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# One-Year Surveillance of ESKAPE Pathogens in an Intensive Care Unit of Monterrey, Mexico

Jorge Martín Llaca-Díaz[a] Soraya Mendoza-Olazarán[b] Adrian Camacho-Ortiz[c] Samantha Flores[d] Elvira Garza-González[a, b]

[a]Departamento de Patología Clínica, [b]Servicio de Gastroenterología and [c]Servicio de Infectología, Hospital Universitario Dr. José Eleuterio González and [d]Departamento de Microbiología, Facultad de Medicina, Universidad Autónoma de Nuevo León, Monterrey, México



**Key Words**
Extended spectrum β-lactamases · Multidrug resistance · Intensive care unit · Vancomycin

**Abstract**
***Background:*** Bacterial species from the ESKAPE group (i.e. *Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa* and *Enterobacter* species) are frequently resistant to antibiotics. The purpose of this study was to monitor the incidence of ESKAPE pathogens at the intensive care unit (ICU) of a tertiary care hospital in Monterrey, Mexico. ***Methods:*** All clinically relevant organisms isolated from June 2011 to June 2012 were included. Identification and susceptibility testing was performed using panels from Sensititre. Resistance to oxacillin, for *S. aureus,* and the production of extended spectrum β-lactamases (ESBLs), for *K. pneumonia,* were determined as defined by the Clinical Laboratory Standards Institute. Also, the presence of *vanA* and *vanB* genes was determined in *E. faecium* vancomycin (VAN)-resistant isolates. ***Results:*** The majority of pathogens (64.5%) isolated in the ICU unit were from the ESKAPE group. The organisms most frequently isolated were *A. baumannii* (15.8%) and *P. aeruginosa* (14.3%). A high resistance to carbapenems was detected for *A. baumannii* (75.3%) while 62% of *S. aureus* isolates were confirmed to be methicillin resistant. Of the *K. pneumoniae* isolates, 36.9% were ESBL producers. We detected three *E. faecium* VAN-resistant isolates, all of which contained the *vanA* gene. ***Conclusion:*** The presence of the ESKAPE group of pathogens is a major problem in the ICU setting. The results of this study support the implementation of special antimicrobial strategies to specifically target these microorganisms.



## Introduction

Antimicrobial resistance among both Gram-positive and Gram-negative bacteria has been on the rise in the past few years [1–3]. The presence of multidrug-resistant (MDR) pathogens has become a cause for serious concern with regard to nosocomial infections. In fact, the World Health Organization has recently recognized antimicrobial resistance as one of the three most important human health concerns [4]. The most common and threatening MDR pathogens have been grouped together under the

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Elvira Garza-González, PhD
Servicio de Gastroenterología, Departamento de Patología Clínica, Hospital Universitario Dr. José Eleuterio González, Universidad Autónoma de Nuevo León
Avenida Francisco I. Madero s/n, Colonia Mitras Centro, Monterrey
NL 64460 (México), E-Mail elvira_garza_gzz@yahoo.com

acronym 'ESKAPE,' which stands for *Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa* and *Enterobacter* spp. [5–8].

Three decades ago, *A. baumannii* was sensitive to most antibiotics, but today it is exceptionally resistant to most antibiotics [9], with carbapenem resistance being greater than 50% in some countries [10]. Recently, data from Monterrey, Mexico, reported a meropenem (MEM) resistance of 69% [11]. A major factor contributing to antibiotic resistance is the production of extended spectrum β-lactamases (ESBLs) by the *Enterobacteriaceae* species, particularly *K. pneumoniae* [12].The dissemination of ESBL-producing Gram-negative pathogens in hospitals is an emerging global problem that deserves special consideration [13, 14].

