

## Prevalence of Carbapenem–Resistant *Enterobacteriaceae* in Seoul, Korea

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The prevalence of carbapenem-resistant *Enterobacteriaceae* (CRE) is increasing globally. However, a few studies have addressed their epidemiology in Seoul, Korea. In this study, we conducted one-year surveillance of CRE among 1,468 clinical isolates of *Enterobacteriaceae* at the hospital in Seoul with molecular characterization of carbapenemase genes. About 85% of CRE-positive samples were isolated from the elderly age group (above 60 years). The most common isolated organisms were *Klebsiella pneumoniae* (*K. pneumoniae*) (56.5%) and *Escherichia coli* (*E. coli*) (17.0%). We detected six different Carbapenemase-producing *Enterobacteriaceae* (CPE) of *bla*<sub>KPC</sub>, *bla*<sub>NDM</sub>, *bla*<sub>OXA</sub>, *bla*<sub>VIM</sub>, *bla*<sub>IMP</sub>, and *bla*<sub>GES</sub> alone or in combination with other *bla* genes. Typically, 853 (58.1%) isolates were tested positive for at least one CPE. KPC (*K. pneumoniae* carbapenemase)-2 was the most common CPE type (46.0%) followed by NDM (New Delhi metallo-β-lactamase)-1 (5.9%). KPC-2 was most commonly found in *K. pneumoniae* (494/676 isolates [73.1%]) and *E. coli* (107/676 isolates [15.8%]), whereas NDM-1 was commonly found in *Enterobacter cloacae* complex (20/86 isolates [23.3%]). Detailed information and molecular characteristics of CPE is essential to prevent the spread of these pathogens.

**Key Words:** Carbapenem-resistant *Enterobacteriaceae* (CRE), Carbapenemase-producing *Enterobacteriaceae* (CPE), *Klebsiella pneumoniae*

No potential conflict of interest relevant to this article was reported.

## INTRODUCTION

Carbapenem-resistant *Enterobacteriaceae* (CRE) is an emerging problematic infectious agent, with reports of its prevalence worldwide (1-3). CRE outbreak in hospitals has become a critical issue. Transmission by patients with CRE, as well as carriers of CRE, contribute significantly to in-hospital CRE transmission (4). Carbapenemase-producing *Enterobacteriaceae* (CPE) are an important and increasing threat to global health (5). Infections due to these organisms are associated with significant morbidity and mortality (1).

CPE produce enzymes that fall into three classes according to the Ambler classification: class A β-lactamases (*Klebsiella pneumoniae* carbapenemase [KPC]), class B metallo-β-lactamases (New Delhi metallo-β-lactamase [NDM], imipenemase [IMP], and Verona integron-encoded metallo-β-lactamase [VIM]), and class D β-lactamases (oxacillinase [OXA]-48). The carbapenemase genes in *Enterobacteriaceae* have been shown to be associated with mobile genetic elements such as plasmids or transposons, thereby facilitating infection outbreaks (6).

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An understanding of the epidemiology of the emergence of CPE and the changing burden over time is critical to the implementation of control programs and the management of individual patients (7). The purpose of this study is to investigate the prevalence and molecular epidemiology of CPE isolates collected from Seoul area in 2018.

## MATERIALS AND METHODS

### Bacterial strains

From January 2018 to December 2018, a total of 1,468 CRE clinical isolates were retrospectively collected from 113 hospitals in Seoul (Korea). Isolation sites were blood, urine, stool, sputum, lesion, bile, pus, tracheal aspiration, and etc. Bacterial identification was performed using Bruker Biotyper MALDI-TOF MS (Bruker Daltonics, Bremen, Germany) and VITEK 2 (bioMérieux, Marcy l'Etoile, France).

### Antimicrobial susceptibility testing

Antimicrobial susceptibility testing was carried out by broth microdilution using customized Sensititre plates (TREK Diagnostic Systems, Cleveland, OH, USA). CRE were found to be resistant to imipenem, meropenem, doripenem, and ertapenem based on the Clinical and Laboratory Standards Institute (CLSI) guidelines (8).

### PCR detection and sequencing of CPE genes

PCR and subsequent sequencing were conducted to detect and identify the main CPE (*bla<sub>KPC</sub>* and *bla<sub>GES</sub>* from class A; *bla<sub>IMP</sub>*, *bla<sub>VIM</sub>*, and *bla<sub>NDM</sub>* from class B; and *bla<sub>OXA</sub>* from class D)-encoding genes, as previously described (9) (Table 1). Briefly, the template DNAs were prepared by boiling, and PCR amplification was conducted using Quick Taq HS DyeMix (TOYOBO, Japan) with specific primer pairs. The PCR conditions were: 94°C for 5 min, followed by 30 cycles of

