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Epidemiological Study of an Outbreak of KPC-2-Producing *Klebsiella pneumoniae* in a Tertiary Hospital in Korea

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Abstract

Background: The prevalence of carbapenemase-producing *Enterobacteriaceae* (CPE), especially the KPC-2-producing *Klebsiella pneumoniae*, is rapidly increasing and becoming a menace to global public health. This study aims to present the molecular epidemiology of the KPC-2-producing *K. pneumoniae* isolates that emerged in a tertiary hospital in South Korea and describe its clinical significance. *Methods:* This study included carbapenem-resistant *K. pneumoniae* isolates collected from a tertiary hospital from April to December 2018. The antimicrobial susceptibility of *K. pneumoniae* isolates was tested using the disk diffusion method. PCR and DNA sequence analyses were performed to identify the resistance genotype. In addition, the molecular epidemiology was investigated using pulsed-field gel electrophoresis (PFGE) and multi-locus sequencing typing (MLST). *Results:* A total of 100 KPC-2-producing *K. pneumoniae* isolates were collected, which were mainly classified into two pulsotypes according to the XbaI restriction digestion pattern by PFGE analysis (pulsotype A, $n = 31$; pulsotype B, $n = 63$). The isolates exhibiting pulsotype A belonged to ST395 and the remaining isolates exhibiting pulsotype B were attributed to ST307 by MLST analysis. *Conclusion:* This study investigated clinical information and molecular bacterial profiles for KPC-2-producing *K. pneumoniae* isolates. These findings indicate that proper infection control activities are needed to prevent the spread of multidrug-resistant organisms such as CPE, which could cause high mortality in the clinical field.

Keywords

Carbapenemase
KPC-2 beta-lactamase
Klebsiella pneumoniae
Pulsed-field gel electrophoresis

1. Introduction

With the spread of gram-negative bacilli that produce extended-spectrum beta-lactamases (ESBLs) that confer resistance to beta-lactam antibiotics [1], The increasing use of carbapenem-based antibiotics as the main therapeutic antibiotic for gram-negative bacterial infections has led to a rapid increase in carbapenem-resistant *Enterobacteriaceae* (CRE), which has become a global problem [2,3]. Domestically, carbapenem resistance rates of less than 1% have been reported in *Escherichia coli* and *Klebsiella pneumoniae* [4], but reports of carbapenemase-producing *Enterobacteriaceae* (CPE) isolates have been continuously increasing in recent years [5]. CRE can be divided into carbapenemase-nonproducing *Enterobacteriaceae* (CNPE) and carbapenemase-producing *Enterobacteriaceae* (CPE) [6]. The main mechanism by which gram-negative bacteria acquire resistance to carbapenem-based antibiotics is antibiotic inactivation by carbapenemase production. The genes encoding carbapenemase are often present on mobile genetic elements such as plasmids and transposons, allowing for the transmission of resistance between species and between species, and are therefore a real target for infection control and surveillance in healthcare facilities and the community [7].

Carbapenemases are categorized into three classes according to Ambler's classification as follows: (i) class A; *Klebsiella pneumoniae* carbapenemase (KPC), Guiana extended-spectrum beta-lactamase (GES), etc; (ii) class B; New Delhi metallo-beta-lactamase (NDM), imipenemase (IMP), Verona integron-encoded metallo-β-lactamase (VIM), etc; and (iii) class D; oxacillinase (OXA)-48-like, etc [1,6]. According to Lee *et al.* [8], the number of carbapenemase *Enterobacteriaceae* isolates reported to the Centers for Disease Control and Prevention increased from 39 in 2012 to 2,953 in 2017. Among carbapenemase *Enterobacteriaceae*, KPC types were the most common, with KPC-2 accounting for the largest proportion. The bla_{KPC-2} gene has been most frequently reported since it was first detected in *K. pneumoniae* in 2010 [9-11]. In a report by Yoon *et al.*, when the isolation status of carbapenemase enterobacteria in Korea was checked, KPC-2-producing *K. pneumoniae* accounted for more than half, followed by NDM-1-producing *E. coli*, and then OXA-48-like-producing *E. coli* [5]. When examining the strain type (ST) of KPC-2-producing *K. pneumoniae*, ST11, and ST258 are the most common worldwide, and widespread transmission of ST11 and ST307 has been reported in Korea [5,8].

