



ORIGINAL ARTICLE

Incidence of Multidrug-Resistant Enterobacteriaceae in Intensive Care Units of the Abel Santamaría Cuadrado Hospital

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ABSTRACT

Introduction: healthcare-associated infections play a predominant role in global sepsis scenarios.

Objective: to assess the incidence of multidrug-resistant Enterobacteriaceae isolated in the intensive care units (ICUs) of Abel Santamaría Cuadrado Hospital.

Methods: an observational, analytical, prospective cross-sectional study was conducted in the Microbiology Laboratory of the "Abel Santamaría Cuadrado" General Teaching Hospital of Pinar del Río from January 2022 to July 2024. Absolute and relative frequencies were calculated.

Results: a total of 209 microbiological samples from ICU patients were analyzed. Of these, 15,79 % were negative and 17,22 % were contaminated. Enterobacteriaceae were identified in 94 cases (44,98 %), with *Enterobacter* being the most frequent genus (42 isolates), particularly *Enterobacter gergoviae* (28 cases, 29,79 %) and *Pantoea agglomerans* (18 cases, 19,15 %). High resistance rates were observed: 100 % of isolates were resistant to penicillins and 96,8 % to first- and second-generation cephalosporins. The lowest resistance was noted against penicillin- β -lactamase inhibitor combinations. *Escherichia*, *Klebsiella*, and *Providencia* showed complete resistance to cephalosporins, whereas *Enterobacter* exhibited no resistance to third-generation cephalosporins and *Klebsiella* showed no resistance to penicillins combined with inhibitors—findings that reveal critical resistance patterns to guide empirical antibiotic therapy.

Conclusions: There is substantial antimicrobial resistance—particularly to penicillins and cephalosporins—in the ICU setting. Knowledge of local resistance profiles guides clinicians in empirical treatment, supports clinical decision-making, and contributes to the development of context-specific antimicrobial stewardship policies.

Keywords: Critical Care; Enterobacteriaceae; Drug Resistance, Microbial; Intensive Care Units.

INTRODUCTION

Antimicrobial resistance is defined as the ability of a microorganism to withstand the effects of antibiotics. This trait may be intrinsic to the bacterium or acquired during the infectious process.⁽¹⁾ The current level of microbial resistance to antimicrobials constitutes a serious global health problem and a major challenge for the future. Research has elucidated the mechanisms and causes underlying this resistance, as well as strategies involving both new and existing pharmaceutical agents to counteract it.^(2,3)

According to World Health Organization (WHO) data, approximately 60 % of hospital-acquired (nosocomial) infections are caused by resistant microorganisms. Notably, antimicrobial resistance mechanisms are in a state of continuous evolution, making it nearly impossible to control large-scale outbreaks.⁽⁴⁾ It is projected that by 2050, antimicrobial resistance could cause 10 million deaths annually worldwide.⁽⁵⁾

Antimicrobial resistance arises through two primary mechanisms:⁽¹⁾

- **Artificial selection**, resulting from inappropriate antibiotic use, which favors the emergence of resistant clones.
- **Natural selection**, involving horizontal gene transfer—particularly via plasmids carrying resistance genes—thereby increasing the prevalence of resistant bacteria.

At the 2015 World Health Assembly, all WHO Member States committed to developing and implementing a Global Action Plan on Antimicrobial Resistance. In Latin America, Brazil reported the first antimicrobial resistance case in 2003, followed by Argentina and Colombia in 2005. In 2010, Ecuador documented its first case: a *Klebsiella pneumoniae* strain producing carbapenemases.⁽⁶⁾

The current level of antibiotic resistance observed in ICUs is deeply concerning and is progressing alarmingly toward a potential return to a pre-antibiotic era—where pan-resistant, untreatable microorganisms colonize ICUs and cause severe, fatal infections. Therefore, it is essential to maintain up-to-date microbiological surveillance across all clinical services.

METHODS

An observational, analytical, prospective cross-sectional study was carried out in the Microbiology Service of the "Abel Santamaría Cuadrado" General Teaching Hospital in Pinar del Río, Cuba, from January 2022 to July 2024. The universe comprised all microbiological samples analyzed in the Miscellaneous Department corresponding to patients admitted to the hospital's ICUs during 2023 and 2024. The study sample included all positive samples identified as Enterobacteriaceae that underwent complete microbiological characterization.