**Table 1.** Primer pairs used for amplification of CPE

| Target genes | Sequences (5'→3')             | Product size (bp) |
|--------------|-------------------------------|-------------------|
| IMP          | F TGA GCA ATG TAT CTG TAT TC  | 740               |
|              | R TTA GTT GCT TGG TTT TGA TG  |                   |
| OXA-48       | F TTG GTG GCA TCG ATT ATC GG  | 743               |
|              | R GAG CAC TTC TTT TGT GAT GGC |                   |
| VIM          | F TGG TCT ACA TGA CCG CGT CT  | 766               |
|              | R CGA CTG AGC GAT TTG TGT G   |                   |
| NDM          | F CAA TAT TAT GCA CCC GGT CG  | 720               |
|              | R ATC ATG CTG GCC TTG GGG AA  |                   |
| KPC          | F ATG TCA CTG TAT CGC CGT CT  | 893               |
|              | R TTT TCA GAG CCT TAC TGC CC  |                   |
| GES          | F GCG CTT CAT TCA CGC ACT AT  | 753               |
|              | R GCG TAA TCT CTC TCC TGG GC  |                   |
| SME          | F AAC GGC TTC ATT TTT G       | 830               |
|              | R GCT TCC GCA ATA GTT TTA TCA |                   |
| GIM          | F TCG ACA CAC CTT GGT CTG AA  | 477               |
|              | R AAC TTC CAA CTT TGC CAT GC  |                   |
| SIM          | F TAC AAG GGA TTC GGC ATC G   | 570               |
|              | R TAA TGG CCT GTT CCC ATG TG  |                   |
| SPM          | F AAA ATC TGG GTA CTC AAA CG  | 271               |
|              | R ACA TTA TCC GCT GGA ACA GG  |                   |

denaturation at 94°C for 30 s, annealing at 56°C for 20 s and elongation at 72°C for 30 s; and a final extension at 72°C for 7 min. PCR products were purified using a QIAquick Gel Extraction Kit (Qiagen, Hilden, Germany). Analyses of nucleotide sequences were carried out by BIOFACT Co. (Daejeon, Korea). Sequences were compared with available sequences in GenBank using the BLAST program of the National Center for Biotechnology Information (NCBI).

## RESULTS

### CRE isolates and their resistance characteristics

While stratifying all CRE isolates by age group, it was observed that 407 (27.7%) isolates were from 70-79 years age group, 392 (26.7%) were from 80-89 years age group, 252 (17.2%) were from 60-69 years age group, 138 (9.4%) were from 50-59 years age group, 58 (4.0%) were from 40-49 years age group, 55 (3.7%) were from above 90 years age group, 49 (3.3%) were from 0-9 years age group, 41 (2.8%) were from 30-39 years age group, 20 (1.4%) were from 20-29 years age group, and 6 (0.4%) were from 10-19 years age group (Table 2). For all the analyzed isolates from patients, 806 (54.9%) were from male patients and 589 (40.1%) were from female patients (Table 2). The types of CRE isolates are shown in Table 3. Of 1,468 study isolates, *Klebsiella pneumoniae* (*K. pneumoniae*) was the most common isolated CRE organism in this study (830 isolates, 56.5%) followed by *Escherichia coli* (*E. coli*) (249 isolates, 17%), *Enterobacter cloacae* complex (136 isolates, 9.3%), *Klebsiella aerogenes* (63 isolates, 4.3%), *Proteus mirabilis* (41 isolates, 2.8%), *Citrobacter koseri* (37 isolates, 2.5%), and *Citrobacter freundii* (34 isolates, 2.3%).

### Genetic characterization of carbapenemases genes among CRE isolates

The distribution of different carbapenemases among the *Enterobacteriaceae* isolates is summarized in Table 4. Of 1,468 samples tested, 853 (58.1%) were tested positive for at least one CPE. KPC-2 was the most common CPE type (46.0%), followed by NDM-1 (5.9%), NDM-5 (1.8%), NDM-5 co-infected with OXA-181 (0.8%), OXA-181 (0.7%), OXA-232 (0.5%), NDM-4 (0.5%), OXA-48 (0.3%), VIM-2 (0.3%), and NDM-1 with OXA-232 (0.2%). Also, a relatively low detection frequency of IMP-1, KPC-2 with NDM-1, KPC-2 with GES-5, KPC-4, and NDM-13, KPC-4 with NDM-1, OXA-48 with NDM-5, IMP-6, GES-5, and GES-5 with VIM-2 at 0.1% was observed, respectively. KPC-2 was most commonly found in *K. pneumoniae* (494/676 isolates [73.1%]) and *E. coli* (107/676 isolates [15.8%]), whereas NDM-1 was mostly found in *Enterobacter cloacae* complex (20/86 isolates [23.3%]) (Table 5).