In this study, we aimed to identify the molecular epidemiological association of KPC-type carbapenemase-producing *K. pneumoniae* isolated from a Korean general hospital from April to December 2018 and to determine their clinical significance.

2. Materials and methods

2.1. Target strains

K. pneumoniae strains isolated from clinical specimens from April to December 2018 in one general hospital in Korea that showed non-susceptibility to carbapenem-based antibiotics including imipenem, meropenem, and ertapenem were collected. If *K. pneumoniae* was isolated repeatedly from the same patient, the initial isolate was collected.

2.2. Strain identification

Strain identification was performed using a Bruker Biotyper (Bruker, Billerica, MA, USA) based on a matrix-assisted laser desorption ionization–time of flight mass spectrometer (MALDI-TOF MS). Collected *K. pneumoniae* isolates obtained by culturing them on MacConkey broth (BANDIO, Pocheon, Korea) were smeared thinly on MALDI-TOF plates and allowed to dry completely by applying matrix solution before using MALDI-TOF MS. The criterion for strain identification score was 2.0 or higher.

2.3. Antibiotic susceptibility test

Carbapenem antibiotic susceptibility testing was performed using the NMIC-203 panel of the Phoenix

M50 (Becton Dickinson, Franklin Lakes, NJ, USA). In addition, randomly selected representative isolates were tested for susceptibility to piperacillin, ampicillin-sulbactam, cefazolin, cefotaxime, ceftazidime, cefepime, aztreonam, cefoxitin, imipenem, meropenem, ertapenem, amikacin, gentamicin, tigecycline, colistin, ciprofloxacin, and trimethoprim-sulfamethoxazole were tested for antibiotic susceptibility by disc diffusion. Readings were made according to Clinical and Laboratory Standard Institute (CLSI) interpretive criteria [12], and *E. coli* ATCC 25922 was used as the standard strain.

2.4. Analysis of resistance mechanisms

Carbapenem-resistant *K. pneumoniae* isolates were subjected to PCR and sequencing for ESBL (CTX-M-1, CTX-M-2, CTX-M-9, and CTX-M-25), AmpC (CMY-1, CMY-2, ACC, ACT, FOX), and carbapenemases (KPC, IMP, VIM, NDM, GES, and OXA-48). PCR conditions were as follows: (1) for ESBL and carbapenemase, amplification with 30 cycles of pre-denaturation 95°C for 5 min, denaturation 94°C for 30 sec, annealing 56°C for 20 sec, and extension 72°C for 40 sec, followed by a reaction at 72°C for 7 min; (2) for AmpC, amplification with 25 cycles of pre-denaturation 94°C for 5 min, denaturation 94°C for 30 sec, annealing 58°C for 30 sec, and extension 72°C for 1 min, followed by a reaction at 72°C for 7 min. The amplification products were sequenced and the results obtained were compared with NCBI's BLAST (https://blast.ncbi.nlm.nih.gov/Blast.cgi) to confirm the genotype. The sequences of the primers used in this study are summarized in **Table 1**.

2.5. Pulsed-field gel electrophoresis (PFGE)

The genome (gDNA) of *K. pneumoniae* was immobilized on a plug, digested with XbaI (TaKaRa biotechnology, Shiga, Japan) restriction enzyme, and electrophoresed on a GenePath System (Bio-Rad Laboratories, Hercules, CA, USA) at 6 V/cm, switch time 2.1 s, 11°C. The criteria for identical pulsotypes were determined as follows: (1) a difference of less

