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Genotypic Characterization by DNA Microarray of Carbapenem-Resistant Enterobacterales

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Introduction :

The detection of antibiotic resistance genes is essential to understand local epidemiology, guide appropriate antimicrobial therapy, and limit the dissemination of multidrug-resistant bacteria.

Aim of the study:

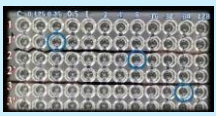
- The aim of this study was to identify antibiotic resistance genes among carbapenem-resistant Enterobacterales (CRE) isolated at Habib Thameur Hospital, Tunis, Tunisia..

Methodology:

Descriptive study

Bacteriology Unit

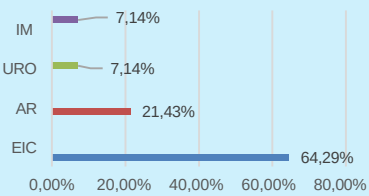
June 2024 and March 2025



70 clinical isolates of carbapenem-resistant Enterobacterales.

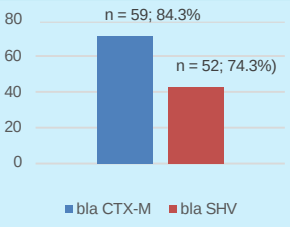
PCR DNA Flow technology with the MDR kit

RESULT:

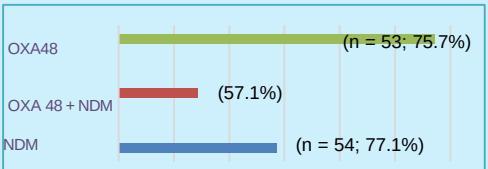


Epidemiological distribution of KPRC by hospital unit

Additional resistance genes were identified, particularly those associated with fluoroquinolone resistance: **qnrS** (n = 47; 67.1%) and **qnrB** (n = 40; 57.1%). Aminoglycoside resistance genes detected included **aac(6')-Ib** (n = 46; 65.7%), **rmtF** (n = 22; 31.4%), **rmtC** (n = 11; 15.7%), **rmtB** (n = 4; 5.7%), and **armA** (n = 6; 8.6%)

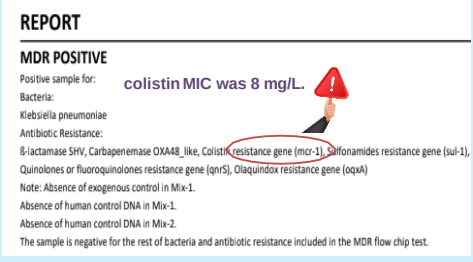


Prevalence and molecular profile of dominant ESBL enzyme



Molecular characterization of carbapenemase types

Colistin resistance (MIN > 4 mg/L) was observed in 22 Klebsiella pneumoniae isolates (31.4%)



Conclusion:

Our study revealed a high prevalence of carbapenemase-producing Enterobacterales, predominantly **blaNDM** and **blaOXA-48**, in our hospital setting. These findings highlight the urgent need for strengthened surveillance, optimized antimicrobial stewardship, and reinforced infection prevention and control measures.