CHARACTERIZATION OF ANTIMICROBIAL RESISTANCE IN ESKAPE-E PATHOGENS FROM FOUR HOSPITALS IN HONDURAS 2023-2025

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Introduction

- Infections caused by ESKAPE-E pathogens (*Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa*, *Enterobacter cloacae* and *Escherichia coli*) pose a world health problem due to their association with high levels of antimicrobial resistance (AMR).[1,2]
- AMR is an emerging threat in Honduras, with limited published data available. Past reports indicate increasing resistance to quinolones and carbapenems, particularly among *Escherichia coli*, *Klebsiella pneumoniae*, and *Acinetobacter baumannii*.[3,4]
- Additionally, an observational study conducted in two hospitals in Honduras from 2011 to 2012, detected the prevalence of methicillin-resistant *Staphylococcus aureus* (MRSA) at 14.3%.[5]

Materials & Methods

- A total of 1,208 ESKAPE-E isolates were collected from wound exudates, blood, soft tissue, and body fluids across four hospitals in Honduras (2023–2025).
- Isolates were sub-cultured and the BD Phoenix system and ComASP® Colistin microdilution assay (for Gram-negative organisms) were used for identification and susceptibility testing (CLSI M100).
- Carbapenemases KPC, OXA-48-like, VIM, IMP, and NDM were detected using NG-Test CARBA-5. The presence of the *mcr-1* gene was detected using the StepOne Plus Real-Time PCR System.
- Multidrug Resistance (MDR) was defined as non-susceptibility to ≥1 agent in ≥3 antimicrobial categories.

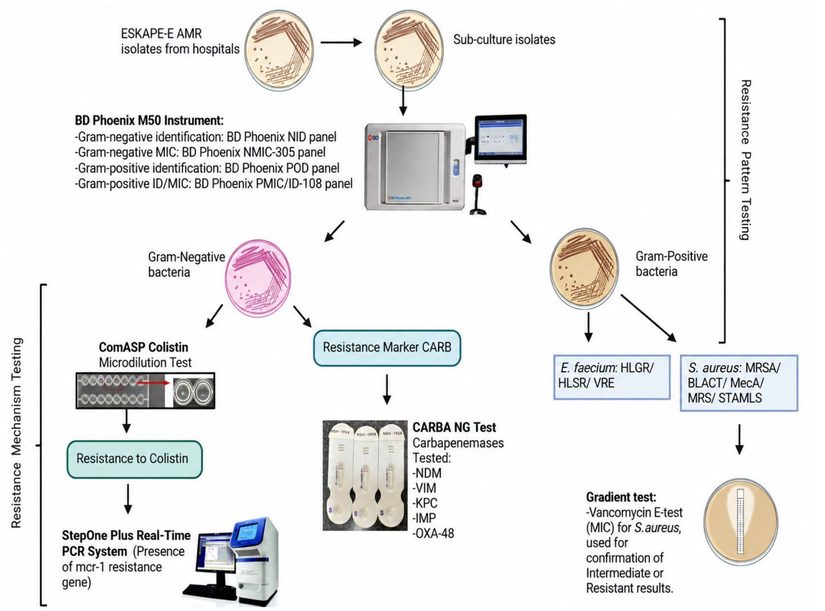
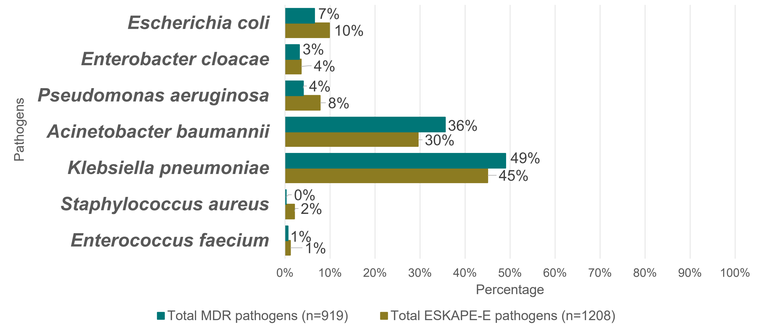


Figure created with BioRender.com using adapted visuals from BD Phoenix™, Applied Biosystems StepOnePlus™, and ComASP® Colistin MIC testing (Liofilchem).

