

Abstract

Prevalence, antibiotic sensitivity pattern and genetic analysis of extended spectrum beta lactamase producing *Escherichia coli* and *Klebsiella* spp among patients with community acquired urinary tract infection in Galle District, Sri Lanka

Introduction.

Community acquired urinary tract infections (CA-UTI) are mainly caused by *Escherichia coli* and *Klebsiella* spp which inducible extended spectrum beta lactamase (ESBL) producers. Study of pathogens in such infections may help to establish antibiotic guidelines in the out-patient setting.

Objectives

To determine, the prevalence of ESBL producing *E. coli* and *Klebsiella* spp in CA-UTI characteristics of the ESBL producing organisms including resistance genes and factor associated with infection with ESBL producers.

Design, setting and methods

A descriptive cross-sectional study was done at the out-patient department of a tertiary care hospital and at 10 selected general practitioners' centers. Following written consent and administration of an interviewer-based questionnaire, urine samples were collected from clinically suspected CA-UTI patients. Significant isolates were identified and antibiotic sensitivity (ABST) were done according to the standards methods. ESBL genes were identified by Conventional multiplex PCR.

Results

Positive cultures were seen in 178 (38%) urine samples of total 465 patients. Most positives from females (103/58%). Predominant isolate was *E. coli* (149, 84%) with 68% ESBL producers followed by 16 (9%) *Klebsiella pneumoniae* with 4 (25%) ESBL producers. ESBL pathogens had high resistance rates for quinolones present (41%) but 80% sensitivity to nitrofurantoin, fosfomycin, mecillinam, aminoglycosides and carbapenems. ESBL genes included were 83% CTX -M, 71% OXA, 24% TEM and 9% SHV with one more than one gene in 29 isolates (71%). Haematuria was

significantly associated with ESBL production ($p < 0.01$). Out of risk factors tested, there was significant association between structural abnormalities the urinary tract and increased ESBL CA-UTI ($p < 0.01$).

Conclusions.

ESBL prevalence was 40% in CA-UTI with *E.coli* predominance. More than eighty percent of ESBL organisms show high sensitivity to aminoglycosides, carbapenems, nitrofurantoin, mecillinam and fosfomycin. The most frequently isolated ESBL gene was CTX-M. Haematuria and structural abnormalities of urinary tract were significantly associated with ESBL CA-UTI.