Inclusion criteria: Microbiological samples positive for Enterobacteriaceae with full susceptibility testing completed.

Data collection employed empirical methods (observation, documentary review), theoretical methods (analysis and synthesis), and historical-logical reasoning. Primary data were extracted from the Microbiology Service's Miscellaneous Department database. Biological samples were collected by trained microbiology technicians or professionals following strict aseptic and antiseptic protocols and site-specific sampling procedures.

Sample types included:

- Endotracheal tube respiratory secretions from ventilated patients
- Pleural catheter cultures from patients with thoracostomy
- Central venous catheter tip cultures
- Skin lesion and surgical wound swabs
- Body fluids (pleural, peritoneal)
- Purulent secretions

All collected data were stored in a database for statistical processing. Analyses were performed using SPSS version 11.0.0. Qualitative variables were summarized using absolute and relative frequencies, cumulative frequencies, simple percentages, and cross-tabulations. Quantitative variables were described using simple percentages, means, standard deviations, rates, and ratios as appropriate. Tables and graphs were generated for clearer interpretation.

The study adhered to the four fundamental ethical principles: respect for persons, beneficence, non-maleficence, and justice. It also complied with the Declaration of Helsinki (1975, revised 1983) and its latest version adopted at the 52nd General Assembly in Edinburgh, Scotland (October 2000). Hospital administrative authorities were informed of the study's objectives and granted formal authorization. The research was approved by the Scientific Council and Ethics Committee of the "Abel Santamaría Cuadrado" General Teaching Hospital.

RESULTS

This study analyzed microbiological samples from patients admitted to intensive care units. Statistical processing yielded the following results:

As shown in Table 1, of the 209 biological samples analyzed, 15,79 % were negative and 17,22 % were contaminated. Enterobacteriaceae were isolated in 94 cases (44,98 %), which constituted the final study sample.

Table 1. Results of the biological samples studied.

Results of the samples			No.	%
Positives	Grampositives		25	11,96
	Gramnegatives	Enterobacteries	94	44,98
		Other	21	10,05
Negatives			33	15,79
Contaminated			36	17,22