Table 1. Oligonucleotide sequence of the primers used in this study

Target gene	Primer name	Primer sequence (5' to 3')	Amplicon size (bp)
$bla_{CTX-M-1}$	CTX-M-1_48–25F	GACTATTCATGTTGTTGTTAWTTC	973
	CTX-M-1_+28–+49R	TAAGGCGATAAACAAAAACGGA	
$bla_{CTX-M-9}$	CTX-M-9_-42–21F	GAATACTGATGTAACACGGATT	962
	CTX-M-9_+23–+44R	ATATAAATAGAAAGTGGGGCAC	
	CTX-M-9_+27–+46R	CTGATCCTTCAACTCAGCAA	
bla_{CMY-1}	MOXM F	GCTGCTCAAGGAGCACAGGAT	520
	MOXM R	CACATTGACATAGGTGTGGTGC	
bla_{CMY-2}	CTTM F	TGGCCAGAACTGACAGGCAAA	462
	CTTM R	TTTCTCCTGAACGTGGCTGGC	
bla_{DHA}	DHAM F	AACTTTCACAGGTGTGCTGGGT	405
	DHAM R	CCGTACGCATACTGGCTTTGC	
bla_{ACC}	ACCM F	AACAGCCTCAGCAGCCGGTTA	346
	ACCM R	TTCGCCGCAATCATCCCTAGC	
bla_{ACT}	EBCM F	TCGGTAAAGCCGATGTTGCGG	302
	EBCM R	CTTCCACTGCGGCTGCCAGTT	
bla_{FOX}	FOXM F	AACATGGGGTATCAGGGAGATG	190
	FOXM R	CAAAGCGCGTAACCGGATTGG	
bla_{KPC}	KPC F	ATGTCACTGTATCGCCGTCT	882
	KPC R	TTTTCAGAGCCTTACTGCCC	

than three bands in the PFGE banding pattern, and (2) band similarity of phylogenetic trees generated on the basis of unweighted pair groups using 1.0% Dice coefficient arithmetic averages, analyzed with InforQuestFP Version 4.5 (Bio-Rad, Hercules, CA, USA), was greater than 80% [19].

2.6. Multi-locus sequence typing (MLST)

Representative pulsotypes were identified based on the similarity of PFGE band types, and one representative strain was randomly selected for each pulsotype and subjected to PCR and sequencing for seven housekeeping genes, *rpoB*, *gapA*, *mdh*, *pgi*, *phoE*, *infB*, and *tonB*, and the analyzed sequences were compared with the *K. pneumoniae* MLST database (http://bigsdb.pasteur.fr/klebsiella/klebsiella.html) to identify allelic type and sequence type.

2.7. Investigate clinical information

The age, sex, type of specimen isolated, route of admission, ward, and prognosis of patients with KPC-generated *K. pneumoniae* were investigated. For transferred patients, the type of hospital (primary care, nursing home, general hospital) was identified; for hospitalized patients, the type of hospital room (general ward or intensive care unit) was identified.

3. Results

3.1. Clinical information of patients with KPC-2-producing *K. pneumoniae* isolates

A total of 100 isolates of KPC-2-producing *K. pneumoniae* were identified. One week of KPC-2-producing *K. pneumoniae* was isolated in April 2018, followed by six weeks in May, 13 weeks each in June and July, and a peak of 25 weeks in August. The number then decreased to 17 in September, followed by 8 in October, 11 in November, and 5 in December (**Figure 1**).

Among the patients isolated with KPC-2-producing *K. pneumoniae*, 56 (56.0%) were male, and 44 (44.0%) were female, with more males than females. The age of the patients ranged from 0 to 96 years, with a mean age of 67 years, and all but one patient aged 0 and 9 years were adults aged 20 years or older. In particular, there was a high proportion of elderly patients, with 78 patients aged 60 years or older. Of the total patients, 21.0% (n = 21) were referred from outside hospitals, of which 42.9% (9/21) were referred from general