**Table 2.** Distribution of CRE by gender and age group

| Age     | No. of male (%) | No. of female (%) | No. of unknown (%) | Total (%)     |
|---------|-----------------|-------------------|--------------------|---------------|
| 0-9     | 24 (1.6)        | 23 (1.6)          | 2 (0.1)            | 49 (3.3)      |
| 10-19   | 5 (0.3)         | 1 (0.1)           | 0 (0.0)            | 6 (0.4)       |
| 20-29   | 12 (0.8)        | 6 (0.4)           | 2 (0.1)            | 20 (1.4)      |
| 30-39   | 17 (1.2)        | 23 (1.6)          | 1 (0.1)            | 41 (2.8)      |
| 40-49   | 41 (2.8)        | 17 (1.2)          | 0 (0.0)            | 58 (4.0)      |
| 50-59   | 95 (6.5)        | 39 (2.7)          | 4 (0.3)            | 138 (9.4)     |
| 60-69   | 161 (11.0)      | 82 (5.6)          | 9 (0.6)            | 252 (17.2)    |
| 70-79   | 247 (16.8)      | 149 (10.1)        | 11 (0.7)           | 407 (27.7)    |
| 80-89   | 177 (12.1)      | 208 (14.2)        | 7 (0.5)            | 392 (26.7)    |
| >=90    | 21 (1.4)        | 34 (2.3)          | 0 (0.0)            | 55 (3.7)      |
| Unknown | 6 (0.4)         | 7 (0.5)           | 37 (2.5)           | 50 (3.4)      |
| Total   | 806 (54.9)      | 589 (40.1)        | 73 (5.0)           | 1,468 (100.0) |

**Table 3.** Distribution of species in CRE isolates

| Types of isolates                   | No. of isolates | Percentage (%) |
|-------------------------------------|-----------------|----------------|
| <i>Klebsiella pneumoniae</i>        | 830             | 56.5           |
| <i>Escherichia coli</i>             | 249             | 17.0           |
| <i>Enterobacter cloacae</i> complex | 136             | 9.3            |
| <i>Klebsiella aerogenes</i>         | 63              | 4.3            |
| <i>Proteus mirabilis</i>            | 41              | 2.8            |
| <i>Citrobacter koseri</i>           | 37              | 2.5            |
| <i>Citrobacter freundii</i>         | 34              | 2.3            |
| <i>Serratia marcescens</i>          | 15              | 1.0            |
| <i>Klebsiella oxytoca</i>           | 15              | 1.0            |
| <i>Providencia rettgeri</i>         | 14              | 1.0            |
| <i>Morganella morganii</i>          | 8               | 0.5            |
| <i>Proteus vulgaris</i>             | 8               | 0.5            |
| <i>Citrobacter braakii</i>          | 4               | 0.3            |
| <i>Raoultella ornithinolytica</i>   | 3               | 0.2            |
| <i>Providencia stuartii</i>         | 2               | 0.1            |
| <i>Citrobacter amalonaticus</i>     | 1               | 0.1            |
| <i>Hafnia alvei</i>                 | 1               | 0.1            |
| <i>Citrobacter youngae</i>          | 1               | 0.1            |
| <i>Escherichia hermannii</i>        | 1               | 0.1            |
| <i>Kluyvera cryocrescens</i>        | 1               | 0.1            |
| <i>Citrobacter farmeri</i>          | 1               | 0.1            |
| <i>Kluyvera intermedia</i>          | 1               | 0.1            |
| <i>Raoultella planticola</i>        | 1               | 0.1            |
| <i>Proteus penneri</i>              | 1               | 0.1            |
| Total                               | 1,468           | 100            |

**Table 4.** Distribution of carbapenemase genotypes by CRE isolates (n=1,468)

| Types of isolates | No. of isolates | Percentage (%) |
|-------------------|-----------------|----------------|
| KPC-2             | 676             | 46.0           |
| NDM-1             | 86              | 5.9            |
| NDM-5             | 26              | 1.8            |
| NDM-5, OXA-181    | 12              | 0.8            |
| OXA-181           | 11              | 0.7            |
| OXA-232           | 8               | 0.5            |
| NDM-4             | 8               | 0.5            |
| OXA-48            | 5               | 0.3            |
| VIM-2             | 4               | 0.3            |
| NDM-1, OXA-232    | 3               | 0.2            |
| IMP-4             | 2               | 0.1            |
| NDM-4, OXA-181    | 2               | 0.1            |
| IMP-1             | 1               | 0.1            |
| KPC-2, NDM-1      | 1               | 0.1            |
| KPC-2, GES-5      | 1               | 0.1            |
| KPC-4             | 1               | 0.1            |
| NDM-13            | 1               | 0.1            |
| KPC-4, NDM-1      | 1               | 0.1            |
| OXA-48, NDM-5     | 1               | 0.1            |
| IMP-6             | 1               | 0.1            |
| GES-5             | 1               | 0.1            |
| GES-5, VIM-2      | 1               | 0.1            |
| NEG*              | 615             | 41.9           |
| Total             | 1,468           | 100            |