Another important species of the ESKAPE group is *S. aureus*, particularly methicillin-resistant *S. aureus* (MRSA), which has an incidence and prevalence that continues to increase rapidly in many regions of the world. The mortality rate associated with invasive MRSA infections is estimated at approximately 20% [15] and bloodstream infections caused by this bacterial species are associated with a high mortality rate and length of hospital stay [16]. Finally, isolates of *Enterococcus faecalis* and *E. faecium* are the third- to fourth-most prevalent nosocomial pathogen worldwide. Acquired resistance, particularly to glycopeptides, is reported for a number of these isolates, thus limiting the number of therapeutic options [17, 18].

Global and regional surveillance of ESKAPE pathogens is fundamental to control the infections caused by these bacterial species [19]. The purpose of this study was to monitor the incidence of ESKAPE pathogens in an intensive care unit (ICU) of a tertiary care hospital in Monterrey, Mexico.

## Methods

*Setting and Clinical Isolates*

This study was conducted at the Dr. José Eleuterio Gonzalez University Hospital, a teaching hospital in Monterrey, Nuevo Leon, Mexico. This hospital provides tertiary medical care in seven wards, including three ICUs spanning pediatric, medical and surgical units. This study was performed in the medical and surgical ICUs with a combined 20-bed area. During the study period (from 3 June 2011 to 3 June 2012), 1,692 clinical isolates were obtained from both ICUs. The first isolate of a particular species per patient, irrespective of the body site, was recorded. Only patient specimens taken for diagnostic purposes were included.

*Antimicrobial Susceptibility and Identification Assays*

The species identification and susceptibility testing were performed using the broth microdilution method. Panels were obtained from Sensititre (TEK Diagnostic Systems Inc., Cleveland, Ohio, USA) and were used as described by the manufacturer. Antimicrobials tested against Gram-negative bacteria included: amikacin (AMK), aztreonam (AZT), cefotaxime (CTX), ceftazidime (CAZ), chloramphenicol (CHL), ciprofloxacin (CIP), gentamicin (GEN), imipenem (IPN), MEM, ticarcillin (TIC) and tobramycin (TOB). Antibiotics included against Gram-positive bacteria included clindamycin (CLI), erythromycin (ERY), high-concentration GEN (GEN500), linezolid (LNZ), oxacillin (OXA), penicillin (PEN), quinupristin/dalfopristin (QUD), teicoplanin (TEI), high-concentration streptomycin (ST1000), tetracycline (TET) and vancomycin (VAN). Antibiotics used against both Gram-positive and Gram-negative organisms included: amoxicillin-clavulanic acid (AMX), ampicillin (AMP), cefepime (FEP), ceftriaxone (CRO), cefuroxime (CXM), levofloxacin (LVX) and trimethoprim/sulfamethoxazole (SXT).

Multidrug resistance was defined as having a resistance to three or more classes of antimicrobials. The class definitions used in this study were: penicillins (PEN), cephalosporins (FEP, CTX, CAZ, CRO, CXM), carbapenems (IPN, MEM), fluoroquinolones (LVX), aminoglycosides (AMK, GEN, TOB) and tetracyclines (TET). Assay control organisms and susceptibility breakpoints were those recommended by the Clinical Laboratory Standards Institute (CLSI) [20].

*ESBL Production and Detection of MRSA*

Presumptive ESBL producers were identified by determining the minimal inhibitory concentrations (MIC) for CAZ and CTX. The combination disk method, alone and in combination with inhibitory clavulanic acid, was used to confirm the expression of ESBLs. Both presumptive and confirmatory tests were performed following CLSI guidelines [20]. Additionally, the MIC of OXA was determined as recommended by the CLSI [20].

*Detection of the van Genes*

Genomic DNA of *E. faecium* VAN-resistant isolates was obtained by phenol chloroform and ethanol precipitation. PCR assays were performed as described previously [21]. Approximately 100 ng of DNA was added to a PCR mixture containing 10× PCR buffer, 0.2 mM deoxyribonucleotide and 1 U of *Taq* DNA polymerase (Bioline). Two different primer sets (one each for *vanA* and *vanB*) were used in the assay. Amplification of DNA was performed with denaturation at 94°C for 2 min, followed by 30 cycles of 1 min at 94°C, 1 min at 54°C and 1 min at 72°C. Amplicons were analyzed by electrophoresis on 1% agarose gels.