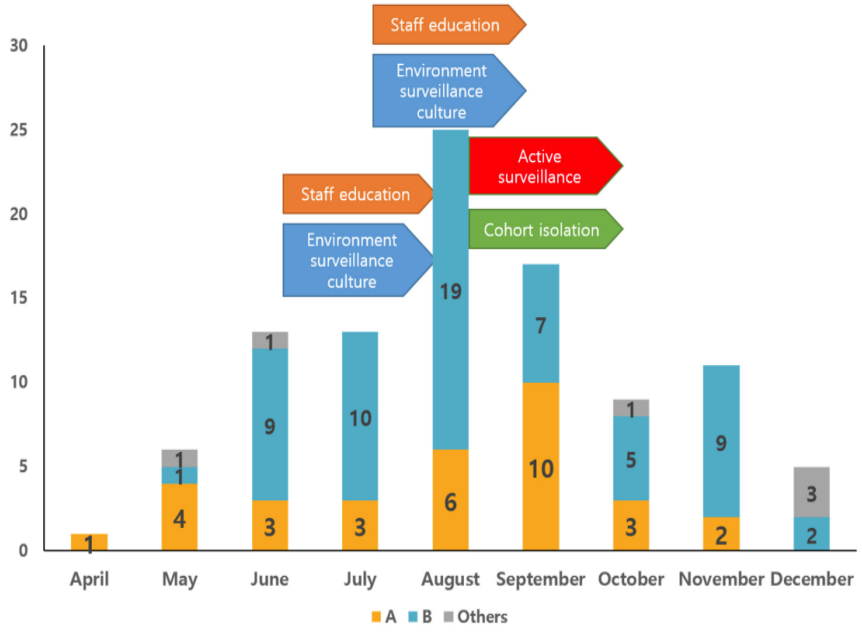

Figure 1. Monthly isolation of KPC-2-producing *K. pneumoniae* isolates stratified by PFGE banding patterns. Bar graphs indicate the numbers of KPC-2-producing *K. pneumoniae* isolates collected in each month during April–December 2018 and arrows indicate the activity performed for eradicating a KPC-type carbapenemase-producing *K. pneumoniae* isolates outbreak. Yellow bar, pulsotype A; Blue bar, pulsotype B; Gray bar, other pulsotypes.

hospitals, 28.6% (6/21) from nursing homes, and 28.6% (6/21) from clinics. As for the type of specimen, 37.0% (*n* = 37) of the isolates were from the respiratory tract, followed by 22.0% (*n* = 22) from the urinary tract and 15.0% (*n* = 15) from the abscess (**Table 2**).

By ward, KPC-2-producing *K. pneumoniae* was most frequently isolated from general wards with 77.0% (*n* = 77), followed by 21.0% (*n* = 21) from intensive care and 2.0% (*n* = 2) from outpatients. Single wards had the highest number of isolates with 17.0% (*n* = 17) in ICU, followed by ward 64 (15.0%, *n* = 15) and ward 63 (13.0%, *n* = 13). The in-hospital mortality rate for KPC-2-producing *K. pneumoniae* isolates was 37.0% (*n* = 37), and the 30-day mortality rate was 25.0% (*n* = 25).

