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Original article

Emergence of extended-spectrum β-lactamase producing *Enterobacter* spp. in patients with bacteremia in a tertiary hospital in southern Brazil

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ABSTRACT

Background: Extended-spectrum β-lactamases (ESBLs) are increasingly prevalent in *Enterobacter* spp., posing a challenge to the treatment of infections caused by this microorganism. The purpose of this retrospective study was to evaluate the prevalence, risk factors, and clinical outcomes of inpatients with bacteremia caused by ESBL and non ESBL-producing *Enterobacter* spp. in a tertiary hospital over the period 2004–2008.

Methods: The presence of bla_{CTX-M}, bla_{TEM}, bla_{SHV}, and bla_{PER} genes was detected by polymerase chain reaction (PCR) and nucleotide sequence analysis. Genetic similarity between strains was defined by pulsed-field gel electrophoresis (PFGE).

Results: *Enterobacter* spp. was identified in 205 of 4907 of the patients who had positive blood cultures during hospitalization. Of those cases, 41 (20%) were ESBL-producing *Enterobacter* spp. Nosocomial pneumonia was the main source of bacteremia caused by ESBL-producing *Enterobacter* spp. The presence of this microorganism was associated with longer hospital stays. The ESBL genes detected were: CTX-M-2 (23), CTX-M-59 (10), CTX-M-15 (1), SHV-12 (5), and PER-2 (2). While *Enterobacter aerogenes* strains showed mainly a clonal profile, *Enterobacter cloacae* strains were polyclonal.

Conclusion: Although no difference in clinical outcomes was observed between patients with infections by ESBL-producing and non-ESBL-producing strains, the detection of ESBL in *Enterobacter* spp. resulted in the change of antimicrobials in 75% of cases, having important implications in the decision-making regarding adequate antimicrobial therapy.

Emergencia de *Enterobacter* spp. productores de β-lactamasas de espectro extendido en pacientes con bacteriemia en un hospital terciário del sur del Brasil

RESUMEN

Antecedentes: Las β-lactamasas de espectro extendido (BLEE) son cada vez más frecuentes en *Enterobacter* spp., lo que representa un desafío para el tratamiento de infecciones causadas por este microorganismo. El propósito de este estudio fue evaluar los factores de riesgo y los resultados clínicos de pacientes ingresados con bacteriemia causada por *Enterobacter* spp. productores de BLEE en un hospital terciario durante los años 2004-2008.

Métodos: La presencia de los genes bla_{CTX-M}, bla_{TEM}, bla_{SHV}, e bla_{PER} se detectó mediante la reacción en cadena de la polimerasa (PCR) y análisis de la secuencia de nucleótidos. La similitud genética entre las cepas fue definida por electroforesis en gel de campo pulsado (PFGE).

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Resultados: *Enterobacter* spp. fue identificado en 205 pacientes de un total de 4.907 que tenían cultivos positivos de sangre durante la hospitalización. De esos 205 casos, 41 (20%) eran *Enterobacter* spp. productores de BLEE. La neumonía nosocomial fue la principal fuente de bacteriemia causada por *Enterobacter* spp. productores de BLEE. La presencia de este microorganismo se asoció con una mayor estancia hospitalaria. Las BLEE detectadas fueron: CTX-M-2 (23), CTX-M-59 (10), CTX-M-15 (1), SHV-12 (5) y PER-2 (2). Mientras que las cepas de *Enterobacter aerogenes* presentaron un perfil principalmente clonal, *E. cloacae* fueron policlonales.

Conclusiones: Si bien no fueron observadas diferencias en los resultados clínicos entre los pacientes con infecciones causadas por cepas productoras de BLEE y no productoras de BLEE, la detección de BLEE en *Enterobacter* spp., resultó en el cambio de los antimicrobianos en el 75% de los casos, habiendo implicaciones importantes en la toma de las decisiones con respecto a la terapia antimicrobiana adecuada.