## Results

*Distribution of Species by Clinical Specimen*

A total of 1,692 clinical isolates were recovered from clinical specimens, which included respiratory, blood, urine, catheter and other sites (table 1). ESKAPE pathogens were identified in 64.5% (1,092/1,692) of isolates. Overall, the organisms most frequently isolated were

**Table 1.** Distribution of ESKAPE pathogens and other species isolated from clinical specimens collected in the ICU of the José Eleuterio González University Hospital from June 2011 to June 2012

| Pathogen | Global | Respiratory | Blood | Urine | Catheter | Other |
|---|---|---|---|---|---|---|
| ESKAPE group | | | | | | |
| *A. baumannii* | 268 (15.8) | 168 (18.8) | 42 (13.6) | 10 (5.7) | 22 (13.8) | 26 (17.2) |
| *P. aeruginosa* | 242 (14.3) | 130 (14.5) | 32 (10.3) | 41 (23.3) | 24 (15) | 15 (9.9) |
| *S. aureus* | 241 (14.2) | 163 (18.2) | 38 (12.3) | 4 (2.3) | 16 (10) | 20 (13.2) |
| *K. pneumoniae* | 192 (11.3) | 113 (12.6) | 23 (7.4) | 18 (10.2) | 24 (15) | 14 (9.3) |
| *E. faecium* | 35 (2.1) | 9 (1) | 8 (2.6) | 11 (6.3) | 1 (0.6) | 6 (4) |
| *E. cloacae* | 69 (4.1) | 28 (3.1) | 15 (4.8) | 7 (4) | 12 (7.5) | 7 (4.6) |
| *E. aerogenes* | 28 (1.7) | 17 (1.9) | 2 (0.6) | 4 (2.3) | 3 (1.9) | 2 (1.3) |
| Other species | 17 (1) | 9 (1) | – | 6 (3.4) | – | 2 (1.3) |
| *Enterobacter* | | | | | | |
| CoNS | 146 (8.6) | 37 (4.1) | 88 (28.4) | 6 (3.4) | 10 (6.3) | 5 (3.3) |
| *E. faecalis* | 121 (7.2) | 42 (4.7) | 13 (4.2) | 29 (16.5) | 21 (13.1) | 16 (10.6) |
| *E. coli* | 90 (5.3) | 36 (4) | 9 (2.9) | 17 (9.7) | 10 (6.3) | 18 (11.9) |
| Other species | 243 (14.4) | 143 (16) | 40 (12.9) | 23 (13.1) | 17 (10.6) | 20 (13.2) |
| Total | 1,692 (100) | 895 (100) | 310 (100) | 176 (100) | 160 (100) | 151 (100) |

Figures in parentheses are percentage. CoNS = Coagulase-negative staphylococci.



*A. baumannii* (15.8%), *P. aeruginosa* (14.3%), *S. aureus* (14.2) and *K. pneumoniae* (11.3%). *A. baumannii* and *S. aureus* were most frequently isolated from respiratory specimens (18.8 and 18.3%, respectively). From blood specimens, the most frequently isolated species were *A. baumannii* and *S. aureus* (13.6 and 12.3%, respectively), while *P. aeruginosa* was the most common isolate in urine (23.3%). In catheters, *K. pneumoniae* and *P. aeruginosa* were the predominant species (15% for both species).

*Antibiotic Resistance*

Data detailing the $MIC_{50}$, $MIC_{90}$ and percentages of antimicrobial resistance for each of the ESKAPE pathogens, as well as for a few other frequent species, are presented in tables 2 and 3. In general, a high prevalence of drug resistance was detected. For *A. baumannii*, the percentages of resistance were higher than 72% for all antimicrobial agents evaluated, except for FEP (23.2%). For *K. pneumoniae*, 3 out of the 16 antimicrobial agents evaluated showed resistance percentages higher than 54%.

