

Occurrence of blaSHV mediated extended spectrum cephalosporin resistance within clinical isolates of Escherichia coli associated with UTI cases from north-east India

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ABSTRACT: *Escherichia coli*, a gut flora, is increasingly responsible for urinary tract infection in the community and hospital settings. The antibiotic resistance of *E. coli*, particularly the production of extended-spectrum beta-lactamases (ESBLs) which confer resistance to extended spectrum cephalosporins and monobactam challenges public health issue and creates increasing difficulty in the diagnosis and therapeutic options. In this study, we have detected the presence of multidrug resistant *E. coli* harboring blaSHV associated with urinary tract infection. This is a prospective study performed in the patients who had attended two different primary health care settings (Kalinagar and Girishganj) of Assam, north eastern India from July 2019 - February 2020. A total number of 246 midstream urine samples were collected from patients suffering from UTI or suspected to have UTI. The significant bacteriuria was determined by culture loop method. The isolates were identified using VITEK® 2 Compact automated system and were phenotypically characterized for ESBL production with an initial screening followed by phenotypic confirmation by combined disc

diffusion method (CLSI 2017). The genotypic characterization of ESBLs was performed using PCR assay targeting different ESBL genes namely blaTEM, blaSHV, blaCTX-M, blaOXA-10, blaOXA-2, blaPER, blaVEB and blaGES. The present study revealed the presence of 19 *E. coli* isolates confirmed using VITEK® 2 automated system. Of which three isolates were found to be ESBL producers by combined disc diffusion method. Molecular characterization of ESBL revealed that these isolates were carrying blaSHV and the susceptibility pattern showed that all these isolates were resistant to cephalosporin and quinolone antibiotics and susceptible to only carbapenem and aminoglycoside group of drugs. The present study has demonstrated the emergence of blaSHV in this part of the world and as this enzyme has kept a stable role in antibiotic resistance over many years so it is important to track down the clonal source and origin of the resistance determinant to implement proper infection control policy and also to prevent the expansion towards novel bacterial hosts and reservoirs.

REFERENCES

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