Table 2. Patient characteristics

Characteristic	Total (*n* = 100) No. (%)	Pulsotype A (*n* = 31) No. (%)	Pulsotype B (*n* = 63) No. (%)	Others (*n* = 6) No. (%)	*P*-value*
Age (yr)†	69.0 [60.1–77.3]	69.0 [60.0–78.0]	70.0 [62.0–76.5]	67.5 [53.0–87.0]	0.974
Male	56 (56.0)	20 (64.5)	33 (52.4)	3 (50.0)	0.371
Comorbidity					
Cardiovascular disease	15 (15.0)	7 (22.6)	7 (11.1)	1 (16.7)	0.246
Cerebrovascular disease	10 (10.0)	4 (12.9)	6 (9.5)	0	0.886
Diabetes mellitus	13 (13.0)	4 (12.9)	8 (12.7)	1 (16.7)	0.999
End-stage renal disease	6 (6.0)	2 (6.5)	4 (6.3)	0	0.999
Chronic liver disease	4 (4.0)	2 (6.5)	2 (3.2)	0	0.844
Malignancy	55 (55.0)	21 (67.7)	31 (49.2)	3 (50.0)	0.139
Charlson comorbidity index†	2.0 [1.0–6.0]	3.0 [2.0–6.0]	2.0 [1.0–6.0]	1.5 [0.0–3.0]	
Specimen					0.163
Sputum	37 (37.0)	15 (48.8)	21 (33.3)	1 (16.7)	
Urine	22 (22.0)	3 (9.7)	18 (28.6)	1 (16.7)	
Pus	15 (15.0)	3 (9.7)	11 (17.5)	1 (16.7)	
Surveillance	13 (13.0)	5 (16.1)	6 (9.5)	2 (33.3)	
Genital	7 (7.0)	2 (6.5)	5 (7.9)	0	
Blood	6 (6.0)	3 (9.7)	2 (3.2)	1 (16.7)	
Colonization	37 (37.0)	9 (29.0)	23 (36.5)	5 (83.3)	0.626
Admission					0.762
Out-patient department	2 (2.0)	0	0	2 (33.3)	
General wards	77 (77.0)	23 (74.2)	50 (79.4)	4 (66.7)	
Intensive care units	21 (21.0)	8 (25.8)	13 (20.6)	0	
Transfer-in	21 (21.0)	7 (22.6)	10 (15.9)	4 (66.7)	0.798
Clinic	6 (6.0)	3 (9.7)	3 (4.8)	0	
General hospital	9 (9.0)	2 (6.5)	4 (6.3)	3 (50.0)	
Geriatric hospital	6 (6.0)	2 (6.5)	3 (4.8)	1 (16.7)	
30-day mortality	25 (25.0)	10 (32.3)	13 (20.6)	2 (33.3)	0.328
In-hospital mortality	37 (37.0)	15 (48.4)	20 (31.7)	2 (33.3)	0.180
Pulsotype					
A	31 (31.0)	-	-	-	
B	63 (63.0)	-	-	-	
Others	6 (6.0)	-	-	-	

**P*-value was calculated comparing two groups including pulsotype A and pulsotype B by Fisher's exact test and Mann Whitney U test in categorical variables and continuous variables, respectively. †Mean [interquartile range].

3.2. Epidemiological analysis of KPC-2-producing *K. pneumoniae* isolates

When the KPC-2-producing *K. pneumoniae* isolates were analyzed based on PFGE clonal similarity of >80%, two pulsotypes accounted for 94.0% (pulsotype A, 31%, n = 31; pulsotype B, 63.0%, n = 63), and six other pulsotypes were identified. The clonal similarity between the two dominant pulsotypes A and B was approximately 70% (**Figure 2**).