From all isolates, 86.2% (231/268) of *A. baumannii* isolates were MDR, as were 100% (114/114) of *Enterobacter* spp., 59.4% (114/192) of *K. pneumoniae* and 28.9% (70/242) of *P. aeruginosa.* Furthermore, 20.9% (56/268) of *A. baumannii* isolates were found to be extensively drug resistant because they showed resistance to all 13 antimicrobial agents evaluated. Among the species isolated that were not part of the ESKAPE group, 76.7% (69/90) of *E. coli* were MDR.

*Prevalence of ESBL-Positive Enterobacteriaceae and MRSA*

For *K. pneumoniae* isolates (n = 192), 89 were determined to be ESBL producers by presumptive assay. Of those, 85.4% (76/89) were further confirmed to be ESBL producers by the double disk method. Given the high level of MDR detected for *E. coli*, we also screened *E. coli* isolates for the production of ESBLs. We determined that 62.2% (56/90) of them were ESBL producers by presumptive assay and 75% (42/56) were positive by double disk method.

Among Gram-positive organisms, 62% (150/242) of *S. aureus* isolates were methicillin resistant and 3 of 35 *E. faecium* isolates were found to be VAN resistant. All of these isolates also typed positive for the *vanA* gene. None of the *S. aureus* isolates were resistant to VAN.

## Discussion

In the hospital setting, different bacterial species may be the causative agents of infectious diseases. Due to their high level of pervasiveness and association with antimi-