Introduction

Enterobacter spp. has been recognized as nosocomial pathogens, mainly affecting patients in the intensive care unit (ICU). *E. cloacae* and *E. aerogenes* are the most common species found in human infections. The frequency of bacteremia has increased in the last decade, and the rate of infection is approximately 1/1000 admissions in university hospitals or tertiary-care centers.[1] In general, the mortality associated with bacteremia caused by *Enterobacter* spp. is as high as bacteremia caused by other enteric bacilli, with mean rates of 20–35%.[1]

β-Lactam resistance in *Enterobacter* spp. challenges the treatment of infections caused by this organism and is associated with unfavorable clinical outcomes.[2] The main resistance mechanism in these organisms is the expression of chromosomally encoded AmpC cephalosporinase,[1] leading to treatment failure when third-generation cephalosporins are used.[2] Moreover, the frequency of extended-spectrum β-lactamase (ESBL) expression is increasing in these species as an important cause of broad-spectrum cephalosporin resistance.[2]

While AmpC cephalosporinase is chromosomally encoded, ESBLs are mediated by transferable plasmids. Therefore, detection of ESBL genes is recommended for the adoption of control measures to prevent spread of resistance.[3]

Several reports have described the high mortality, time, and cost of hospitalization as well as delays in choosing the appropriate antibiotic therapy associated with infections caused by *Klebsiella pneumoniae*, *Escherichia coli*, and *Proteus mirabilis* ESBL-producing microorganisms.[4–6] However, studies evaluating the effects of ESBL production in *Enterobacter* spp. are rare. One report compared the clinical significance of ESBLs produced in *Enterobacter* spp., *Citrobacter* spp., *Serratia* spp., and *Morganella morganii* and found no differences in the outcome of bacteremia between those microorganisms.[7] However, further clinical studies are hindered by the difficulty of detecting ESBLs in species that also express genes encoding inducible AmpC, since the latter may mask the detection of the former.[8]

This study evaluated the prevalence, risk factors, and clinical outcomes of bacteremia caused by ESBL- and non-ESBL-producing *Enterobacter* spp. strains.

Materials and methods

Study setting

This study was conducted at the Clinics Hospital of Federal University of Paraná (HC/UFPR), a 643-bed teaching hospital located in Curitiba, Brazil, over a 5-year period (January 2004–December 2008). Over the past 10 years, HC/UFPR has had an average of 18,699 admissions per year, including 159 ICU admissions, per year. The Clinics Hospital offers a broad range of complex care including bone marrow transplants, liver transplants, cardiovascular surgery, chemotherapy, and other high-risk procedures.

The study was approved by the Institutional Review Board of the HC/UFPR (project number 2288.182/2010-07). All patients received an individual identification number, and their names were not disclosed to maintain confidentiality.

Study design and bacterial strains

A retrospective comparative study was performed to assess risk factors and clinical outcomes of nosocomial infection by ESBL-producing *Enterobacter* spp. vs. non-ESBL-producing *Enterobacter* spp. strains. All patients included in this study developed bacteremia after 48 h of hospitalization and yielded positive blood culture for *Enterobacter* spp. (either ESBL-producing or non-producing strains). One isolate per patient was included in the study. The total number of patients with positive blood culture collected during the period of study was considered to assess prevalence.

Clinical data were obtained from medical records of the patients. The following clinical data were evaluated: age and sex, underlying disease (cancer, digestive tract diseases, respiratory diseases, heart diseases, central nervous system diseases, or kidney disease), invasive procedures (central venous catheter, mechanical ventilation, tracheotomy, surgery, transplant, or urinary catheter), ward and/or intensive care unit (ICU) admission, use of antimicrobial agents, immunosuppressant or chemotherapy prior to culture, primary focus of bacteremia, length of hospital stay (days), before and after blood culture results (with ESBL or non-ESBL producing *Enterobacter* spp.), changes in antimicrobial therapy after physicians were informed of the ESBL results, and clinical outcome (death, discharge, or related death).