\*carbapenemase gene negative

Table 5. Distributions of genotypes of CRE isolates (n=1,468)

| Types of <i>Enterobacteriaceae</i>  | Types of CPE |       | KPC |     | GES-5, NEG |      | ND   |    | NDM-5, OXA |    | OXA |    | NDM |    | OXA |    | VIM |    | NDM-1, IMP |    | KPC-2, KPC-4, OXA-48, IMP |    | GES |    | NEG* |    |     |
|-------------------------------------|--------------|-------|-----|-----|------------|------|------|----|------------|----|-----|----|-----|----|-----|----|-----|----|------------|----|---------------------------|----|-----|----|------|----|-----|
|                                     | -2           | VIM-2 | M-1 | M-5 | OXA-181    | -181 | -232 | -4 | -48        | -2 | -48 | -4 | -4  | -4 | -4  | -4 | -4  | -4 | -4         | -4 | -4                        | -4 | -4  | -4 | -4   | -4 | -4  |
| <i>Klebsiella pneumoniae</i>        | 494          | 279   | 18  | 8   | 2          | 4    | 8    | 6  | 1          | 2  | 3   | 2  | 2   | 1  | 1   | 1  | 1   | 1  | 1          | 1  | 1                         | 1  | 1   | 1  | 1    | 1  | 279 |
| <i>Escherichia coli</i>             | 107          | 80    | 18  | 18  | 10         | 6    | 2    | 4  |            |    |     |    |     |    |     |    |     |    |            |    |                           |    |     |    |      |    | 80  |
| <i>Enterobacter cloacae</i> complex | 5            | 108   | 20  |     |            |      |      |    | 2          | 1  |     | 1  |     |    |     |    |     |    |            |    |                           |    |     |    |      |    | 108 |
| <i>klebsiella aerogenes</i>         | 5            | 54    | 2   |     | 1          |      |      |    |            |    |     |    |     |    |     |    |     |    |            |    |                           |    |     |    |      |    | 54  |
| <i>Proteus mirabilis</i>            |              | 39    | 1   |     |            |      |      |    |            |    |     |    |     |    |     |    |     |    |            |    |                           |    |     |    |      |    | 39  |
| <i>Citrobacter koseri</i>           | 37           |       |     |     |            |      |      |    |            |    |     |    |     |    |     |    |     |    |            |    |                           |    |     |    |      |    |     |
| <i>Citrobacter freundii</i>         | 9            | 10    | 15  |     |            |      |      |    |            |    |     |    |     |    |     |    |     |    |            |    |                           |    |     |    |      |    | 10  |
| <i>Serratia marcescens</i>          | 7            | 1     | 7   |     |            |      |      |    |            |    |     |    |     |    |     |    |     |    |            |    |                           |    |     |    |      |    | 7   |
| <i>Klebsiella oxytoca</i>           | 10           |       | 4   |     |            |      |      |    |            |    |     |    |     |    |     |    |     |    |            |    |                           |    |     |    |      |    | 14  |
| <i>Providencia rettgeri</i>         |              | 14    |     |     |            |      |      |    |            |    |     |    |     |    |     |    |     |    |            |    |                           |    |     |    |      |    | 8   |
| <i>Proteus vulgaris</i>             |              | 8     |     |     |            |      |      |    |            |    |     |    |     |    |     |    |     |    |            |    |                           |    |     |    |      |    | 7   |
| <i>Morganella morganii</i>          |              | 7     | 1   |     |            |      |      |    |            |    |     |    |     |    |     |    |     |    |            |    |                           |    |     |    |      |    | 7   |
| <i>Citrobacter braakii</i>          |              | 3     | 1   |     |            |      |      |    |            |    |     |    |     |    |     |    |     |    |            |    |                           |    |     |    |      |    | 3   |
| <i>Raoultella ornithinolytica</i>   |              |       | 3   |     |            |      |      |    |            |    |     |    |     |    |     |    |     |    |            |    |                           |    |     |    |      |    | 2   |
| <i>Providencia stuartii</i>         |              | 2     |     |     |            |      |      |    |            |    |     |    |     |    |     |    |     |    |            |    |                           |    |     |    |      |    | 1   |
| <i>Citrobacter youngae</i>          |              | 1     |     |     |            |      |      |    |            |    |     |    |     |    |     |    |     |    |            |    |                           |    |     |    |      |    | 1   |
| <i>Kluyvera intermedia</i>          | 1            |       |     |     |            |      |      |    |            |    |     |    |     |    |     |    |     |    |            |    |                           |    |     |    |      |    | 1   |
| <i>Citrobacter amalonaticus</i>     |              | 1     |     |     |            |      |      |    |            |    |     |    |     |    |     |    |     |    |            |    |                           |    |     |    |      |    | 1   |
| <i>Kluyvera cryocrescens</i>        | 1            |       |     |     |            |      |      |    |            |    |     |    |     |    |     |    |     |    |            |    |                           |    |     |    |      |    | 1   |
| <i>Escherichia hermannii</i>        |              |       | 1   |     |            |      |      |    |            |    |     |    |     |    |     |    |     |    |            |    |                           |    |     |    |      |    | 1   |
| <i>Raoultella planticola</i>        |              |       | 1   |     |            |      |      |    |            |    |     |    |     |    |     |    |     |    |            |    |                           |    |     |    |      |    | 1   |
| <i>Hafnia alvei</i>                 |              | 1     |     |     |            |      |      |    |            |    |     |    |     |    |     |    |     |    |            |    |                           |    |     |    |      |    | 1   |
| <i>Proteus penneri</i>              |              | 1     |     |     |            |      |      |    |            |    |     |    |     |    |     |    |     |    |            |    |                           |    |     |    |      |    | 1   |
| <i>Citrobacter farmeri</i>          |              |       |     |     |            |      |      |    |            |    |     |    |     |    |     |    |     |    |            |    |                           |    |     |    |      |    | 1   |