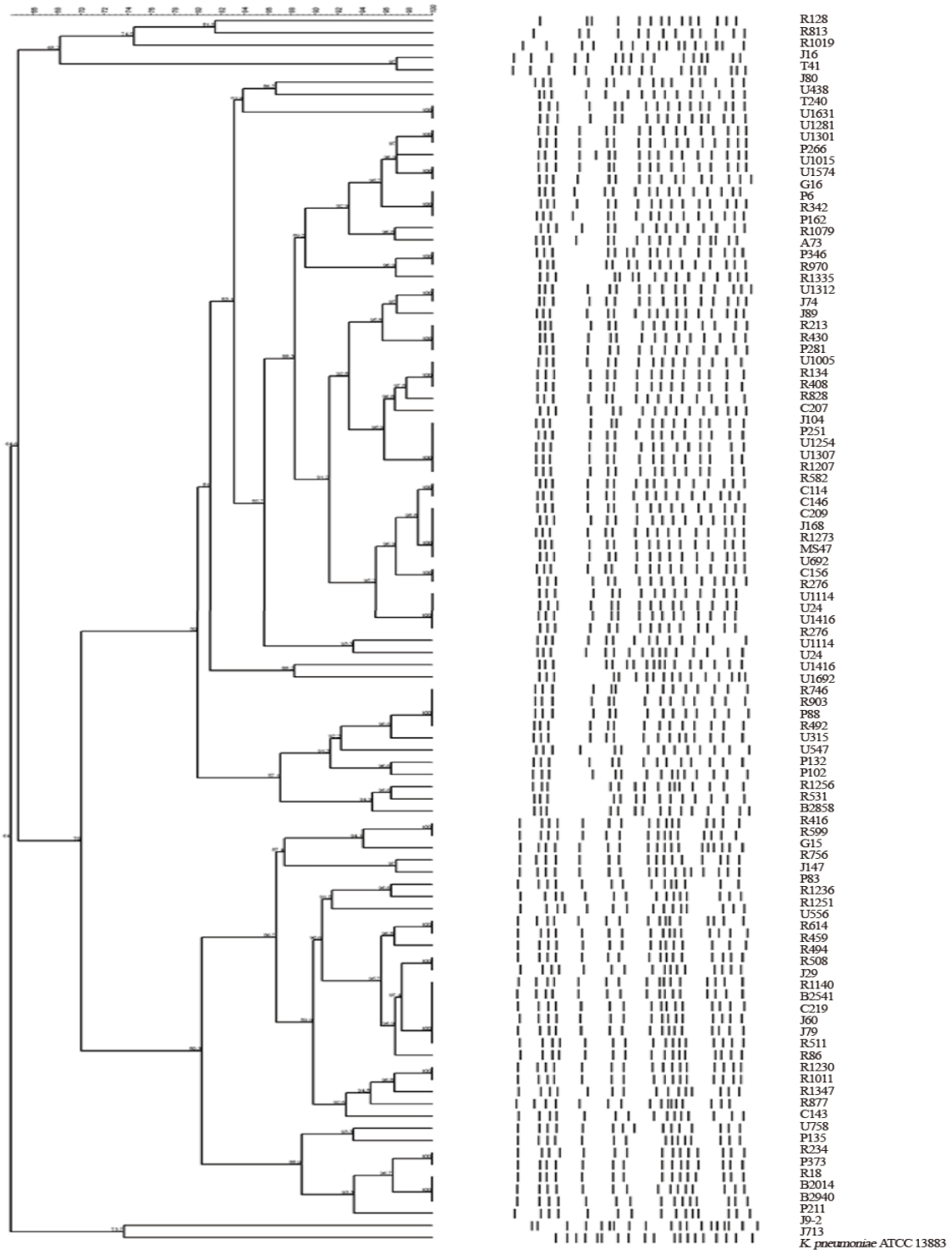

Figure 2. Dendrogram of KPC-2-producing *K. pneumoniae* isolates according to the PFGE band pattern.

The *K. pneumoniae* isolates belonging to pulsatype A were tested for antibiotic susceptibility by the Phoenix system (Becton Dickinson), all showed a resistant phenotype to ampicillin, piperacillin-tazobactam, cefazolin, ceftazidime, cefotaxime, aztreonam, ertapenem, meropenem, and levofloxacin, and all but one showed a susceptible phenotype to gentamicin and amikacin (**Table 3**). The susceptibility confirmation test by disc diffusion method showed similar results to those of the Phoenix system (Becton Dickinson) and corresponded to ST395 (*rpoB-gapA-mdh-pgi-phoE-infB-tonB*, 3-1-2-4-1-1-4) according to the MLST assay (**Figure 3**). In addition, the $bla_{\text{CTX-M-15}}$ gene was identified in addition to $bla_{\text{KPC-2}}$, and no other ESBL transcribing genes or AmpC β-lactamase were identified. *K. pneumoniae* isolates belonging to pulsotype B showed a resistant phenotype to all betalactam antimicrobials, and all but two isolates showed gentamicin co-resistance. The susceptibility confirmation test by disc diffusion method showed similar results to those of the Phoenix system (Becton Dickinson), corresponding to ST307 (4-1-2-52-1-1-7) (**Figure 4**). The *K. pneumoniae* strains showing pulsotype B also co-carried $bla_{\text{CTX-M-15}}$.