Results

Figure 2. ESKAPE-E pathogen distribution with corresponding MDR frequencies



- From 1,208 ESKAPE-E pathogens evaluated, 76% of isolates were MDR.
- *K. pneumoniae* (49%) and *A. baumannii* (36%) were the most prevalent MDR pathogens.
- Carbapenem resistance was highly prevalent in *A. baumannii* (97%) and *K. pneumoniae* (82%), based on BD Phoenix antimicrobial susceptibility testing. Quinolone resistance was similarly frequent (97% and 95%, respectively).

Table 1. Resistance mechanisms identified in Gram-negative ESKAPE-E pathogens

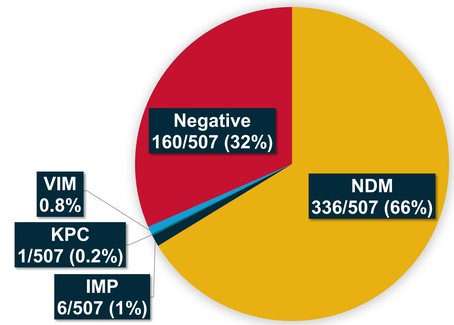
Resistance mechanisms	Total Gram-negative ESKAPE-E (n=1169)	Pathogen	Total per pathogen
ESBL* (BD Phoenix)	626 (54%)	*Klebsiella pneumoniae*	525 (83%)
		Acinetobacter baumannii	1 (0.2%)
		Escherichia coli	100 (16%)
CPO** (BD Phoenix)	920 (79%)	*Klebsiella pneumoniae*	438 (48%)
		Acinetobacter baumannii	350 (38%)
		Escherichia coli	62 (6%)
		Enterobacter cloacae	28 (3%)
		Pseudomonas aeruginosa	42 (5%)
ESBL* + CPO** (BD Phoenix)	501 (43%)	*Klebsiella pneumoniae*	439 (87%)
		Acinetobacter baumannii	1 (0.2%)
		Escherichia coli	61 (12%)
Colistin resistance (Microdilution)	22 (2%)	*Klebsiella pneumoniae*	10 (45%)
		Acinetobacter baumannii	5 (23%)
		Enterobacter cloacae	5 (23%)
		Pseudomonas aeruginosa	2 (9%)

**ESBL: Extended-spectrum beta-lactamase. **CPO: Carbapenemase-producing organisms.*

- *K. pneumoniae* was the most frequent CPO (48%) and ESBL-producing bacteria (84%).
- Among 39 Gram-positive isolates, 19/25 (76%) of *S. aureus* were methicillin-resistant, and 6/14 (43%) of *E. faecium* were vancomycin-resistant.

Results (Continued)

Figure 3. Carbapenem resistance markers among Gram-negative ESKAPE-E pathogens



- NDM was the most prevalent carbapenemase, with 73% detected in *K. pneumoniae*. A combination of NDM and KPC was also observed in one *K.pneumoniae* strain.
- No OXA-48-like carbapenemases were detected.

Conclusions

- Carbapenemase and ESBL producers were the most frequent resistance mechanisms identified among the 1,169 Gram-negative ESKAPE-E pathogens tested.
- High carbapenem and quinolone resistance among ESKAPE-E pathogens in four hospitals in Honduras was observed, aligning with previous national reports.
- ESKAPE-E isolates frequently harbor multiple resistance mechanisms, limiting treatment options and reinforcing the need for robust infection control, antimicrobial stewardship and MDR ongoing surveillance.

References

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