\* carbapenemase gene negative

## DISCUSSION

CRE is of significant concern to public health, both at the community level and for the health-care facilities (10). The worldwide global increase in infections with CRE is of great concern due to the association of infections with the highly virulent bacteria with high morbidity and mortality rates (10). Until now, the carbapenem resistance rate among *Enterobacteriaceae* isolates from Korea has been relatively low and stable (11).

When we considered CRE isolates, the age distribution was skewed toward older patients, accounting for 85% of isolates (above 60 years of age).

Our findings that *K. pneumoniae* was the dominant type (identified in 56.5% of isolated), followed by *E. coli* (only 17.0%) is in agreement with those of previous studies done in community hospitals in Bahrain, Taiwan, and US where *K. pneumoniae* was the most prevalent species (91%) (10, 12, 13). *K. pneumoniae* will play a major role in carbapenem resistance because it has been repeatedly identified to be the most common species among CRE, hereafter called carbapenem-resistant *K. pneumoniae* (CRKP) (14).

It was found that the emergence of CRE has become a formidable public health threat as it had increased four-fold over the past 10 years worldwide (15), particularly among *K. pneumoniae* and *E. coli*, as has been reported in the global antibiotic resistance estimates published by the World Health Organization in 2014 (16). The results of the present study on the leading causes of CRE were similar to those of previous studies that focused on community hospitals. However, the prevalence rate of *E. coli* and *K. pneumoniae* was either on a little lower or higher side than the rate specified in previous reports. This may be due to the difference between countries and the reporting years (10, 17, 18).

Three main carbapenemases are reported worldwide: KPC, NDM, and OXA-48-like (18). KPC the most common transmissible class A genes are mostly found worldwide (19, 20). KPC-2, NDM-1, NDM-5, and OXA-181 are the most common carbapenemases identified in the present study, and the outcome is similar to previous findings describing the detection of KPC, NDM, and OXA-48 worldwide (21, 22). Korea is known for outbreaks of *K. pneumoniae* that produce KPC-2, NDM-1, and OXA-232 (20, 23, 24). After the first KPC producer (KPC-2 in *K. pneumoniae*) was identified in 1996 in the eastern United States (25), reports of KPC-2 in the New York, NY, area began to appear in 2004; KPC-expressing *K. pneumoniae* is currently an alarming problem (26-28). This report is especially disturbing because New York demonstrated large outbreaks of extended-spectrum  $\beta$ -lactamase (ESBL)-producing *Klebsiella* (29, 30) for which carbapenems were considered to be one of the few treatment options (16). Since numerous studies on KPC-2 genes have been carried out worldwide (31, 32), we need to carefully monitor CPE and perform in-depth research on CPE using surveillance systems.