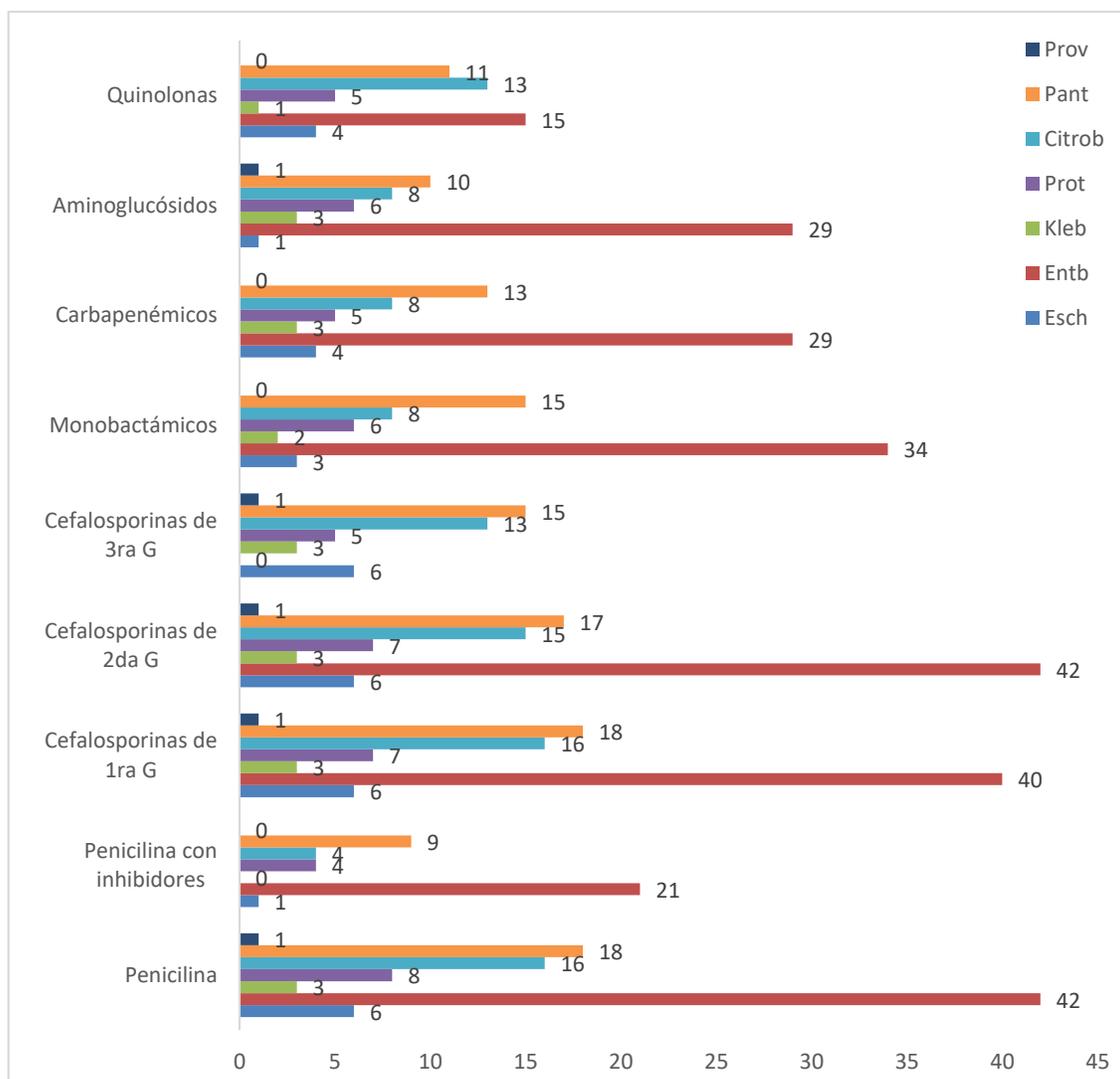
In Table 2, it is observed that among the Enterobacteriaceae isolated from the cultured biological samples, the genus *Enterobacter* was the most frequent, identified in 42 samples. Within this group, the most common species was *Enterobacter gergoviae*, detected in 28 cases (29,79 %), followed by *Pantoea agglomerans*, which was found in 18 biological samples (19,15 %).

Table 2. Distribution of the sample by genus and species of the cultured bacteria.

Family	Genre	Specie	No.	%
<i>Enterobacteriaceae</i>	Escherichia (n=6)	<i>Escherichia coli</i>	6	6,38
	Enterobacter (n=42)	<i>Enterobacter cloacae</i>	6	6,39
		<i>Enterobacter gergoviae</i>	28	29,79
		<i>Enterobacter amnigenes</i>	8	8,51
	Klebsiella (n=3)	<i>Klebsiella pneumoniae</i>	2	2,13
		<i>Klebsiella aerogenes</i>	1	1,06
	Proteus (n=8)	<i>Proteus mirabilis</i>	7	7,45
		<i>Proteus vulgaris</i>	1	1,06
	Citrobacter (n=16)	<i>Citrobacter freundii</i>	6	6,38
		<i>Citrobacter koseri</i>	3	3,19
		<i>Citrobacter amalonaticus</i>	7	7,45
	Pantoea (n=18)	<i>Pantoea agglomerans</i>	18	19,15
	Providencia (n=1)	<i>Providencia rettgeri</i>	1	1,06

Among the most important information shown in Figure 1 is the fact that 100 % of the biological samples analyzed across all Enterobacteriaceae genera exhibited resistance to penicillins, and resistance to first- and second-generation cephalosporins was observed in 96,8 % of cases. The lowest resistance rates were recorded for penicillins combined with β -lactamase inhibitors.

The genus *Escherichia* demonstrated 100 % resistance to cephalosporins, as did the genera *Klebsiella* and *Providencia*. In contrast, *Enterobacter* showed no resistance to third-generation cephalosporins, and *Klebsiella* exhibited no resistance to penicillin-inhibitor combinations.



Legend: Esch: *Escherichia*; Entb: *Enterobacter*; Kleb: *Klebsiella*; Prot: *Proteus*; Citr: *Citrobacter*; Pant: *Pantoea*; Prov: *Providencia*

Fig. 1. Antimicrobial groups to which different Enterobacteriaceae genera showed resistance.

