. pneumoniae isolates. In addition, 163 nonduplicate ESBL-producing E. coli clinical isolates from the same period were also analyzed for comparison. Isolates were randomly selected to span the entire study year with an approximately equal number of isolates per quarter; only 1 isolate from each patient was chosen and tested. The center is a 643-bed academic tertiary-care medical center in Westchester County, New York. The Institutional Review Board of New York Medical College approved this study.

The bacterial isolates were identified and evaluated for antimicrobial drug susceptibility with the MicroScan WalkAway 96 system (Siemens, Sacramento, CA, USA). ESBL production was phenotypically confirmed by a double-disk or broth microdilution method for suspected ESBL isolates according to the Clinical and Laboratory Standards Institute (CLSI) guidelines (19). The antimicrobial drug susceptibility of CTX-M–producing K. pneumoniae isolates against selected antimicrobial drugs was also assessed with standardized CLSI disk diffusion and Etest methods. Bacterial isolates were refrigerated on nutrient agar slants or were frozen (-80°C) in MicroBank cryovials containing 20% glycerol (Pro-Lab Diagnostics, Round Rock, TX, USA).

PCR Detection of blaCTX-M, blaSHV, blaTEM, and blaKPC Genes

For PCR, bacterial genomic DNA was extracted directly from colonies on nutrient slants or from fresh subcultures grown on Trypticase soy agar with 5% sheep blood (TSA II, BBL, Sparks, MD, USA) by boiling a dense suspension of an approximately no. 1 McFarland standard in sterile distilled water. As the DNA template in the PCR assays, 2–3 μL of the boiled cell suspension was used. PCR amplification of blaCTX-M, blaSHV, blaTEM, and blaKPC genes in K. pneumoniae and E. coli clinical isolates was performed by using a consensus primer pair specific to each type of β-lactamase as described (20–22). A multiplex PCR was developed and used for simultaneous detection of blaCTX-M (551 bp) and blaTEM (972 bp) genes. Two PCRs were performed for blaSHV-ESBL and blaKPC, respectively. PCRs were carried out by using the HotStart DNA polymerase master mix (QIA-GEN, Germantown, MD, USA) with 30–35 cycles at an annealing temperature of 50°C for blaCTX-M and blaTEM, and 52°C for blaSHV and blaKPC. PCR products were analyzed by agarose gel electrophoresis or by using the QIAxcel system (QIAGEN). The specificity of PCR amplicons on representative isolates was confirmed by DNA sequencing.

DNA Sequencing

For DNA sequencing, PCR products were purified by using the PCR Purification kit (QIAGEN) or the ExoSAP-IT PCR Clean-up kit (Affymetrix, Cleveland, OH, USA), according to the manufacturer’s instructions. The purified DNA amplicons were sequenced by using an ABI Prism BigDye Terminator (version 1.1) cycle sequencing ready reaction kit on the ABI Prism 3730xl or ABI 3500xl DNA Analyzers (Applied Biosystems, Foster City, CA, USA) in-house, or by a commercial facility (GeneWiz, South Plainfield, NJ, USA). The CTX-M, TEM, and SHV gene sequences were compared with sequences in GenBank by using the NCBI basic local alignment search tool (www.ncbi.nlm.nih.gov/BLAST).

Multilocus Sequence Typing

Multilocus sequence typing (MLST) was performed by using primers and conditions as described by Diancourt et al. (23). PCR products from MLST were sequenced as described above. Allelic profiling and sequence types (STs) were determined by querying the K. pneumoniae MLST database maintained by the Pasteur Institute (www.pasteur.fr/recherche/genopole/PF8/mlst/Kpneumoniae.html).

Pulsed-field Gel Electrophoresis (PFGE)

Pulsed-field gel electrophoresis (PFGE) on CTX-M ESBL–producing K. pneumoniae isolates representing each CTX-M genotype was performed as described (24). The GelCompare II software, (version 2.0; Applied Maths, Austin, TX, USA) was used to calculate the Dice similarity coefficients and generate dendrograms by cluster analysis with the unweighted-pair group method using average linkages. Pulsotype designations were assigned at the ≥80% profile similarity level.