Definitions

Patients with ESBL-producing *Enterobacter* spp. were defined as "group 1" and patients with non-ESBL-producing *Enterobacter* spp. were defined as "group 2". Death was considered related to infection when the cause of death was septic shock and the last microorganism isolated from blood cultures was identified as *Enterobacter* spp. Antimicrobial therapy with carbapenems for ESBL-producing *Enterobacter* spp., and carbapenem or fourth-generation cephalosporins for non-ESBL *Enterobacter* spp. was considered appropriate therapy. Third-generation cephalosporins were considered inadequate therapies for both groups, and other antibiotics were deemed appropriate or not according to the antimicrobial susceptibility test.

Microbiology studies

Blood cultures were performed with the BactAlert® system (bioMérieux, Hazelwood, MO). The Vitek system (bioMérieux) was used for species identification (ID 32 GN card) and antimicrobial

sensitivity tests (AST N105 card). Isolates showing reduced sensitivity to cephalosporins were tested (ceftriaxone, ceftazidime, cefotaxime, or aztreonam), according to the Clinical Laboratory Standard Institute (CLSI) breakpoints for ESBL screening in *Klebsiella* spp. and *E. coli*,[9] were tested for the presence of ESBL-encoding genes.

Molecular detection of ESBL genes

All isolates of *Enterobacter* spp. with a positive phenotypic screening test were tested for the presence of bla_{CTX-M}, bla_{TEM}, bla_{SHV}, and bla_{PER} genes by polymerase chain reaction (PCR) as previously described.[10–12] Positive controls *K. pneumoniae* A30397 ($bla_{CTX-M-2}$), *E. coli* E27 (bla_{TEM-9}), and *K. pneumoniae* A32048-3 (bla_{SHV-5}), and the negative control *E. coli* ATCC 25922 were run simultaneously. Samples that were PCR-positive for bla_{CTX-M} were submitted to a second PCR using the primers: $bla_{CTX-M-1}$ 5′-TGTTAGGAAGTGTGCCGCTG-3′; 5′-GACGGCTTTCT-GCCTTAGGTTG-3′ and $bla_{CTX-M-2}$ 5′-ATGTTAACGGTGATGGCGAC-3′; 5′-GCATCAGAAACCGTGGGTTAC-3′. Amplicons from all isolates were purified using a GFX-TM PCR purification kit (Amersham Bioscience, NJ, USA) and sequenced using the same set of primers. The nucleotide sequences were identified using a BigDye terminator v3.1 Cycle Sequencing kit and an automated DNA capillary sequencer (ABI PRISM 3700 DNA Analyzer; PE Applied Biosystems, Hitachi), analyzed with ChromasPro version 1.33 (Technelysium Pty LTDA), and compared with the GenBank database sequences using the BLAST tool (http://www.ncbi.nih.gov/BLAST). Isolates with ESBL genes were classified as ESBL-producing.

Pulsed-field gel electrophoresis (PFGE)

DNA of all ESBL-producing strains was extracted as described previously[13] and digested with *Xba*I (10 U; Fermentas, Maryland, USA) at 37 °C. Electrophoresis was performed on a CHEF-DR III (Bio-Rad Laboratories, USA) instrument for 24 h at 6 V/cm and 12 °C and pulse times from 5 to 30 s. Gels were analyzed with the Gel-Pro Analyzer 4.0 and NTSYS 2.02 software. Clusters of possibly related isolates were identified using the Dice similarity coefficient and unweighted pair-group method with arithmetic averages (UPGMA). Identical isolates were assigned the same capital letter and different pulsed-field gel electrophoresis (PFGE) profiles were named with different capital letters. Isolates with more than 80% similarity were assigned as a subtype and given the same capital letter as the major type, followed by an Arabic number (e.g., A1, A2, A3, and A4).

