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Abstract Discussion Forum **(0)**

Number: Mo1410

EXTREMELY HIGH PREVALENCE OF MULTIDRUG-RESISTANT ORGANISMS IN THE GUT FLORA OF HOSPITALISED PATIENTS WITH GASTROINTESTINAL ILLNESS: A CROSS-SECTIONAL STUDY AT A TERTIARY CARE HOSPITAL IN NORTH INDIA

Society: AGA
Track: Stomach and Small Bowel Disorders

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Introduction

Gut colonisation with multidrug resistant organisms (MDRO) is associated with poor outcomes in hospitalised patients. We undertook a cross-sectional study to find out prevalence of MDRO colonisation in patients admitted in Gastroenterology ward and intensive care unit (ICU) at a tertiary care centre.

Methods

Rectal swab for bacterial culture was obtained from all consecutive patients admitted in Gastroenterology ward and ICU at All India Institute of Medical Sciences, New Delhi over 2-month period (October-November 2022). Isolates were assessed for antibiotic sensitivity using VITEK 2 compact (bioMÃ©rieux Inc.). Organism was labelled â€œmulti-drug resistantâ€□ based on non-susceptibility to any agent in at least 3 antimicrobial classes. Polymerase chain reaction (PCR) for antimicrobial resistance (AMR) genes was done using PCR system (Bio-Rad TM). Prevalence of MDRO in other clinical samples, concordance between fecal and other samples, and association of mortality with MDR colonization was also assessed.

Results

One hundred-seven patients with chronic liver disease and its complications (41.1%), acute pancreatitis(27.1%), inflammatory bowel disease(7.5%), acute cholangitis(6.5%) and other gastrointestinal disorders(17.8%) were included. Mean hospitalisation duration was 14+13 days, with 59.2%, 52.5% and 22.5% requiring central venous catheterization, Foley catheterization and mechanical ventilation, respectively. 106(99.1%) samples were positive for MDRO, predominantly E.coli(75.7%), Klebsiella pneumoniae(16.8%) and Enterococcus
fecium(9.3%). NDM(New-Delhi-metallo-Î²-lactamase, carbapenemase)(64.5%) was most prevalent AMR gene, followed by TEM(extended-spectrum-beta-lactamase,ESBL)(58.9%) and OXA(carbapenemase)(55.1%). 15% of other clinical samples were positive for MDRO, most common pathogen being K.pneumoniae(50%). Concordance for MDRO was highest in acute pancreatitis (16.7% for E.coli and 33.3% for Klebsiella pneumoniae). Isolated gut MDR colonization was associated with 22%(n=20) mortality, while patients with MDRO in both stool and another clinical sample had 50%(n=8) mortality.

Conclusions

We report extremely high prevalence of gut colonisation with MDR organisms in hospitalised patients with GI illness. Urgent policy measures are needed to address the imminent threat of MDR infections.

Keywords
Antibiotic resistance genes, acute pancreatitis, cirrhosis, multidrug resistance
organism, gut colonisation

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DDW ePoster Library. Narang H. 05/05/2025; 4153297; Mo1410

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