Results

CTX-M in ESBL-producing, non-KPC K. pneumoniae Clinical Isolates

Of the 121 ESBL–producing K. pneumoniae isolates originally recovered during 2005–2009, blaSHV and blaTEM genes were detected in 102 (84.3%) and 61 (50.4%) of 121 isolates, respectively (Table 1). Overall, 25 CTX-M-type
ESBL *K. pneumoniae* were identified. However, none of the 81 *K. pneumoniae* isolates from 2005 through 2008 was positive for bla<sub>CTX-M</sub> genes. CTX-M-type ESBL was first detected in 2 (5.0%) of 40 *K. pneumoniae* isolates from 2009. The prevalence of *K. pneumoniae* isolates carrying the CTX-M–encoding genes increased to 6 (17.6%) of 34 in 2010 and 12 (34.3%) of 35 in 2011. The level remained high (27.8%, 5/18) in the first 7 months of 2012. Overall, only 2 (1.7%) of 121 ESBL-producing *K. pneumoniae* isolates from 2005 through 2009 carried the bla<sub>CTX-M</sub> genes, compared with 23 (26.4%) of 87 isolates from 2010 through 2012 (p<0.0001, Fisher exact test), indicating the rapid emergence and spread of CTX-M enzymes among ESBL-producing *K. pneumoniae* clinical isolates since 2009.

CTX-M in ESBL-producing *E. coli* Clinical Isolates

One hundred sixty-three ESBL-producing *E. coli* clinical isolates from 2005 through 2012 were analyzed by PCR for detection of bla<sub>SBLE</sub> genes of the SHV, TEM, and CTX-M types (Table 2). Unlike the situation with *K. pneumoniae*, bla<sub>CTX-M</sub> genes were detected in ESBL-producing *E. coli* isolated as early as 2005. Overall, 89 (54.6%) of 163 ESBL *E. coli* isolates from the 8-year period carried bla<sub>CTX-M</sub> genes. CTX-M was the leading ESBL type in all years examined except 2008. The bla<sub>CTX-M</sub> genes from 47 (52.8%) of 89 CTX-M–producing *E. coli* isolates were sequenced. CTX-M-15 was determined in 45 (95.7%) of 47 CTX-M–producing *E. coli* isolates analyzed. CTX-M-1 and CTX-M-3 genotypes were each found in 1 ESBL *E. coli* isolate.

CTX-M in KPC-producing *K. pneumoniae* Clinical Isolates

Two hundred twenty-eight KPC-producing *K. pneumoniae* isolates from 2005 to 2012 were examined by PCR for detection of bla<sub>KPC</sub> genes. All *K. pneumoniae* isolates were positive for the bla<sub>KPC</sub> gene by PCR as described (22). None was positive for the bla<sub>CTX-M</sub> gene.

Clinical and Microbiological Characteristics of CTX-M–producing *K. pneumoniae*

Selected clinical/epidemiologic features of the 25 patients with CTX-M–producing *K. pneumoniae* and certain microbiological characteristics of the isolates are shown in Table 3, Appendix (wwwnc.cdc.gov/EID/article/19/11/12-1470-T3.htm). Mean patient age was 56 years, and 13 (52%) of the patients were male. Sixteen patients (64%) had bacteriuria. CTX-M–producing *K. pneumoniae* isolates were recovered from 13 (52%) patients within 72 hours of hospital admission; however, 18 (72%) of these patients had been hospitalized in the 8 months before the current admission.

The bla<sub>CTX-M</sub> genes from all 25 CTX-M ESBL–producing *K. pneumoniae* isolates from 2009 through 2012 were sequenced. CTX-M-15 was identified in 19 (76.0%) and was the dominant CTX-M genotype. The remaining 6 isolates were determined to be CTX-M-3 (n = 4), CTX-M-1 (n = 1), and CTX-M-2 (n = 1), respectively. Twenty-four (96.0%) had coexisting bla<sub>SHV</sub> β-lactamases, which were predominantly non-ESBL bla<sub>SHV-11</sub> (n = 15) and bla<sub>SHV-1</sub> (n = 5). Four additional *K. pneumoniae* carried ESBL-type bla<sub>SHV</sub> β-lactamases, including bla<sub>SHV-12</sub> (n = 1), bla<sub>SHV-2</sub> (n = 1), and bla<sub>SHV-25</sub> (n = 2). Seventeen (68.0%) were positive for TEM-type β-lactamases, and all were confirmed to be bla<sub>TEM-1</sub>.