Statistical analyses

Epidemiological data were recorded and analyzed using Epi Info version 3.5.1. and Statistics v.8.0, using the following statistical parameters: Kruskal–Wallis test for nonparametric continuous variables and chi-square (degree of freedom = 1) or Fisher's exact test (expected value less than 5) for categorical variables. A logistic regression for multivariate analyses was included for variables with $P < 0.05$ in univariate analyses. The results were considered statistically significant when the P value was less than 0.05.

Results

During the study period (2004–2008), 4907 patients had positive blood cultures, and *Enterobacter* spp. were isolated from 205 (4.1%) patients, showing an increasing prevalence of 2.7% in 2004 to 5.8% in 2008 (data not shown). The *Enterobacter* spp. species found were *E. cloacae* (109 cases, 53.2%), *E. aerogenes* (91, 44.4%), and *E. gergoviae* (5, 2.4%).

Table 1
Risk factors of ESBL- and non-ESBL-producing *Enterobacter* spp. bacteremia.

	ESBL (n = 41) N (%)	Non-ESBL (n = 164) N (%)	Odds ratio	P
Previous ICU stay	27 (65.9)	79 (48.2)	2.08	0.042
Gastrointestinal diseases	8 (19.5)	69 (42.1)	0.33	0.007
Respiratory diseases	11 (26.8)	36 (22.0)	1.30	0.506
Neoplasia	12 (29.3)	46 (28.0)	1.06	0.876
Neurological diseases	9 (22.0)	53 (32.3)	0.59	0.196
Kidney diseases	5 (12.8)	27 (19.0)	0.63	0.369
Heart diseases	18 (43.9)	80 (48.8)	0.82	0.575
Urinary catheter	14 (35.0)	55 (33.5)	1.07	0.860
Central venous catheter	17 (41.5)	87 (53.0)	0.63	0.184
Mechanical ventilation	27 (65.9)	82 (50.0)	1.93	0.068
Tracheostomy	16 (39.0)	42 (25.6)	1.86	0.088
Surgery	6 (14.6)	76 (46.3)	0.20	0.0002
Previous infections	26 (63.4)	91 (55.5)	1.39	0.359
Pneumonia	23 (56.1)	51 (31.1)	2.83	0.003
Urinary infection	10 (25.0)	32 (19.5)	1.37	0.441
Abdominal infection	1 (2.5)	13 (7.9)	0.30	0.197
Surgical wound	2 (5.0)	15 (9.2)	0.52	0.309
Prior antibiotic use	37 (90.2)	157 (96.3)	0.36	0.117
Quinolone	9 (22.0)	26 (16.0)	1.47	0.371
Ceftriaxone or Ceftazidime	6 (14.6)	56 (34.6)	0.32	0.021
Cefepime	19 (46.3)	67 (41.6)	1.21	0.584
Carbapenem	7 (17.1)	62 (38.5)	0.33	0.009
Piperacilin/tazobactam	5 (12.2)	30 (19.0)	0.59	0.308

ICU = intensive care unit; *n* = number of patients.

Out of the 205 *Enterobacter* spp. isolated, 41 (20%) were ESBL-producing (20 were *E. cloacae* and 21 were *E. aerogenes*) while 164 (78%) were non-ESBL-producing *Enterobacter* spp.

Patient age ranged between 15 days and 97 years old. We compared the ESBL- and non-ESBL groups and their distribution according to the following age strata <18 (pediatric, *n* = 22), 18–64 (adults, *n* = 119) and ≥65 (elderly, *n* = 64); ESBL-producing strains were observed in 22.7% of pediatric patients, 21% of adult patients and 17.2% of elderly patients. There was no significance difference between groups. There was also no gender difference between ESBL- and non-ESBL-producing groups.