4. Discussion

CPEs are one of the most important multidrug-resistant bacteria for nosocomial infections and community transmission of antibiotic resistance, and according to the statistics of the Korea Centers for Disease Control and Prevention in 2017, the number of CPEs in Korea was reported to be gradually increasing from 175 cases in 2014, 565 cases in 2015, 1,453 cases in 216, and 2,657 cases in 2017 [8], and KPC-producing *K. pneumoniae* was the most common among CPEs. No other type of carbapenemase-producing gram-negative bacteria other than the KPC type were isolated during the strain collection period of this study.

In this study, two pulsotypes accounted for 94% (pulsotype A, 31%, $n = 31$; pulsotype B, 63.0%, $n = 63$) of the isolates, with PFGE patterns matching more than 80%. The strains of the two main pulsotypes showed a multidrug-resistant phenotype, resistant to most beta-lactam antibiotics except amikacin or gentamicin.

Table 3. Antimicrobial susceptibility results of KPC-producing *K. pneumoniae* isolates obtained by Phoenix system

Antimicrobials	Total ($n = 100$) No. (%)	Pulsotype A ($n = 31$) No. (%)	Pulsotype B ($n = 63$) No. (%)	Others ($n = 6$) No. (%)
Resistant to				
Ampicillin	100 (100.0)	31 (100.0)	63 (100.0)	6 (100.0)
Ampicillin-sulbactam	87 (87.0)	29 (93.5)	52 (82.5)	6 (100.0)
Piperacillin-tazobactam	99 (99.0)	31 (100.0)	63 (100.0)	5 (83.3)
Cefazolin	100 (100.0)	31 (100.0)	63 (100.0)	6 (100.0)
Ceftazidime	100 (100.0)	31 (100.0)	63 (100.0)	6 (100.0)
Cefotaxime	100 (100.0)	31 (100.0)	63 (100.0)	6 (100.0)
Cefepime	80 (80.0)	12 (38.7)	63 (100.0)	5 (83.3)
Cefoxitin	99 (99.0)	30 (96.8)	63 (100.0)	6 (100.0)
Aztreonam	100 (100.0)	31 (100.0)	63 (100.0)	6 (100.0)
Ertapenem	97 (97.0)	31 (100.0)	63 (100.0)	3 (50.0)
Meropenem	100 (100.0)	31 (100.0)	63 (100.0)	6 (100.0)
Gentamicin	62 (62.0)	1 (3.2)	61 (96.8)	0
Amikacin	0	0	0	0
Levofloxacin	97 (97.0)	31 (100.0)	63 (100.0)	3 (50.0)
Trimethoprim-sulfamethoxazole	96 (96.0)	31 (100.0)	63 (100.0)	2 (33.3)
Tigecycline	56 (56.0)	1 (3.2)	55 (87.3)	0

(A)

(B)

(C)

Antimicrobials	Susceptibility
Piperacillin	R
Ampicillin-sulbactam	R
Cefazolin	R
Cefotaxime	R
Cefazidime	R
Cefepime	R
Aztreonam	R
Cefoxitin	R
Imipenem	R
Meorpenem	R
Ertapenem	R
Amikacin	S
Gentamicin	S
Ciprofloxacin	R
Trimethoprim-sulfamethoxazole	R
Tigecycline	I
Colistin	S

Figure 3. Representative results of disk diffusion method for antimicrobial susceptibility testing in KPC-2 producing *K. pneumoniae* isolates exhibiting pulsotype A (ST395). (A) Results of zone diameter for 12 antibiotics on MH 150 Ø agar; (B) results of zone diameter for remaining 6 antibiotics on MH 90 Ø agar; and (C) results of antimicrobial susceptibility. Abbreviations: R, resistant; I, intermediate; S, susceptible.