Previous studies indicated increasing numbers of *Enterobacteriaceae* as frequent carriers of genes encoding two of the most concerning subclasses of carbapenemases: KPC, which has become endemic in parts of America, Southern Europe, Israel, and China; and the New Delhi Metallo- $\beta$ -lactamase (NDM), which has become endemic in Northern Europe and the Asia Pacific region, most remarkably in the UK and India (33-35). Mechanisms of carbapenem nonsusceptibility can be divided broadly into carbapenemase production CPE and a combination of  $\beta$ -lactamase (ESBL and AmpC) production with porin loss, and efflux pump overexpression (non-carbapenemase-producing carbapenem nonsusceptible *Enterobacteriaceae* [NCPCRE]) (36). These mechanisms generally appear paired among themselves or with carbapenemase-production (1). All three alternative mechanisms aim to block the penetration of the antibiotics within the bacterial cell (37). The data from a case-control study comparing patients with NCPCRE (cases) and patients with CPE (controls) reported in the United States indicate 843 unique patients with first-episode CRE, including 387 (45.9%) NCPCRE and 456 (54.1%) CPE (38). Orsi and colleagues (39) demonstrated that compared to *Klebsiella pneumoniae* carbapenemase (KPC)-producing CRE, NCPCRE were associated with prior antibiotic exposure, demonstrating that patient-level risk factors may differ according to mechanisms of resistance. Another study performed in Taiwan from 2010 to 2012 presented the detection of Carbapenemase in 5.0% of the CRE isolates but the prevalence and carbapenemase differed by species (40).

Although KPC is the most common carbapenemase worldwide, NDM has also been shown to be important sporadic outbreaks around the globe (41, 42). The prevalence of NDM was in agreement with a study on Global distribution (43). The analysis of a total of 1,468 isolates of *Enterobacteriaceae* for the presence of CPE demonstrated NDM as the second gene (9.6%, 141/1,468) and mostly NDM-1 (64.5%, 91/141) in *Enterobacteriaceae*. CPE distribution likely appears to vary geographically; for example, high rates in Greece (VIM and KPC), Romania, Poland and Denmark (NDM), and in the Indian subcontinent (NDM, KPC, and OXA-181) (44, 45). MBL-producing *Enterobacteriaceae* isolates have also been reported in several Latin American countries and Europe (45). In a multinational survey spanning 2012-2014, VIM-producing CPE were recovered in Mexico and NDM-1-producing CPE in Venezuela (45).

CRE continues to evolve, posing an increasing threat to patients of all ages (1). Early identification of carbapenemase producers in clinical infections, at the carriage state, or both, is therefore mandatory to prevent the development of hospital-based outbreaks (44). Consequently, it is hypothesized that constant surveillance and regular education are important for the successful mitigation of health-care-associated infection and to decrease the incidence rate of CRE. Molecular characterization of CPE is essential for epidemiological surveillance to monitor the resurgence of the CPE pandemic.

In conclusion, this study revealed the overall prevalence of CRE in Seoul, Korea and highlights the need for continued studies as a way to control the emergence of new CPE varieties as a basis for further epidemiological surveillance

## CONFLICT OF INTEREST

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

## REFERENCES

- 1) Logan LK, Weinstein RA. The Epidemiology of Carbapenem-Resistant *Enterobacteriaceae*: The Impact and Evolution of a Global Menace. *J Infect Dis* 2017;215:S28-S36.
- 2) Livorsi DJ, Chorazy ML, Schweizer ML, Balkenende EC, Blevins AE, Nair R, et al. A systematic review of the epidemiology of carbapenem-resistant *Enterobacteriaceae* in the United States. *Antimicrob Resist Infect Control* 2018;7:55.
- 3) Zhang Y, Wang Q, Yin Y, Chen H, Jin L, Gu B, et al. Epidemiology of carbapenem-resistant *Enterobacteriaceae* infections: report from the China CRE network. *Antimicrob Agents Chemother* 2018;62:e01882-17.
- 4) Lerner A, Adler A, Abu-Hanna J, Meitus I, Navon-Venezia S, Carmeli Y. Environmental contamination by carbapenem-resistant *Enterobacteriaceae*. *J Clin Microbiol* 2013;51:177-81.
- 5) van Duin D, Doi Y. The global epidemiology of carbapenemase-producing *Enterobacteriaceae*. *Virulence* 2017;8:460-9.
- 6) Queenan AM, Bush K. Carbapenemases: the versatile beta-lactamases. *Clin Microbiol Rev* 2007;20:440-58.
- 7) Kohler PP, Melano RG, Patel SN, Shafinaz S, Faheem A, Coleman BL, et al. Emergence of Carbapenemase-Producing *Enterobacteriaceae*, South-Central Ontario, Canada. *Emerg Infect Dis* 2018;24:1674-82.
- 8) Clinical and Laboratory Standards Institute (CLSI). Performance Standards for Antimicrobial Susceptibility Testing M100-S26. Wayne, PA: CLSI, 2016.