The antimicrobial drug susceptibilities of CTX-M–producing *K. pneumoniae* isolates are summarized in Table 4. Of the 25 CTX-M–producing *K. pneumoniae* isolates examined in this study, only 12% (n = 3) and 36% (n = 8) of isolates were susceptible to ciprofloxacin and gentamicin, respectively. Low susceptibility rates were also observed for piperacillin/tazobactam (36%), tetracycline (20%) and trimethoprim/sulfamethoxazole (4%). Twenty-three of the 25 (92%) isolates tested were susceptible to carbapenems. Notably, the 2 carbapenem-resistant *K. pneumoniae* isolates (PK30 and PK107) carried bla<sub>CTX-M-3</sub> and bla<sub>SHV-11</sub>. One of these *K. pneumoniae* isolates also showed resistance to colistin with an MIC of 64µg/mL. Both patients died of complications associated with bloodstream and respiratory tract infections. Three of 22 CTX-M–producing *K. pneumoniae* isolates examined by Etest were nonsusceptible to tigecycline (MICs 3 µg/mL, 3 µg/mL, and 8 µg/mL).

All 25 CTX-M–producing *K. pneumoniae* isolates examined were resistant to cefotaxime, and all but 1 isolate and certain microbiological characteristics of the isolates are shown in Table 3, Appendix (wwwnc.cdc.gov/EID/article/19/11/12-1470-T3.htm). Mean patient age was 56 years, and 13 (52%) of the patients were male. Sixteen patients (64%) had bacteriuria. CTX-M–producing *K. pneumoniae* isolates were recovered from 13 (52%) patients within 72 hours of hospital admission; however, 18 (72%) of these patients had been hospitalized in the 8 months before the current admission.

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The 50% minimum inhibitory concentration (MIC_{50}) for cefotaxime among these isolates was >256 µg/mL. By contrast, the MIC_{50} and 90% inhibitory concentration for ceftazidime were 16 µg/mL and 128 µg/mL, respectively. Two CTX-M–producing K. pneumoniae isolates (8.0%) were susceptible (MIC ≤4 µg/mL) and 5 isolates (20%) were intermediate in susceptibility (8 µg/mL) to ceftazidime according to the 2010 revised CLSI breakpoints (Figure 1). In addition, we determined the susceptibilities of 22 CTX-M–producing K. pneumoniae isolates against cefotaxime and ceftazidime by using the standard disk diffusion method. All CTX-M–producing K. pneumoniae isolates examined were resistant to cefotaxime by disk diffusion (mean inhibitory zone size 8.3 mm; range 6–13 mm). Two of these isolates were susceptible (≥21 mm) and 5 had intermediate (18–20 mm) susceptibility to ceftazidime by disk diffusion (Table 3, Appendix). The disk diffusion results showed a category agreement with the Etest MIC of 100% for cefotaxime and 90.9% for ceftazidime with 2 minor errors.

**PFGE and MLST Analysis of CTX-M–producing K. pneumoniae**

Of 17 representative CTX-M–producing K. pneumoniae isolates analyzed by PFGE, 8 different pulsotypes (PF1–8) were identified with Dice coefficients of ≥80% similarity (Figure 2). Ten of 17 K. pneumoniae isolates examined belonged to 3 major groups (PF3, PF4, PF5) with 3–4 isolates in each group. The remaining pulsotypes contained only 1 or 2 K. pneumoniae isolates. No clear temporal relationship was shown among the highly related isolates.

MLST was performed on 18 CTX-M–producing K. pneumoniae isolates. These isolates were selected to represent different CTX-M genotypes, pulsotypes, antimicrobial susceptibility profiles, and years of isolation. Twelve STs were recognized for the K. pneumoniae isolates examined (Table 3, Appendix). Notably, all 3 CTX-M group 1, non–CTX-M-15 K. pneumoniae isolates analyzed (KP38, PK107, and PK135) had ST11, whereas 10 different STs (ST15, ST16, ST17, ST48, ST147, ST252, ST258, ST280, ST392, and ST437) were identified for the 14 CTX-M-15 K. pneumoniae isolates. Isolate F351 was the only non–CTX-M-1 group K. pneumoniae isolate identified in this study and was determined to be a separate group (ST792) by MLST. Of the 14 CTX-M–producing K. pneumoniae isolates evaluated simultaneously by DNA sequencing, PFGE and MLST, a high genetic divergence was demonstrated by the detection of 4 CTX-M genotypes (CTX-M-1, CTX-M-2, CTX-M-3, and CTX-M-15), 8 pulsotypes (PF1–8) and 11 STs (ST11, ST15, ST16, ST17, ST48, ST147, ST252, ST280, ST392, ST437, and ST792) (Figure 2).

