

## The Frequency of Extended-spectrum $\beta$ -lactamase-producing Isolates of Enteropathogenic *Escherichia Coli*

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**Background & Objectives:** Acute diarrheal disease is still an important cause of infectious morbidity in children in many developing countries, enteropathogenic *Escherichia coli* (EPEC) being the most frequently found bacterial pathogen. It is usually associated with infants from the poorer social groups. Antimicrobial treatment is not recommended for diarrheal diseases caused by enteropathogenic bacteria other than shigellae (i.e., EPEC). Therefore, antibiotic resistance genes harbored by these microorganisms can remain unnoticed and may be silently transferred between different bacterial species in the community or among patients. Extended-spectrum  $\beta$ -lactamases (ESBLs) are plasmid-encoded  $\beta$ -lactamases that confer significant resistance to penicillins, cephalosporins and aztreonam. In recent years, ESBL production in Enterobacteriaceae, particularly in *Escherichia coli*, has significantly increased in numerous countries. The objective to this study is to determine the antibiotic resistance pattern and considering the prevalence rate of Extended-Spectrum  $\beta$ -Lactamases (ESBLs) genes coding, including TEM, SHV, CTX-M and OXA gene and insertion sequence of ISE-CP1 in Enteropathogenic *Escherichia coli* (EPEC) strains isolated from children with diarrhea.

**Methods:** Totally, 192 strains of Enteropathogenic *Escherichia coli* (EPEC) isolated from children with diarrhea were studied. The susceptibility of isolates to 14 antimicrobial agents was determined using the disk diffusion Methods. Disks containing ceftazidime, cefotaxime, ceftazidime/clavulanic acid, and cefotaxime/clavulanic acid were used in the Double Disk Synergy Test (DDST) Methods to detect ESBL isolates. All the strains were examined for the presence of genetic determinants encoding Extended-Spectrum  $\beta$ -Lactamases (ESBLs) including CTX-M, SHV, TEM, OXA and insertion sequence of ISE-CP1 with PCR technique.

**Results:** Resistance to cefpodoxime, trimethoprom, tetracycline and ampicillin were found in 97%, 60.7%, 58.4%, and 45.8%, respectively. Multidrug resistance was 68.7 percent. The most sensitivity was found to imipenem, ceftriaxone, and ciprofloxacin antibiotics. Out of a total of 192 isolates, 153(79.7%) isolates possessed the resistance phenotypes consistent with possible ESBL production. PCR were used to determine the genetic determinant(s) responsible for ESBL phenotypes. A total of 26 (13.5 %), 23 (11.9 %), 21 (10.9%), and 14 (7.3%) isolates were TEM, SHV, CTX-M, and OXA ESBLs producers, respectively. Nineteen CTX-M producers carried the insertion sequence ISEcpI gene.

**Conclusion:** The antibiotic resistance of these bacteria has to be monitored. Based on the results, it is recommended that prescription of cephalosporins be restricted to susceptible isolates and that the usage of other effective antibiotics be considered. This is of great concern as the gene is also found in association with the ISEcpI gene, which may easily facilitate its spread

**Keywords:** EPEC; Extended Spectrum Betalactamase; Antibiogram; Antibiotic Resistance; Diarrhea