ESBL- and non-ESBL-producing strains showed similar distributions between different hospital wards, except in the ICU where the frequency of ESBL-producing strains was higher. Similarly, the length of hospital stay before infection was similar between the 2 groups, varying only in ICU, where a longer stay was a significant risk factor for ESBL-producing *Enterobacter* spp. infection (Table 1).

Among all underlying diseases and co-morbidities evaluated, none represented independent risk factors for infection by ESBL-producing strains (Tables 1 and 2). Moreover, invasive procedure during hospitalization was not a risk factor for infection by ESBL-producing *Enterobacter* spp. On the other hand, the use of carbapenem and third-generation cephalosporins during

Table 2
Multivariate analysis of the risk factors of ESBL- and non-ESBL-producing *Enterobacter* spp. bacteremia.

	ESBL (n = 41) N (%)	Non-ESBL (n = 164) N (%)	Odds ratio	P
Patient unit				
Previous ICU stay	27 (65.9)	79 (48.2)	2.08	<0.05
Invasive procedures				
Surgery	6 (14.6)	76 (46.3)	0.20	<0.05
Previous antimicrobial therapy				
Ceftriaxone/ceftazidime	6 (14.6)	56 (34.6)	0.21	<0.05
Carbapenem	7 (17.1)	62 (38.5)	0.21	<0.05

ICU = intensive care unit; n: number of patients.

Table 3
Clinical outcomes of ESBL- and non-ESBL-producing *Enterobacter* spp. bacteremia.

	ESBL (n = 41) N (%)	Non-ESBL (n = 164) N (%)	Relative risk	P
Discharge	23 (56.1)	83 (50.6)	1.25	0.529
Mortality	18 (43.9)	81 (49.4)	0.80	0.529
Related mortality	8 (19.5)	22 (13.4)	1.56	0.323

n: number of patients.

hospitalization proved to be a risk factor for infections by non-ESBL-producing *Enterobacter* spp. (Tables 1 and 2).

Regarding the clinical outcome, the mortality among patients with bacteremia by ESBL-producing *Enterobacter* spp. was 43.9%; among patients with bacteremia by non-ESBL-producing *Enterobacter* spp., mortality was 49.4%. ESBL- and non-ESBL-producing *Enterobacter* spp.-related mortality was 19.5% and 13.4%, with no significant difference between groups. The patients infected with ESBL-producing strains had a longer hospital stay after the culture results than patients with non-ESBL-producing *Enterobacter* spp. bacteremia. The mean hospital stay in this study was 8 days in the ICU and 7 days in other wards. During the course of this study, bacteremia caused by *Enterobacter* spp. increased the mean length of hospital stay to 15 days and ESBL-producing *Enterobacter* spp. increased the mean duration of hospitalization to 22 days (Table 3).

Patients infected with ESBL-producing strains that were using empirically ceftriaxone or ceftazidime were considered to have received inappropriate therapy, and totaled 85.4% of the study population. The microbiological diagnostic results led to a change in antimicrobial therapy in 75.6% (31/41) of patients. In most of these cases (97%), the exchange occurred from cephalosporins to carbapenems. On the other hand, ineffective empirical treatment (third generation cephalosporin) was not a risk factor for death or related death in patients with bacteremia in both groups.

Three different groups of β-lactamases were identified from the total number of ESBL-producing strains: CTX-M (34 isolates), SHV (5 isolates), and PER (2 isolates). CTX-M-2 was the most prevalent type, accounting for 83% of all ESBL-producing strains, including 8 isolates of *E. aerogenes* and 15 isolates of *E. cloacae*. CTX-M-59 was detected in 10 isolates of *E. aerogenes* and CTX-M-15 in 1 isolate of *E. cloacae*. SHV-12 enzymes were found in 3 *E. cloacae* and 2 *E. aerogenes*. PER-2 was found in 2 *E. cloacae* strains. The high degree of genetic similarity of the *E. aerogenes* isolates identified in this study