**Table 2.** MIC and percent of resistant strains data for Gram-negative species of the ESKAPE group plus *E. coli*

| Antimicrobial Agent | *A. baumannii* (n = 268) | | | | *P. aeruginosa* (n = 242) | | | | *K. pneumoniae* (n = 192) | | | | *Enterobacter* spp. (n = 114) | | | | *E. coli* (n = 90) | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | $MIC_{50}$ µg/ml | $MIC_{90}$ µg/ml | range | %R | $MIC_{50}$ µg/ml | $MIC_{90}$ µg/ml | range | %R | $MIC_{50}$ µg/ml | $MIC_{90}$ µg/ml | range | %R | $MIC_{50}$ µg/ml | $MIC_{90}$ µg/ml | range | %R | $MIC_{50}$ µg/ml | $MIC_{90}$ µg/ml | range | %R |
| AMK | >32 | >32 | ≤16–>32 | 72.4 | ≤16 | >32 | ≤16–>32 | 18.2 | ≤16 | 32 | ≤16–>32 | 7.3 | ≤16 | >32 | ≤16–>32 | 9.6 | ≤16 | ≤16 | ≤16–>32 | 3.3 |
| TOB | >8 | >8 | ≤4–>8 | 80.1 | >8 | >8 | ≤4–>8 | 22.7 | ≤4 | >8 | ≤4–>8 | 46.9 | ≤4 | >8 | ≤4–>8 | 23.7 | >8 | >8 | ≤4–>8 | 51.1 |
| GEN | >8 | >8 | ≤2–>8 | 83.2 | ≤2 | >8 | ≤2–>8 | 21.5 | ≤2 | >8 | ≤2–>8 | 44.8 | ≤2 | >8 | ≤2–>8 | 14.9 | ≤2 | >8 | ≤2–>8 | 40 |
| FEP | 16 | >16 | ≤8–>16 | 23.2 | ≤8 | >16 | ≤8–>16 | 14.9 | ≤8 | >16 | ≤8–>16 | 11.5 | ≤8 | >16 | ≤8–>16 | 9.6 | ≤8 | 16 | ≤8–>16 | 8.9 |
| CRO | >32 | >32 | ≤8–>32 | 85.8 | 32 | >32 | ≤8–>32 | 47.1 | 16 | >32 | ≤8–>32 | 47.4 | ≥8 | >32 | ≤8–>32 | 26.3 | >32 | >32 | ≤8–>32 | 50 |
| CXM | ND | ND | ND | ND | ND | ND | ND | ND | >16 | >16 | ≤2–>16 | 54.7 | 16 | >16 | 16–>16 | 44.7 | >16 | >16 | ≤2–>16 | 61.1 |
| CTX | >32 | >32 | ≤8–>32 | 86.1 | 16 | >32 | ≤8–>32 | 31.5 | ≤8 | >32 | ≤8–>32 | 36.5 | ≤8 | >16 | ≤8–>32 | 27.2 | ≤8 | >32 | ≤8–>32 | 42.4 |
| CAZ | >16 | >16 | ≤2–>16 | 85 | ≤2 | >16 | ≤2–>16 | 24.5 | ≤8 | >16 | ≤2–>16 | 37 | ≤2 | >16 | ≤2–>16 | 23.7 | 8 | >16 | ≤2–>16 | 14.4 |
| CIP | >1 | >1 | ≤0.2–5>2 | 85.8 | ≤0.25 | >1 | ≤0.25–>1 | 22.3 | 1 | >1 | ≤0.25–>2 | 50 | ≤0.25 | >1 | <0.25–>2 | 25.4 | >1 | >1 | ≤0.25–>1 | 63.3 |
| LVX | >4 | >4 | ≤0.5–>4 | 81.6 | ≤0.5 | >4 | ≤0.5–>4 | 19.4 | ≤0.5 | >4 | ≤0.5–>4 | 26.6 | ≤0.5 | >4 | ≤0.5–>4 | 15.8 | >4 | >4 | ≤0.5–>4 | 62.2 |
| IPN | >8 | >8 | ≤4–>8 | 75.7 | ≤4 | >8 | ≤4–>8 | 28.5 | ND | ND | ND | ND | ND | ND | ND | ND | ND | ND | ND | ND |
| MEM | >8 | >8 | ≤4–>8 | 75.3 | ≤4 | >8 | ≤4–>8 | 20.2 | ND | ND | ND | ND | ND | ND | ND | ND | ND | ND | ND | ND |
| AMX | ND | ND | ND | ND | ND | ND | ND | ND | 16 | >16 | ≤8–>16 | 19.8 | >16 | >16 | >16–>16 | 100 | 16 | >16 | ≤8–>16 | 23.3 |
| AMP | ND | ND | ND | ND | ND | ND | ND | ND | >16 | >16 | >16–>16 | 100 | >16 | >16 | 16–>16 | 93 | >16 | >16 | ≤4–>16 | 86.6 |
| AZT | ND | ND | ND | ND | ≤8 | >16 | ≤8–>16 | 17.8 | 16 | >16 | ≤8–>16 | 46.9 | ≤8 | >16 | >16–>16 | 28.9 | ≤8 | >16 | ≤8–>16 | 43.3 |
| CHL | ND | ND | ND | ND | >16 | >16 | ≤4–>16 | 95.4 | ≤4 | >16 | ≤4–>16 | 24.5 | 8 | >16 | ≤4–>16 | 17.5 | 8 | >16 | ≤4–>16 | 20 |
| TIC | >64 | >64 | ≤16–>64 | 77.2 | 32 | >64 | ≤16–>64 | 26 | >64 | >64 | >64–>64 | 100 | ≤16 | >64 | ≤16–>64 | 23.7 | >64 | >64 | ≤16–>64 | 83.3 |
| SXT | >2 | >2 | ≤2–>2 | 86.9 | ND | ND | ND | ND | ≤2 | >2 | ≤2–>2 | 45.3 | ≤2 | >2 | ≤2–>2 | 27.2 | >2 | >2 | ≤2–>2 | 56.7 |

crobial resistance, the ESKAPE group of pathogens deserves particular attention. To control the incidence of infections due to ESKAPE pathogens, site-by-site surveillance studies are necessary to establish hospital-specific guidelines for effective empirical therapy [22]. In this study, we report a 1-year surveillance of ESKAPE pathogens and describe the incidence of ESBL-producing *K. pneumoniae*, of MRSA and of the presence of VAN-resistant *E. faecium* isolates in an ICU of a Mexican tertiary care teaching hospital.