(A)

(B)

(C)

Antimicrobials	Susceptibility
Piperacillin	R
Ampicillin-sulbactam	R
Cefazolin	R
Cefotaxime	R
Cefazidime	R
Cefepime	R
Aztreonam	R
Cefoxitin	R
Imipenem	R
Meorpenem	R
Ertapenem	R
Amikacin	S
Gentamicin	R
Ciprofloxacin	R
Trimethoprim-sulfamethoxazole	R
Tigecycline	I
Colistin	S

Figure 4. Representative results of disk diffusion method for antimicrobial susceptibility testing in KPC-2 producing *K. pneumoniae* isolates exhibiting pulsotype B (ST307). (A) Results of zone diameter for 12 antibiotics on MH 150 Ø agar; (B) results of zone diameter for remaining 6 antibiotics on MH 90 Ø agar; and (C) results of antimicrobial susceptibility. Abbreviation: R, resistant; I, intermediate; S, susceptible.

Thus, the results indicate a nosocomial outbreak caused by two multidrug-resistant *K. pneumoniae* clones (ST395, ST307). ST307 was a clone that was first reported in Korea in 2014 and then increased from 14 cases in 2014 to 82 cases in 2015 [5], while ST395 has not yet been reported in Korea but has been reported in Italy [13]. However, since only one week per pulsotype was randomly selected for MLST in this study, there is a possibility that the remaining strains within each pulsotype may not be included in the same ST, but since the PFGE band similarity is more than 80%, it is judged to be included in the same clonal complex.

Of the 100 KPC-2-producing *K. pneumoniae* isolates, 78 patients were elderly patients aged 60 years or older, and as reported in the literature, elderly patients are thought to be more susceptible to infection. There were more male patients than female patients, but the difference in gender by pulsotype was not statistically significant (P = 0.371). Sputum samples were the most common source of isolates at 37%, indicating that carriage or colonization of multidrug-resistant bacteria contributed to respiratory tract infections such as pneumonia. When looking at the wards from which KPC-2-producing *K. pneumoniae* was isolated, the most common single ward isolates were from the central intensive care unit at 17%.

There are many reports that ICU inpatients are also a risk factor for infection with KPC-2-producing *K. pneumoniae* [14-17]. Due to the high proportion of immunocompromised patients and the severity of their illness, ICU inpatients are at high risk for multidrug-resistant infections and should therefore be a major target for infection control activities.

In-hospital mortality among patients with KPC-2-producing *K. pneumoniae* isolates was 37%, and mortality within 30 days was 25%. In Italy, a study of the prognosis of patients with KPC-producing *K. pneumoniae* infections in five general hospitals from 2010 to 2013 reported that 225 (34.1%) of a total of 661 patients died within 14 days, with 217 patients receiving three or more concurrent antibiotics [18]. These results suggest that, unlike other bacteria, the multidrug-resistant phenotype of CPE infections leads to a delay in appropriate antibiotic use, which is associated with a high mortality rate.

In the KPC-2-producing *K. pneumoniae* isolates in the present study, the number of monthly isolates increased gradually after the first outbreak in April, reaching a peak of 25 isolates in August, after which it gradually decreased to 5 isolates in December. Due to the increase in CPE isolates, the hospital implemented infection control training for staff and environmental cultures in July and August, and began active surveillance and cohort isolation of patients at high risk for carriage of multidrug-resistant bacteria in September, after which the number of isolates decreased significantly. This indicates the importance of infection control activities to prevent nosocomial transmission of multidrug-resistant bacteria (**Figure 1**).

Surveillance for multidrug-resistant bacteria and infection control activities to prevent transmission are essential for reducing mortality in hospitalized patients. In this study, we investigated the clinical information and infection factors of a KPC-2-producing *K. pneumoniae* outbreak and identified two clonal strains of KPC-2-producing *K. pneumoniae*, which were simultaneously resistant to other classes of antibiotics. In addition, the mortality rate of infected patients was very high, confirming the importance of infection control activities to prevent the transmission of multidrug-resistant bacteria. Therefore, rapid identification of nosocomial transmission clones and appropriate infection control activities are necessary to prevent nosocomial outbreaks of multidrug-resistant bacteria.

Disclosure statement

The authors declare no conflict of interest.

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