

## Bacteremia Caused by Carbapenem-Resistant *E. coli* In Children from A Tertiary Care Hospital

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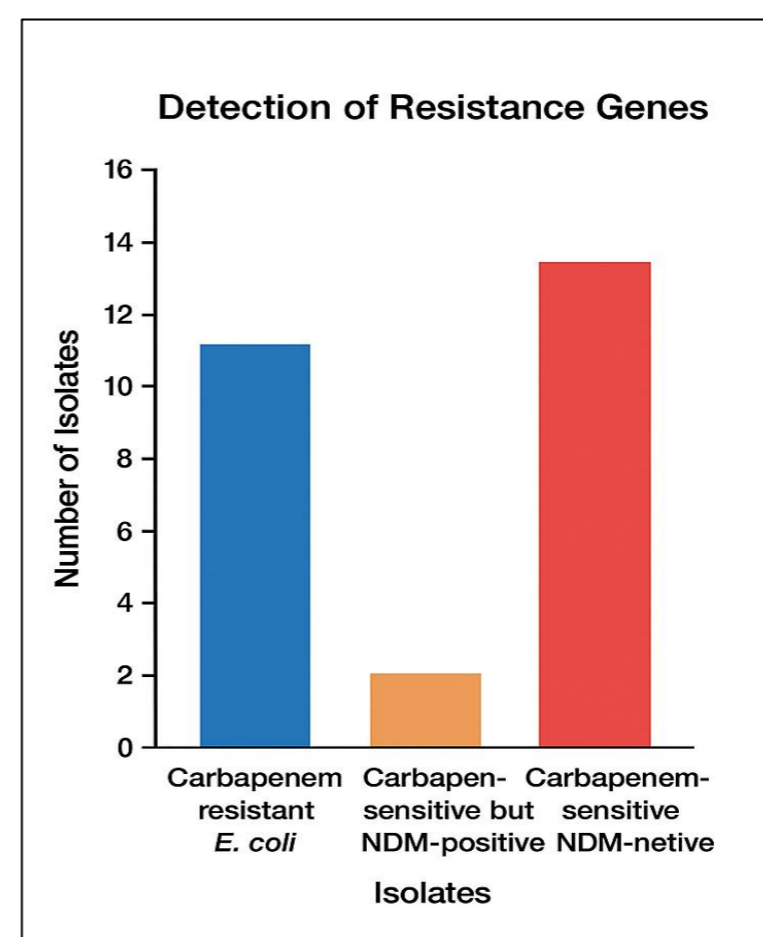
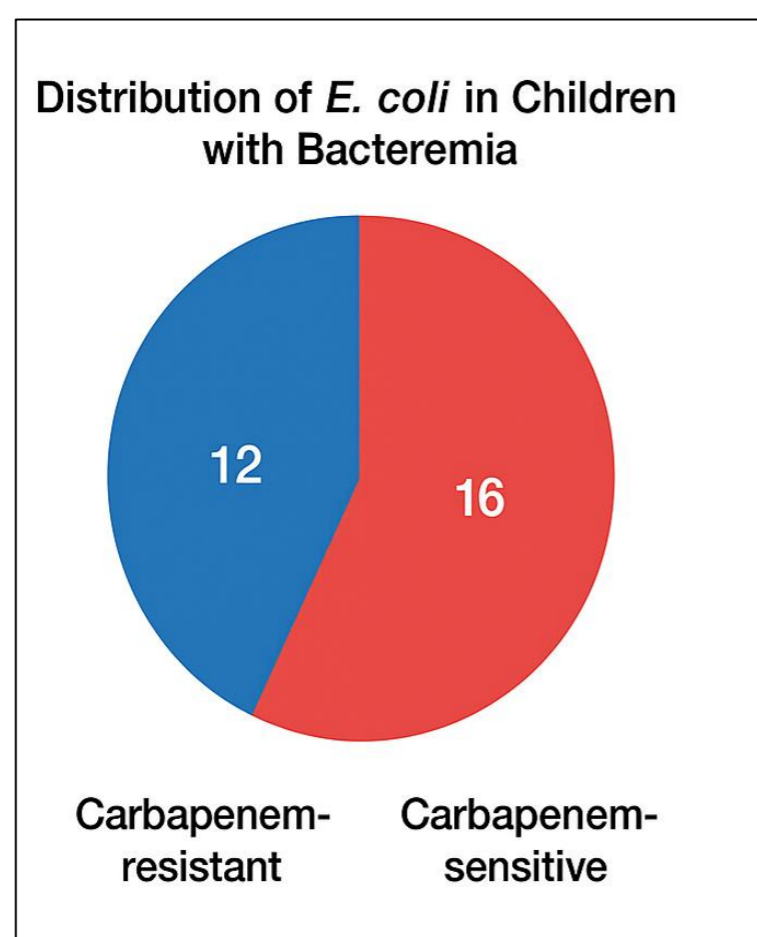
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**Introduction:** Antimicrobial resistance (AMR) has emerged as a significant global public health challenge, especially in developing countries like India, where infectious diseases are prevalent, and antibiotic use often lacks proper regulation. This research aimed to explore the epidemiological connection among patients infected with carbapenem-resistant *Escherichia coli*.

**Methods:** A total of 80 isolates were collected from children suffering from diarrhea. Conventional phenotypic methods were performed, and antibiotic susceptibility testing was conducted using CLSI guidelines. Bacteremias caused by *E. coli* were registered in 28 children. Various bacteriological and molecular biological methods (PCR-RT and MLST) were used to identify isolates.

**Results:** All 28 children with bacteremia were in isolated wards. Out of these, carbapenem resistance in *E. coli* was detected in 12 children. In two carbapenem-sensitive *E. coli* isolates, the NDM-1 gene was detected. No antibiotic resistance genes were found in the hospital environment or other samples. Comparative genomic analyses of 8 *E. coli* isolates revealed differences in common loci, possibly due to variations in plasmid sequences.



**Conclusion:** This study established group colonization in *E. coli* strains due to translocation of intestinal flora. Genomic surveillance of priority pathogens will help identify high-risk AMR clones regionally and globally, and groups at risk of infection. This will enable correlation of virulence factors with patient outcomes, aiding in early outbreak detection.