DISCUSSION

In intensive care units (ICUs), Enterobacteriaceae exhibit heightened infective potential due to the vulnerability and fragile clinical condition of admitted patients. These pathogens can prolong ICU stays, delay recovery, and even cause fatal infections.⁽⁷⁾ The acquisition and transmission of ICU infections are associated with multiple risk factors, including advanced age, disease severity, presence of invasive devices, prior antibiotic exposure, immunosuppression, comorbidities, prolonged hospitalization, and selective pressure from antimicrobial use.^(8,9)

The positivity rate for Enterobacteriaceae in our study aligns with findings by Rodríguez et al., who reported that 56,94 % of samples were positive for these organisms,^(10,11) with high resistance rates, identifying them as the leading etiological agents of infections at the same healthcare center in 2020.

Over the past decade, a global rise in Gram-negative bacilli infections has been documented—a trend confirmed in our study and consistent with international literature.^(12,13) This may be linked to their remarkable capacity to develop antimicrobial resistance.

Guaraca,⁽¹⁴⁾ also reported a predominance of Gram-negative bacteria in ICUs. In 2021, Béja,⁽¹⁵⁾ conducted a study in the ICU of the Adolfo Guevara Velasco National Hospital and found that the second most frequently isolated microorganism belonged to the Enterobacteriaceae family. Other authors have similarly reported high rates of positive cultures for these pathogens.⁽¹⁶⁾

These findings may reflect the diversity of circulating microbiota in the hospital environment under study. In a Cuban institute's microbiological surveillance report, the most frequently identified Gram-negative bacteria were *Pseudomonas* spp., *Enterobacter* spp., *Klebsiella* spp., and *Escherichia coli*.⁽¹¹⁾ Other studies have identified *E. coli*,⁽¹⁴⁾ or *Pseudomonas*,⁽¹⁷⁾ as the predominant isolate—differences potentially related to the clinical indication for testing, as certain bacteria are more commonly associated with specific disease types.

In a study conducted in Camagüey on nosocomial infections in an ICU, *Acinetobacter baumannii* showed a prevalence of 22,9 %, followed by *Enterobacter gergoviae* and *E. coli* (17,80 % each).⁽¹⁸⁾ These results are consistent with published literature.^(19,20,21,22)

Research from a hospital in Mayabeque identified *K. pneumoniae* and *E. coli* isolates with resistance levels that progressively increased over time against all tested antimicrobials.⁽¹⁹⁾ Chávez,⁽²³⁾ found that among 107 Enterobacteriaceae-positive samples, 19 showed resistance to β -lactams. Another study reported that 5,7 % of *E. coli* isolates were resistant to imipenem, while 20% of *K. pneumoniae* isolates showed resistance to meropenem.⁽²¹⁾ Additionally, numerous publications highlight widespread resistance among these bacteria—particularly to β -lactams such as ampicillin and ceftriaxone.⁽¹⁴⁾

Cohen et al,⁽²⁴⁾ emphasized the high resistance of Enterobacteriaceae to carbapenems, associating it with prior ICU admission, prolonged use of invasive devices, and previous antibiotic exposure. Multiple studies corroborate the substantial antimicrobial resistance of Enterobacteriaceae, aligning with our findings.^(10,20,25,26)

Antibiograms for *Proteus vulgaris* revealed high bacterial resistance, especially to β -lactams (penicillins and first-, second-, and third-generation cephalosporins).⁽¹⁴⁾ Ponce,⁽¹⁷⁾ reported carbapenem resistance among Enterobacteriaceae as follows: *Klebsiella pneumoniae* (53,2 %), *Escherichia coli* (34,6 %), *Proteus mirabilis* (7,5 %), *Proteus* spp. (1,9 %), *Enterobacter cloacae* (1,9 %), and other *Enterobacteriaceae* spp. (0,9 %).

CONCLUSIONS

Knowledge of the prevalence and in vitro resistance patterns of Enterobacteriaceae to specific antimicrobials—as reported by the Microbiology Laboratory in this study—enables clinicians to guide empirical therapy in the absence of confirmed bacteriological results and to design context-specific antimicrobial stewardship policies for the management of bacterial infections.

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