is reflected in the results of the PFGE profiling analysis. Out of eleven distinct PFGE types, a PFGE group with at least 80% similarity was identified (group C) (Fig. 1). This group included 85% (17/20) of the isolates and was divided in eight subgroups (C, C1, C2, C3, C4, C5, C6 and C7). For the subgroups C, C1 and C6, clones (100% identity on the basis of PFGE analysis) with four isolates were found. The other PFGE types (A, B and D) showed less than 80% similarity and represented unrelated isolates. CTX-M-59 and CTX-M-2-producing *E. aerogenes* were frequently found. ESBL groups comprised ten isolates of CTX-M-59 (50%), eight of CTX-M-2 (40%), and two of SHV-12 (10%).

Twenty distinct PFGE types were identified in *E. cloacae* isolates on the basis of dendrogram analysis (Fig. 2). Two PFGE groups possessed above 80% similarity, group D that contained two isolates and group L that clustered four isolates. Furthermore, these groups included only CTX-M-2-producing *E. cloacae*. The other PFGE types showed to be unrelated isolates (<80% similarity), and also included CTX-M-2-producing *E. cloacae*, besides SHV-12, PER-2 and CTX-M-15-producing *E. cloacae*. Only a clonal group was observed (group C) that comprised two PER-2-producing *E. cloacae*. This ESBL group has never been described in previous Brazilian studies.

Discussion

The emergence of bacteremia caused by *Enterobacter* spp. has been described in recent years. In this study, *Enterobacter* spp. was isolated in 4.3% of patients with bacteremia in a teaching hospital in southern Brazil during the period 2004–2008, with an increased frequency (2.7–5.8%) of isolation over the 5-year study period. A previous study showed similar results,[14] and another reported an average of 2.2% (range, 1.4–3.4%).[15] These results highlight *Enterobacter* spp. as a pathogen frequently present in nosocomial bacteremia.

The prevalence of *E. cloacae*, followed by *E. aerogenes*, and less participation from other species of this genus as agents of bacteremia, is consistent with the results obtained in other studies.[1,15]

ESBL production has been found with increased frequency in *Enterobacter* spp. The frequency of ESBL among *Enterobacter* spp. in this study was 20%. A study conducted in Korea found 43% of ESBL-producing *Enterobacter* spp. isolated from blood cultures[16]; another study conducted in Hong Kong found a frequency of 6.5%.[2] These data show that prevalence of ESBL in these species varies, and can be high in some countries.
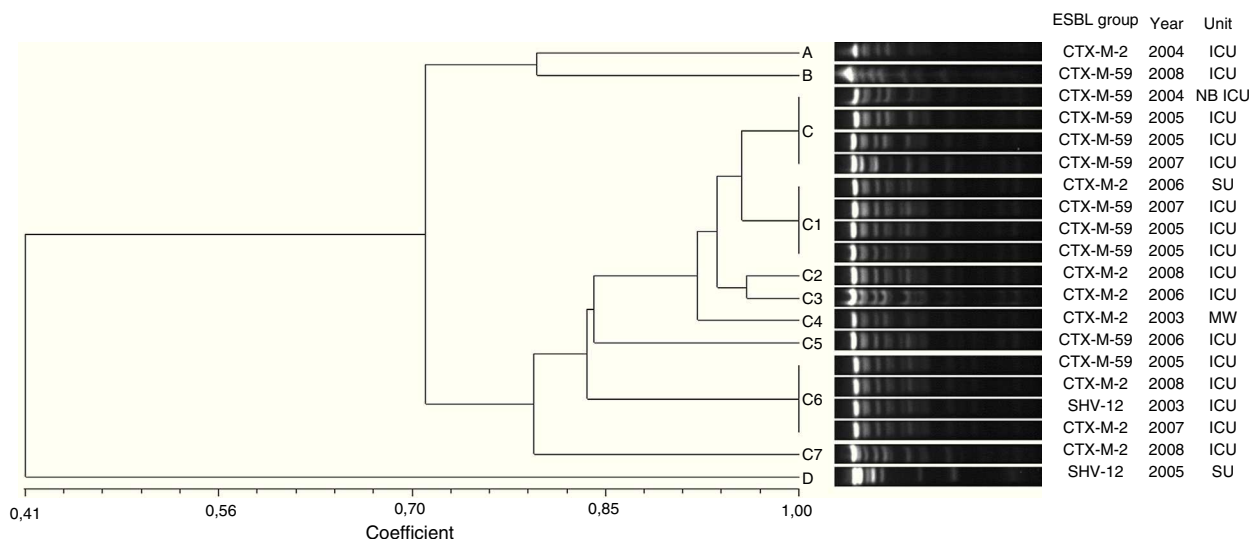

