Abstract

**Background and Objective:** CTX-M type extended spectrum beta-lactamases is a rapidly expanding group of enzymes encountered with increasing frequency, especially, in *Escherichia coli* (*E. coli*). There are a few reports on phylogenetic background of *E. coli* isolates from clinical sources of under five-year-old children in Iran. The purpose of this study was phylotyping of *E. coli* isolates having *blaCTX-M* and *blaCTX-M-15* genes from under five-year-old children with diarrhea and urinary tract infection (UTI).

**Material and Methods:** A total of 121 *E. coli* isolates (75 diarrheas and 46 UTI) were obtained and identified as *E. coli* based on standard bacteriological tests. DNA was extracted from *E. coli* isolates by alkaline lysis method. PCR assay was used because of high frequency of *blaCTX-M* and *blaCTX-M-15* genes in the isolates and also determination of phylogenetic group/subgroups by detection of yjaA and chuA genes and fragment TspE4.C2.

**Results:** The isolates belonged to four phylogenetic groups A (48.77%), B1 (14.04%), B2 (11.57%), and D (25.62%). In the diarrheic isolates, 17.37% were positive for *blaCTX-M* and 14.04% of isolates possessed both *blaCTX-M* and *blaCTX-M-15* genes. Out of 46 UTI isolates, 21.73% were positive for *blaCTX-M* and 15.21% for *blaCTX-M and blaCTX-M-15* genes.

**Conclusion:** A rather high prevalence of *E. coli* isolates with *blaCTX-M* and *blaCTX-M-15* genes was observed in fewer than five-year-old children in Khoramabad city. Phylotyping of isolates possessing *blaCTX-M* and *blaCTX-M-15* genes showed that most of them belong to A and D phylo-groups.

**Keywords:** *Escherichia Coli*, Phylogenetic Group, Extended-Spectrum Beta-Lactamase