**Discussion**

CTX-M ESBL–producing E. coli, especially ST131 strains, have emerged in recent years in several US states (5–7,25,26). In this study, we detected bla\textsubscript{CTX-M} genes in ESBL-producing E. coli strains isolated from patients at a tertiary care medical center in suburban New York City as early as 2005. Eighty-nine (54.6%) of 163 ESBL-producing E. coli isolates in the study period (2005–2012) carried bla\textsubscript{CTX-M}. Our findings confirm the emergence and dominance of CTX-M enzymes in ESBL-producing E. coli since the mid-2000s in the New York City metropolitan area (9,10).

Despite this high prevalence of CTX-M in ESBL-producing E. coli since 2005, none of 81 ESBL-producing K. pneumoniae isolates recovered from patients at the same tertiary care medical center from 2005 through 2008 was positive for bla\textsubscript{CTX-M}. CTX-M–type ESBL was first detected in K. pneumoniae isolates from our institution in 2009. The percentage of K. pneumoniae isolates carrying bla\textsubscript{CTX-M} has increased significantly since then. During 2010–2012, bla\textsubscript{CTX-M} genes were identified in 23 of 87 (26.4%) ESBL-producing K. pneumoniae isolates. These data demonstrate the rapid emergence and spread of CTX-M ESBL–producing K. pneumoniae in our patients. To date, CTX-M–producing K. pneumoniae has been recognized in several US states, including Texas (2004–2007, n = 11) (5,12), Nebraska (2005, n = 1)
In clinical strains, CTX-M–encoding genes have common
grounds. This hypothesis contrasts with findings regarding
likely occurred among isolates with diverse genetic back
polyclonal spread of CTX-M–producing
K. pneumoniae
isolates in the mid- to late-2000s in the United States.
CTX-M in
penicillin–tazobactam than CTX-M-14–producing isolates
32
K. pneumoniae
isolates in the Calgary Healthcare Region of Cana
demonstrates that involves several motile
involves several motile
K. pneumoniae
isolates by PFGE and MLST. Of
17 representative isolates examined by PFGE, 8 differ
clusters were determined. Similarly, 12 MLST STs
were identified for the 18 CTX-M–producing isolates ana
Our data provide strong evidence for the recent, rapid
emergence, and polyclonal spread of the CTX-M-1 group,
especially CTX-M-15 ESBL-producing K. pneumoniae
in a US hospital setting. In this study, 24 (96.0%) of 25
bla_{CTX-M}–positive E. coli isolates. In addition, 1 K. pneu
moniae isolate had the CTX-M-2 genotype. No CTX-M-14
was detected in these K. pneumoniae and E. coli isolates.
CTX-M-14 has also been reported in K. pneumoniae
isolates in the Calgary Healthcare Region of Canada (32).
Why CTX-M-14 is absent in the ESBL-producing E. coli and K. pneumoniae isolates from the New York,
NY, metropolitan area is unknown. Because CTX-M-15–
producing K. pneumoniae isolates may exhibit significantly
higher resistance rates to ciprofloxacin and piperacillin-tazo
bactam than CTX-M-14–producing isolates (27,28), CTX-
M genotypes and their antimicrobial drug profiles should
be monitored among CTX-M–producing E. coli and K. pneumoniae isolates in regions where they are emerging.
We investigated the genetic relatedness of CTX-M–
producing K. pneumoniae isolates by PFGE and MLST. Of
the 17 representative isolates examined by PFGE, 8 differ
clusters were determined. Similarly, 12 MLST STs
were identified for the 18 CTX-M–producing isolates ana
Our data, in combination with findings from other groups (1), suggest that CTX-M–producing K. pneumoniae
isolates are genetically heterogeneous. The emergence and
polyclonal spread of CTX-M–producing K. pneumoniae
likely occurred among isolates with diverse genetic back
This hypothesis contrasts with findings regarding
KPC-producing K. pneumoniae: a clonal spread of KPC-
producing K. pneumoniae isolates belonging to the ST258
lineage was observed by us (33) and Pournaras et al. (34).
In clinical strains, CTX-M–encoding genes have commonly
been located on plasmids that vary in size from 7 kb to
160 kb (2). Plasmid-mediated transmission of CTX-M
genes in Enterobacteriaceae that involves several motile