The organisms most frequently recovered from our ICU were ESKAPE pathogens (64.5%, 1,092/1,692), with a predominance of Gram-negative bacteria. The most common ESKAPE organisms were *A. baumannii*, *P. aeruginosa* and *K. pneumoniae*. These common bacterial pathogens were found to be similar to other prevalent pathogens reported in other countries [1, 8].

In general, a high MDR was observed for *A. baumannii* and *P. aeruginosa*. *E. coli* deserves special attention because it also showed a high level of MDR (76.7%), even though this bacterial species is not included within the ESKAPE group. It seems that, for our hospital, surveillance monitoring should include *E. coli.* As such, it could be added to the ESKAPE group, thus forming a new acronym: ESKAPEE. In this hospital, the MDR ESKAPE pathogens were responsible for a considerable number of infections and represented the majority of isolates for which resistance to multiple antimicrobial agents reduces therapeutic alternatives for physicians.

*A. baumannii* was the most commonly isolated species in our ICU (15.8%). In recent years, *A. baumannii* has emerged with an extensive antibiotic resistance spectrum [23]. In our study, 20.9% of *A. baumannii* were detected to be pan resistant to the antimicrobial agents evaluated. The alternative therapeutics that could be used include tigecycline or colistin; however, these antibiotics were not evaluated in this study.

A regional difference in *A. baumannii* resistance to carbapenems has been reported with resistance rates ranging from 3 to 59% [24–26]. The surveillance data presented in this study showed that 75.3% of *A. baumannii* clinical isolates were resistant to MEM. This value is greater than that previously reported for this hospital by our group (59%) [11], which suggests a potential selection

**Footnote to Table 2**
% R = Percent of resistant strains; ND = not determined.

**Table 3.** MIC and percent of resistant strains data for Gram-positive species of the ESKAPE group

| Antimicrobial agent | *S. aureus* (n = 242) | | | | *Enterococcus* spp. (n = 156) | | | |
|---|---|---|---|---|---|---|---|---|
| | $MIC_{50}$ μg/ml | $MIC_{90}$ μg/ml | range | %R | $MIC_{50}$ μg/ml | $MIC_{90}$ μg/ml | range | %R |
| AMX | >16 | >16 | ≤4–>16 | 62.4 | ND | ND | ND | ND |
| AMP | ≥0.25 | >0.25 | ≤0.25–>0.25 | 90 | ND | ND | ND | ND |
| OXA | >4 | >4 | ≤0.5–>4 | 61.9 | ND | ND | ND | ND |
| PEN | >0.25 | >0.25 | ≤0.25–>0.25 | 89.3 | ND | ND | ND | ND |
| ST1000 | ND | ND | ND | ND | ≤1,000 | >1,000 | ≤1,000–>1,000 | 49.3 |
| FEP | >16 | >16 | ≤8–>16 | 63.6 | ND | ND | ND | ND |
| CRO | >64 | >64 | ≤8–>64 | 62.0 | ND | ND | ND | ND |
| CXM | >16 | >16 | ≤4–> 16 | 50.0 | ND | ND | ND | ND |
| CLI | >2 | >2 | ≤0.5–>2 | 74.8 | ND | ND | ND | ND |
| ERY | >4 | >4 | ≤0.5–>4 | 76.9 | >4 | >4 | ≤0.25–>4 | 75.6 |
| GEN500 | ND | ND | ND | ND | >500 | >500 | ≤500–>500 | 51.9 |
| LVX | >2 | >2 | ≤1–>2 | 53.3 | ND | ND | ND | ND |
| LNZ | ≤2 | ≤2 | ≤2–>4 | 0.8 | ≤2 | ≤2 | ≤2–>4 | 3.8 |
| QUD | ≤1 | 2 | ≤1–>2 | 4.9 | >2 | >2 | ≤1–>2 | 75 |
| TEI | ≤8 | ≤8 | ≤8–>16 | 4.9 | ≤8 | >16 | ≤8–>16 | 10.2 |
| TET | ≤2 | 8 | ≤2–>16 | 9.5 | >8 | >8 | ≤2–>8 | 56.4 |
| SXT | ≤2 | >2 | ≤2–>2 | 12.4 | ND | ND | ND | ND |
| VAN | 2 | 2 | ≤1–>16 | 4.5 | 2 | >16 | ≤1–>16 | 10.2 |

