

Geographical and phylogenetic distribution of antimicrobial resistance among extra intestinal pathogenic *Escherichia coli*

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Introduction and Objectives: This study compared antibiotic resistance profiles of extra-intestinal pathogenic *Escherichia coli* (ExPEC) isolated from humans in two geographical locations in Sri Lanka with distinct environmental attributes, with the objective of determining geographic and phylogenetic variations in resistant proportions of ExPEC to individual antimicrobials and antimicrobial classes.

Methods: ExPEC isolated between January 2020 to March 2021 were collected from the diagnostic microbiology laboratories at Teaching Hospitals of Peradeniya (n=88) and Batticaloa (n=53). The isolates were identified by biochemical and molecular methods and tested for resistance to 15 antimicrobials representing eight classes - penicillins, penicillins + β -lactamase inhibitors, folate pathway inhibitors, quinolones, cephalosporins including extended spectrum cephalosporins (ESC), aminoglycosides and carbapenems, by standard disk diffusion method (EUCAST). Phylogroups of the isolates were determined by quadruplex PCR. Data were analyzed both as individual drug resistance phenotypes and as composite antibiograms. Association of geographical location and the phylogroup with the incidence of antibiotic resistance was statistically estimated.

Results: Comparable resistance profiles were observed in isolates of two locations except for quinolones ($p = 0.02$), and ceftazidime ($p = 0.01$) that showed significant association with Batticaloa isolates and trimethoprim sulfamethoxazole with Peradeniya isolates ($p = 0.006$). According to the antibiograms, of the 141 isolates tested, 106 (75%) were multidrug-resistant (MDR) and were distributed as follows; 4.2% resistant to eight, 9.9% to seven, 18.4% to six, 16.3% to five, 15.6% to four and 10.6% to three classes of antimicrobials. Resistance was most prevalent to ampicillin (86%), cefpodoxime (62%), ciprofloxacin (60%), trimethoprim sulfamethoxazole (59%), levofloxacin (56%), and cefuroxime/cefepime (55%). The majority of the isolates (78%) belonged to phylogroup B2 and were equally present in both locations. Resistance to the ESC antibiotics, namely ceftriaxone ($p = 0.002$), ceftazidime ($p = 0.008$) and cefpodoxime ($p = 0.001$) showed significant association with phylogroup B2.

Conclusions: Regional variations in antimicrobial resistance of ExPEC was evident. The B2, main phylogroup of ExPEC, showed significant resistance to ESC antibiotics. This suggested the presence of antimicrobial resistant clones in the phylogroup B2.

Keywords: Extra intestinal *E coli*, phylogenetic, antimicrobial resistance

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