(15), Pennsylvania (2007, n = 5) (11), and 1 isolate in 2007
each from California, Massachusetts, Michigan, New Jersey,
New York, Washington, and Wisconsin (12). In addition,
a few CTX-M K. pneumoniae isolates have been reported from 2 collections of the SMART surveillance program
with isolates recovered during 2008–2009 (16) and 2009–2010
(18). No CTX-M was detected in US ESBL-producing K.
K. pneumoniae isolates collected before 2000 (3), with all
CTX-M–producing K. pneumoniae isolates recovered from
US patients in or after 2004. Therefore, we speculate that
the emergence and spread of bla_{CTX-M} in K. pneumoniae are
recent evolutionary events that most likely occurred in the
mid- to late-2000s in the United States.

The particular CTX-M enzyme type in ESBL-produ
K. pneumoniae and E. coli varies geographically.
CTX-M-15, which belongs to the CTX-M-1 group, is
the most prevalent CTX-M allele with a worldwide distribution
(1,2,26). CTX-M-14, which belongs to the CTX-M-9 group,
is another common variant that is highly prevalent in some
European and Asian countries (27–30), whereas CTX-M-2
in the CTX-M-2 group and CTX-M-8 seem to be dominant
in South America (1,31). In the United States, CTX-M-15
is the most frequently detected genotype among CTX-M–
producing K. pneumoniae isolates, followed by CTX-M-14
(5,11,12). CTX-M-2 group and CTX-M-8 group ESBL-produc
K. pneumoniae each was identified in 1 isolate (16).

Our data provide strong evidence for the recent, rapid
emergence, and polyclonal spread of the CTX-M-1 group,
especially CTX-M-15 ESBL-producing K. pneumoniae
in a US hospital setting. In this study, 24 (96.0%) of 25
bla_{CTX-M}–positive K. pneumoniae were categorized as
group 1 CTX-M, including isolates encoding CTX-M-15
(n = 19), CTX-M-1 (n = 1), and CTX-M-3 (n = 4). Similarly,
group 1 CTX-M was detected in 47 (100%) of 47

<table>
<thead>
<tr>
<th>Antimicrobial agent</th>
<th>No. isolates tested</th>
<th>No. (%) susceptible isolates</th>
<th>MIC range</th>
</tr>
</thead>
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<tr>
<td>Cefotaxime†</td>
<td>22</td>
<td>0</td>
<td>&gt;256–256</td>
</tr>
<tr>
<td>Cefazidime†</td>
<td>22</td>
<td>2 (9.1)</td>
<td>64–64</td>
</tr>
<tr>
<td>Pip/Tazo</td>
<td>25</td>
<td>9 (36.0)</td>
<td>&gt;2–2</td>
</tr>
<tr>
<td>Ertapenem</td>
<td>25</td>
<td>23 (92.0)</td>
<td>0.094–0.125</td>
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<tr>
<td>Meropenem†</td>
<td>22</td>
<td>21 (95.5)</td>
<td>&gt;2–2</td>
</tr>
<tr>
<td>Imipenem†</td>
<td>22</td>
<td>20 (90.1)</td>
<td>&gt;2–2</td>
</tr>
<tr>
<td>Ciprofloxacin</td>
<td>25</td>
<td>3 (12.0)</td>
<td>&gt;2–2</td>
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<tr>
<td>Amikacin</td>
<td>25</td>
<td>18 (72.0)</td>
<td>&gt;16–32</td>
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<td>8 (32.0)</td>
<td>&gt;8–8</td>
</tr>
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<td>5 (20.0)</td>
<td>&gt;8–8</td>
</tr>
<tr>
<td>TMP/SMX</td>
<td>25</td>
<td>1 (4.0)</td>
<td>&gt;2/38–&gt;38</td>
</tr>
<tr>
<td>Tigecycline†‡</td>
<td>22</td>
<td>19 (86.4)</td>
<td>1–3</td>
</tr>
<tr>
<td>Colistin†§</td>
<td>22</td>
<td>21 (95.5)</td>
<td>0.25–0.38</td>
</tr>
</tbody>
</table>

* n = 25; MIC<sub>50</sub>; 50% minimum inhibitory concentration; MIC<sub>90</sub>; 90% minimum inhibitory concentration; Pip/Tazo, piperacillin/tazobactam; TMP/SMX,
trimethoprim/sulfamethoxazole. MICs were determined by the MicroScan system, except for certain antimicrobial agents that were tested by Etest as specified.
†MICs were determined by Etest.
‡Susceptibility defined by Food and Drug Administration breakpoints.
§Susceptibility defined by Clinical Laboratory and Standards Institute breakpoints for Acinetobacter baumannii (19).
genetic elements has been described (2,35,36). Given the dominance of CTX-M-15 genotypes among genetically heterogeneous K. pneumoniae isolates, our study also implies the probable horizontal transfer of a genetic element carrying bla\textsubscript{CTX-M} among K. pneumoniae isolates.