Fig. 1. Genetic similarity among ESBL-producing *Enterobacter aerogenes* by PFGE and ESBL type, unit, and year of microorganism isolation. Legend: ICU = intensive care unit; SU = surgical unit; NB ICU = newborn intensive care unit; MW = male ward.
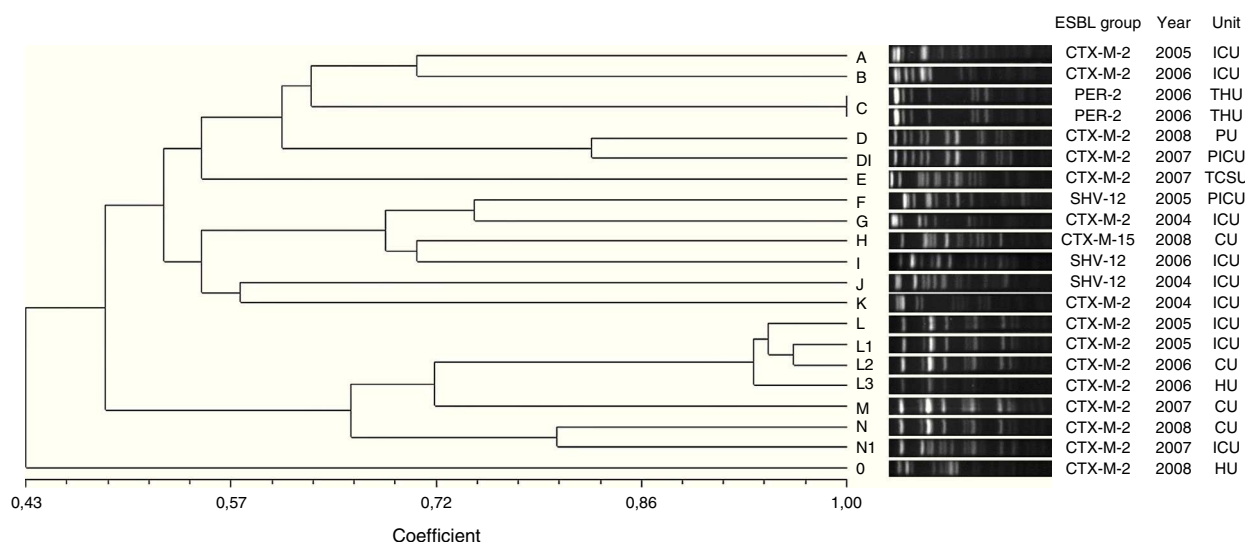
Fig. 2. Genetic similarity among ESBL–producing *Enterobacter cloacae* by PFGE and ESBL type, unit, and year of microorganism isolation. Legend: HU = hematology unit; CU = chemotherapy unit; ICU = intensive care unit; CTCV= Thoracic and Cardiovascular Surgery unit; THU = transplant hepatic unit; P ICU = pediatric intensive care unit; PU = pediatric unit.

