Carbapenemases in Gram-Negative Bacteria: Frequency and Distribution at Military Medical Center in Guatemala

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Introduction

Antimicrobial resistance in Gram-negative bacteria, particularly carbapenemase producers, is a significant global health challenge. This study aims to identify the distribution of carbapenemases in carbapenemase-producing Gram-negative organisms isolated from clinical samples from patients at the Military Medical Center and assess their link to comorbidities and clinical factors

Objectives

To identify the types and distribution of carbapenemases in carbapenem-resistant Gram-negative bacteria at the Military Medical Center in Guatemala. To evaluate the association between carbapenemase types and patient comorbidities as well as other clinical factors

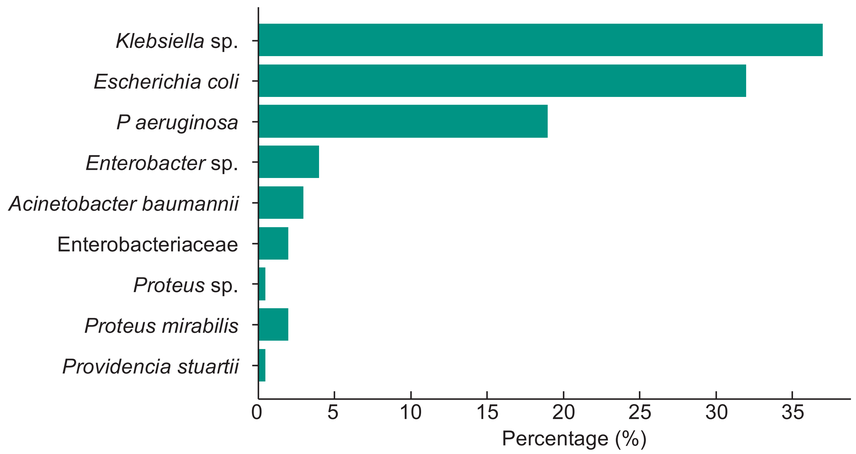
Methods

A non-interventional, prospective, descriptive study was conducted on clinical isolates collected over 12 months. The cohort included 450 Gram-negative isolates, of which 120 were collected consecutively, corresponding mainly to urine samples, soft tissue secretions, and respiratory samples (72.5%). All these isolates showed resistance to carbapenems. Of these, 111 isolates tested positive for carbapenemase and were analyzed by PCR to identify the carbapenemase type. Comorbidities, medical device use, ICU stays, and other clinical factors were also evaluated. Isolate collection was performed sequentially.

Results

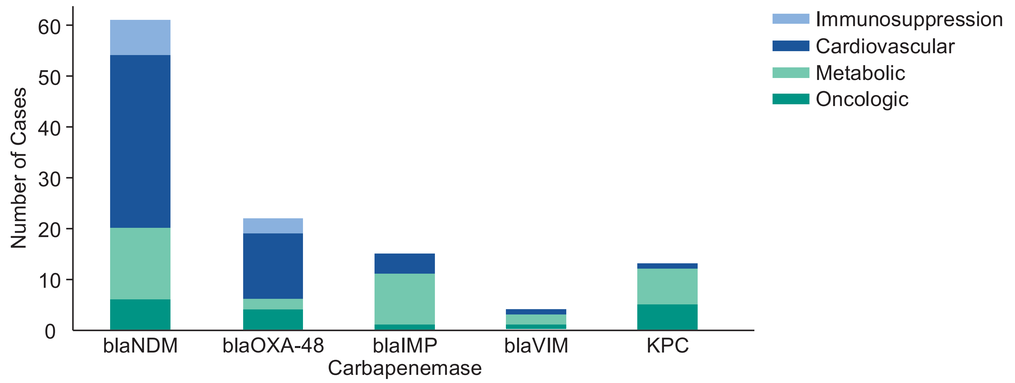
Bacteria with carbapenemases: *Klebsiella* sp., 41 (37%); *Escherichia coli,* 36 (32%); *P aeruginosa*, 21 (19%); *Enterobacter* sp., 4%; *Acinetobacter baumannii*, 3%; Enterobacteriaceae, 2%; *Proteus* sp., 0.5%; *Proteus mirabilis*, 2%; and *Providencia stuartii*, 0.5%

Figure 1. Distribution of bacteria in carbapenemase-positive isolates



The following carbapenemases were identified (pheno-genotype): Klebsiella sp. blaNDM (33), blaOXA-48 (22), blaIMP (1); *Escherichia coli* blaNDM (24), blaIMP (1), KPC (1), blaOXA-48 (1); *P. aeruginosa* blaVIM (8), KPC (8), blaIMP (5), blaOXA-48 (2); *Enterobacter sp.* blaNDM (3), KPC (1); *Acinetobacter baumannii* blaNDM (3); Enterobacteriaceae blaNDM (2). Only blaOXA-48 was found across multiple bacterial species. Key comorbidities associated with carbapenemases: Immunosuppression: blaNDM (6), blaIMP (1), blaOXA-48 (4); Cardiovascular: blaNDM (14), blaIMP (10), blaVIM (1), KPC (5), blaOXA-48 (2); Metabolic: blaNDM (34), blaIMP (4), blaVIM (2), KPC (7), blaOXA-48 (13); Oncologic: blaNDM (7), blaVIM (1), KPC (1), blaOXA-48 (3)

Figure 2. Comorbidities associated with each carbapenemase



Clinical Associations and Mortality: Prolonged ICU stays, and invasive medical devices were associated with the presence of blaNDM (p= 0.00039). Mortality Rates: blaOXA-48 21.1%, blaNDM 20.5%.

Table 1. Key findings summary table

Category	Key data points
Total Isolates	450 Gram-negative bacteria; 120 carbapenem-resistant; 111 positive for carbapenemases
Top Bacteria	*Klebsiella* sp. (37%), *E coli* (32%), *P aeruginosa* (19%)
Main Carbapenemases	blaNDM and blaOXA-48
Species with blaNDM	*Klebsiella* sp., *E coli, P aeruginosa, A baumannii,* Enterobacteriaceae
Species with blaOXA-48	Found across multiple species; only OXA-type carbapenemase detected
Comorbidities (most frequent)	Metabolic (34 blaNDM, 13 blaOXA-48), cardiovascular, immunosuppression
ICU/Device Association	Strongly associated with blaNDM cases
Mortality Rates	blaNDM: 20.5%, blaOXA-48: 21.1%
Sample Origin	72.5% from urine, secretions, respiratory specimens

Conclusion

This study highlights the following key fining: The predominance of *Klebsiella* sp. and *Escherichia coli* with blaNDM and blaOXA-48. A strong association between these carbapenemases and specific comorbidities, such as the use of invasive medical devices, and prolonged ICU stays. Notably, blaOXA-48 was the only OXA-type carbapenemase found in the study. This was explained with the fact that Acinetobacter was detected only in 3% in this cohort. AMR remains a significant clinical challenge. Novel therapies, including aztreonam-based combinations, may offer valuable treatment options for affected patients.

References

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Disclosure
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