Of the 12 STs determined for the CTX-M ESBL–producing K. pneumoniae isolates, ST11, ST15, ST17, ST48, ST147, and ST258 have been reported in CTX-M–positive K. pneumoniae in Spain, Hungary, or Korea (28,37,38). Among these, only ST17 was reported among CTX-M–producing K. pneumoniae isolates in Canada (39). In this study, we determined the STs among CTX-M–producing K. pneumoniae isolates evaluated in this study showed several notable epidemiologic, clinical, and microbiological features. First, most CTX-M–producing isolates were recovered from patients with bacteriuria, which is similar to that observed for infections caused by CTX-M–producing E. coli in New York, NY, (9,10). Although CTX-M–producing K. pneumoniae was isolated in clinical specimens collected within 72 hours of hospitalization in about half of the patients, 18 (72%) of 25 patients had been hospitalized in the prior 8 months. This factor highlights the potential for acquiring CTX-M–producing K. pneumoniae in health care settings and differs from the experience with CTX-M–producing E. coli that are associated with infections arising in the community setting unrelated to exposure to health care facilities (26). Second, the CTX-M–producing K. pneumoniae study isolates exhibited high rates of resistance to gentamicin (68%), trimethoprim-sulfamethoxazole (96%), and tetracycline (80%), in addition to resistance to ciprofloxacin (88%) and piperillin-tazobactam (64%) as described previously in Europe and Asia (27,28,37). Whether such high rates of resistance are associated with the dominant spread of CTX-M-15–producing, rather than CTX-M-14–producing, K. pneumoniae, in these patients is not known. The coexistence of CTX-M ESBL and TEM-1 and SHV-type β-lactamases in these isolates may have also contributed to the observed high rate of antimicrobial drug resistance. All except 1 of our CTX-M–positive K.

![Figure 1](image1.png)

**Figure 1.** MIC distribution for cefotaxime (CTX) and ceftazidime (CAZ) in CTX-M extended-spectrum β-lactamase–producing Klebsiella pneumoniae clinical isolates from a tertiary care medical center, in suburban New York, New York, USA, 2005–2012 (n = 22). The MICs were determined by Etest.

![Figure 2](image2.png)

**Figure 2.** Dendrogram of pulsed-field gel electrophoresis (PFGE) patterns showing the genetic relatedness of CTX-M extended-spectrum β-lactamase (ESBL)–producing Klebsiella pneumoniae isolates from patients in suburban New York, NY, USA (n = 17). Eight PFGE pulsetypes (PF1–8) were identified with ≥80% similarity, which is marked by the vertical line. The corresponding CTX-M genotype, sequence type (ST), if available, and year of isolation for each isolate are listed on the right side of the dendrogram.
**Klebsiella pneumoniae** isolates produced SHV- and CTX-M-type ESBLs. These findings have clinical implications for selecting empiric antimicrobial drug therapy when infection caused by ESBL-producing *K. pneumoniae* is suspected. The rapid emergence of such CTX-M–producing *K. pneumoniae* isolates, mainly in US hospitals, is also raising new concerns for public health and infection control practice. Third, none of the 228 KPC-producing *K. pneumoniae* isolates examined carried *bla* 

**CTX-M**. Coexistence of *bla* 

K. pneumoniae in China (40). Whether certain genetic mechanisms prevent KPC-producing *K. pneumoniae* from acquiring *bla* 

**CTX-M** is unclear.

This study reveals the rapid emergence and polyclonal spread of CTX-M–producing *K. pneumoniae* in patients in Westchester County, New York. A limitation of our study is that the clinical isolates were collected from patients at a single tertiary-care medical center. Investigations of CTX-M–producing *K. pneumoniae* isolates from a variety of geographic regions should be undertaken to clarify the epidemiology and clinical and public health effects of the emergence of CTX-M–producing *K. pneumoniae* in the United States.

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