- 9) Kim JS, Jin YH, Park SH, Han S, Kim HS, Park JH, et al. Emergence of a multidrug-resistant clinical isolate of *Escherichia coli* ST8499 strain producing NDM-13 carbapenemase in the Republic of Korea. *Diagn Microbiol Infect Dis* 2019;94:410-2.
- 10) Saeed NK, Alkhawaja S, Azam NFAEM, Alaradi K, Al-Biltagi M. Epidemiology of carbapenem-resistant *Enterobacteriaceae* in a Tertiary Care Center in the Kingdom of Bahrain. *J Lab Physicians* 2019;11:111-7.
- 11) Korea Centers for Disease Control and Prevention (KCDC). Korean Antimicrobial Resistance Monitoring System (KARMS) annual report, 2014. Korea Centers for Disease Control and Prevention, 2015.
- 12) Jean SS, Lee NY, Tang HJ, Lu MC, Ko WC, Hsueh PR. Carbapenem-Resistant *Enterobacteriaceae* Infections: Taiwan Aspects. *Front Microbiol* 2018;9:2888.
- 13) Thaden JT, Lewis SS, Hazen KC, Huslage K, Fowler VG Jr, Moehring RW, et al. Rising rates of carbapenem-resistant *Enterobacteriaceae* in community hospitals: A mixed-methods review of epidemiology and microbiology practices in a network of community hospitals in the Southeastern United States. *Infect Control Hosp Epidemiol* 2014;35:978-83.
- 14) Netikul T, Kiratisin P. Genetic Characterization of Carbapenem-Resistant *Enterobacteriaceae* and the Spread of Carbapenem-Resistant *Klebsiella pneumoniae* ST340 at a University Hospital in Thailand. *PLoS One* 2015; 10:e0139116.
- 15) Weiner LM, Webb AK, Limbago B, Dudeck MA, Patel J, Kallen AJ, et al. Antimicrobial-resistant pathogens associated with healthcare-associated infections: Summary of data reported to the national healthcare safety network at the centers for disease control and prevention, 2011-2014. *Infect Control Hosp Epidemiol* 2016;37:1288-301.
- 16) Paterson DL, Bonomo RA. Extended-spectrum beta-lactamases: a clinical update. *Clin Microbiol Rev* 2005;18:657-86.
- 17) Pan F, Tian D, Wang B, Zhao W, Qin H, Zhang T, et al. Fecal carriage and molecular epidemiology of carbapenem-resistant *Enterobacteriaceae* from outpatient children in Shanghai. *BMC Infect Dis* 2019; 19:678.
- 18) Rizzo K, Horwich-Scholefield S, Epton E. Carbapenem and Cephalosporin Resistance among *Enterobacteriaceae* in Healthcare-Associated Infections, California, USA. *Emerg Infect Dis* 2019;25:1389-93.
- 19) Patel G, Bonomo RA. "Stormy waters ahead": global emergence of carbapenemases. *Front Microbiol* 2013;4:48.
- 20) Jeong SH, Kim HS, Kim JS, Shin DH, Kim HS, Park MJ, et al. Prevalence and Molecular Characteristics of Carbapenemase-Producing *Enterobacteriaceae* From Five Hospitals in Korea. *Ann Lab Med* 2016;36:529-35.
- 21) Nordmann P, Poirel L. The difficult-to-control spread of carbapenemase producers among *Enterobacteriaceae* worldwide. *Clin Microbiol Infect* 2014;20:821-30.
- 22) Sugawara E, Kojima S, Nikaido H. *Klebsiella pneumoniae* Major Porins OmpK35 and OmpK36 allow more efficient diffusion of beta-lactams than their *Escherichia coli* homologs OmpF and OmpC. *J Bacteriol* 2016;198:3200-8.
- 23) Kim MN, Yong D, An D, Chung HS, Woo JH, Lee K, et al. Nosocomial clustering of NDM-1-producing *Klebsiella pneumoniae* sequence type 340 strains in four patients at a South Korean tertiary care hospital. *J Clin Microbiol* 2012;50:1433-6.
- 24) Hong SK, Yong D, Kim K, Hong SS, Hong SG, Khosbayan T, et al. First outbreak of KPC-2-producing *Klebsiella pneumoniae* sequence type 258 in a hospital in South Korea. *J Clin Microbiol* 2013;51:3877-9.
- 25) Yigit H, Queenan AM, Anderson GJ, Domenech-Sanchez A, Biddle JW, Steward CD, et al. Novel carbapenem-hydrolyzing beta-lactamase, KPC-1, from a carbapenem-resistant strain of *Klebsiella pneumoniae*. *Antimicrob Agents Chemother* 2001;45:1151-61.