% R = Percent of resistant strains; ND = not determined.

for MEM-resistant strains. Of note, the previous study we refer to was performed in all hospital wards, while this study was restricted to only two ICUs.

ESBL-producing strains have been reported around the world in different genera of the *Enterobacteriaceae* family and have been isolated from different clinical specimens [27–30]. In this study, 39.6% of *K. pneumoniae* isolates were found to be ESBL producers. Higher values were detected for *E. coli*, as 46.7% of isolates were ESBL positive. This finding supports the importance of monitoring *E. coli* strains at this particular site. Of interest, the ESBL type has been previously studied within our hospital. For *E. coli* the dominant type was CTX-M-15 (66.7%), and for *K. pneumoniae* the dominant type was SHV-12 (51.5%) [31]. There was also an important clonal relatedness among *K. pneumoniae* ESBL isolates [30].The spread of ESBLs in hospitals is an important challenge for clinicians, as the therapeutic options for these organisms are limited. Additionally, infections attributed to ESBL-producing *E. coli* and *K. pneumoniae* are associated with increased mortality, length of hospital stay and increased cost [29].

The most common Gram-positive organism recovered from our ICUs was *S. aureus*. Among these isolates, MRSA made up 62% of all *S. aureus* isolates. This rate is higher than that reported in the USA (55%), Canada (22.3%) and Europe (ranging between >1 and 24%), but lower than values observed in Turkey (75%) [15, 16, 32, 33].

Different types of potentially influential genes have been reported in VAN-resistant isolates. In a wide variety of enterococcal species, the *vanA* genotype is associated with a high level of resistance, the *vanB*, *vanB2* and *vanD* genotype with a moderate to high level of resistance, and the *vanC* (*C1*, *C2*, *C3*) with an intrinsically low level of resistance [17, 34]. Accordingly, in this study, three *E. faecium* isolates were VAN-resistant and were also typed for the *vanA* gene. There is only one previous report of the presence of VAN-resistant *E. faecium* isolates in Mexico that were also typed for the *vanA* gene [35]. Our results highlight the presence of a high-level resistance to VAN in Mexico. Over the past few years, our ICUs have predominately used IPN and VAN for the treatment of many complicated infections, including ventilator-associated pneumonia, central line-associated bloodstream infections and many complicated intra-abdominal infections. This fact may explain, at least in part, the high level of drug resistance observed.

One weakness of this study is that we used the commercial methodology of Sensititre, which includes a range

of concentrations that sometimes does not allow one to detect the exact MIC. Nonetheless, as the purpose of this study is to assess resistant strains, the testing of concentrations around each breakpoint was deemed acceptable and the data were analyzed with the knowledge of this bias.

The high rate of antibiotic resistance in our ICU underlines the urgent need for strategies for the prevention and control of infections caused by the ESKAPE pathogens. The results of this study will help us to implement an appropriate infection control of these highly resistant species.

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