Risk factors for infection by ESBL-producing strains include previous antibiotic therapy, severity of disease, cross transmission,[17] longer hospital stays,[17] advanced age, and chronic diseases,[15] among others. When bacteremia caused by ESBL- and non-ESBL-producing *Enterobacter* spp. was evaluated in this study, there were no major differences in the risk factors for infections between the 2 groups. These findings suggest that ESBL has less influence on the selection of resistant organisms in this species, probably because *Enterobacter* spp. harbored chromosomal AmpC, which confers resistance during therapy with third-generation cephalosporins.

In this study, pneumonia was the main source of bacteremia by ESBL-producing strains, suggesting that ESBL strains have a hospital origin. Moreover, ESBL-producing strains presented mainly a clonal profile, and in 74% of cases, pneumonia was associated with mechanical ventilation. Likewise, ICU stay was relevant for the acquisition of ESBL-producing *Enterobacter* spp. Furthermore, clonality of *E. aerogenes* isolated from ICU patients during the 5-year study suggested the hospital origin of the strains.

Studies have associated ESBL production with higher mortality, longer hospital stay, delay in appropriate therapy, and higher treatment costs. Most of these studies compared *E. coli*, *Klebsiella* spp., and *Proteus mirabilis* ESBL- and non-ESBL-producing strains.[5,6,15] The present study shows a similar risk of mortality in the group of patients harboring ESBL- and non-ESBL-producing strains. This finding may be explained by the high resistance of *Enterobacter* spp. to antibiotics, even in the absence of ESBL production. However, ESBL-producing infectious agents increased hospital stay, which typically leads to higher costs of patient care. Costs were not directly assessed, but they are higher because the average length of stay was 7 days longer in patients with ESBL-producing *Enterobacter* spp. than in patients infected with non-ESBL-producing strains.

The main cause of mortality in infections by *E. coli* and *Klebsiella* ESBL-producing strains is the delay in administration of appropriate antibiotic therapy.[5,15,18] These data were not evaluated in infections by ESBL-producing *Enterobacter* spp. in this study.

Beyond the epidemiological significance of ESBL detection, there is also the therapeutic importance. During this study, ESBL detection was used to adjust therapy in 75% of patients with ESBL-producing *Enterobacter* spp. bacteremia. This action could have affected the association between ESBLs and outcome, suggesting that if ESBL was not detected, mortality might have been even greater.

CTX-M is a type of ESBL widely prevalent in the world, mainly in South America.[19] It was also the predominant type identified in this study. PER-2 represents another important type of ESBL, which is prevalent in South America,[12] but has never been reported in Brazil and was found in 2 isolates from this study. Similarly, the SHV-12 type, which is commonly found in the USA[7] but not in Brazil, was detected in 5 strains.

Cross transmission was more prevalent in *E. aerogenes* than in *E. cloacae*. The same type of ESBL was detected in strains not genetically related and different ESBLs were detected in genetically related strains, indicating that transfer of plasmids is probably the most important mechanism of resistance dissemination by ESBLs in this study. ESBL detection in *Enterobacter* spp. is important to prevent increased frequency of ESBL in *Enterobacter* spp. as well as in other species of Gram-negative bacilli present in the hospital environment; moreover, the plasmid that carries ESBL genes often carries multiple genes for resistance to other antimicrobials.[3]

Enterobacter spp. is a pathogen with increasing importance in bacteremia. ESBL production is an important mechanism of resistance to broad-spectrum cephalosporins, reducing the therapeutic options for infection by this microorganism. The predominant type of ESBL was CTX-M, with minor participation of other types such as SHV and PER. The PFGE typing showed the occurrence of clonal and non-clonal spread of the strains, suggesting that the ESBL genes have been horizontally disseminated. ESBL detection in *Enterobacter* spp could help to control the spread of this kind of resistance. Moreover, the ESBL production had not contributed to mortality but increased the length of hospital stay.

Funding

Conflict of interest

Authors have no conflict of interest to declare.

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