- 26) Bradford PA, Bratu S, Urban C, Visalli M, Mariano N, Landman D, et al. Emergence of carbapenem-resistant *Klebsiella* species possessing the class A carbapenem-hydrolyzing KPC-2 and inhibitor-resistant TEM-30 beta-lactamases in New York City. *Clin Infect Dis* 2004;39:55-60.
- 27) Bratu S, Landman D, Haag R, Recco R, Eramo A, Alam M, et al. Rapid spread of carbapenem-resistant *Klebsiella pneumoniae* in New York City: a new threat to our antibiotic armamentarium. *Arch Intern Med* 2005;165:1430-5.
- 28) Bratu S, Tolaney P, Karumudi U, Quale J, Mooty M, Nichani S, et al. Carbapenemase-producing *Klebsiella pneumoniae* in Brooklyn, NY: molecular epidemiology and in vitro activity of polymyxin B and other agents. *J Antimicrob Chemother* 2005;56:128-32.
- 29) Meyer KS, Urban C, Eagan JA, Berger BJ, Rahal JJ. Nosocomial outbreak of *Klebsiella* infection resistant to late-generation cephalosporins. *Ann Intern Med* 1993;119:353-8.
- 30) Quale JM, Landman D, Bradford PA, Visalli M, Ravishankar J, Flores C, et al. Molecular epidemiology of a citywide outbreak of extended-spectrum beta-lactamase-producing *Klebsiella pneumoniae* infection. *Clin Infect Dis* 2002;35:834-41.
- 31) Nordmann P, Cuzon G, Naas T. The real threat of *Klebsiella pneumoniae* carbapenemase-producing bacteria. *Lancet Infect Dis* 2009;9:228-36.
- 32) Navon-Venezia S, Chmelnitsky I, Leavitt A, Schwaber MJ, Schwartz D, Carmeli Y. Plasmid-mediated imipenem-hydrolyzing enzyme KPC-2 among multiple carbapenem-resistant *Escherichia coli* clones in Israel. *Antimicrob Agents Chemother* 2006;50:3098-101.
- 33) National Institute of Allergy and Infectious Diseases (NIAID). NIAID's Antibacterial Resistance Program: current status and future directions 2014. <https://www.niaid.nih.gov/sites/default/files/arstrategicplan2014.pdf>.
- 34) Bush K. Proliferation and significance of clinically relevant  $\beta$ -lactamases. *Ann N Y Acad Sci* 2013;1277:84-90.
- 35) Schwaber MJ, Lev B, Israeli A, Solter E, Smollan G, Rubinovitch B, et al. Containment of a country-wide outbreak of carbapenem-resistant *Klebsiella pneumoniae* in Israeli hospitals via a nationally implemented intervention. *Clin Infect Dis* 2011;52:848-55.
- 36) Goodman KE, Simner PJ, Tamma PD, Milstone AM. Infection control implications of heterogeneous resistance mechanisms in carbapenem-resistant *Enterobacteriaceae* (CRE). *Expert Rev Anti Infect Ther* 2016;14:95-108.
- 37) Suay-García B, Pérez-Gracia MT. Present and Future of Carbapenem-resistant *Enterobacteriaceae* (CRE) Infections. *Antibiotics (Basel)*. 2019;8:122.
- 38) Marimuthu K, Ng OT, Cherng BPZ, Fong RKC, Pada SK, De PP, et al. Antecedent Carbapenem Exposure as a Risk Factor for Non-Carbapenemase-Producing Carbapenem-Resistant *Enterobacteriaceae* and Carbapenemase-Producing *Enterobacteriaceae*. *Antimicrob Agents Chemother* 2019;63:e00845-19.
- 39) Orsi GB, Bencardino A, Vena A, Carattoli A, Venditti C, Falcone M, et al. Patient risk factors for outer membrane permeability and KPC-producing carbapenem-resistant *Klebsiella pneumoniae* isolation: results of a double case-control study. *Infection* 2013;41:61-7.
- 40) Wang JT, Wu UI, Lauderdale TL, Chen MC, Li SY, Hsu LY, et al. Carbapenem-nonsusceptible *Enterobacteriaceae* in Taiwan. *PLoS One* 2015;10:e0121668.
- 41) Kim Y, Cunningham MA, Mire J, Tesar C, Sacchettini J, Joachimiak A. NDM-1, the ultimate promiscuous enzyme: substrate recognition and catalytic mechanism. *FASEB J* 2013;27:1917-27.

- 42) Zmarlicka MT, Nailor MD, Nicolau DP. Impact of the New Delhi metallo-beta-lactamase on beta-lactam antibiotics. *Infect Drug Resist* 2015; 8:297-309.
- 43) Kazmierczak KM, Rabine S, Hackel M, McLaughlin RE, Biedenbach DJ, Bouchillon SK, et al. Multiyear, multinational survey of the incidence and global distribution of metallo-beta-lactamase-producing *Enterobacteriaceae* and *Pseudomonas aeruginosa*. *Antimicrob Agents Chemother* 2015;60:1067-78.
- 44) Nordmann P, Naas T, Poirel L. Global spread of Carbapenemase-producing *Enterobacteriaceae*. *Emerg Infect Dis* 2011;17:1791-8.
- 45) Albiger B, Glasner C, Struelens MJ, Grundmann H, Monnet DL. Carbapenemase-producing *Enterobacteriaceae* in Europe: assessment by national experts from 38 countries, May 2015. *Euro Surveill* 2015;20.