Determination of Phylogenetic Group and Prevalence of $bla_{\text{CTX-M}}$ and $bla_{\text{CTX-M-15}}$ Genes in Escherichia Coli Isolates from Intestinal and Urinary Tract Infections in under Five- Year-Old Children

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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 $bla_{CTX-M-15}$ 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 $bla_{\text{CTX-M}}$ and $bla_{\text{CTX-M-15}}$ 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 $bla_{\text{CTX-M}}$ and 14.04% of isolates possessed both $bla_{\text{CTX-M}}$ and $bla_{\text{CTX-IS}}$ genes. Out of 46 UTI isolates, 21.73% were positive for $bla_{\text{CTX-M}}$ and 15.21% for $bla_{\text{CTX-M}}$ and $bla_{\text{CTX-M}}$

Conclusion: A rather high prevalence of E. coli isolates with blaCTX_{-M} and $bla_{\text{CTX-M-15}}$ genes was observed in fewer than five-year- old children in Khoramabad city. Phylotyping of isolates possessing blaCTX_{-M} and $bla_{\text{CTX-15}}$ genes showed that most of them belonge to A and D phylo-groups.

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