

**Prevalence of Virulence Genes of Escherichia Coli O157:H7 Isolated from Patients
with Urinary Tract Infections in Shiraz, Iran**

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Abstract

Background and Objective: Escherichia coli O157:H7 is one of the most well-known pathogenic bacteria worldwide that can develop severe diseases such as hemolytic uremic syndrome (HUS). This study aimed to assess the prevalence of virulence genes of E. coli O157:H7 in patients with suspected urinary tract infections (UTIs).

Material and Methods: This cross-sectional study was conducted on 10,372 urine samples collected from patients with suspected UTI from six hospitals and clinical laboratories in Shiraz city. CT-SMAC medium, β -glucosidase activity test (MUG), specific antiserum, and the presence of O157 and H7 genes by PCR were used to confirm E. coli O157:H7 isolates. Then, stx1, stx2, eaeA, and hlyA genes were evaluated using multiplex PCR.

Results: In this study, 16 (7.8%) and 13 (6.3%) bacteria had O157 and H7 genes, respectively. Evaluation of virulence genes showed that genes eaeA (15.4%), stx1 and eaeA (15.4%), stx2 (7.7%), and stx2 and eaeA (7.7%) had the highest frequency in E. coli O157:H7.

Conclusion: Due to the severity of pathogenicity, low infectious dose of E. coli O157: H7, and its pathogenic genes, more extensive studies and genotyping of E. coli O157: H7 are required to be conducted in other areas of Iran in order to measure the frequency in UTIs and control the infections caused by E. coli O157: H7.

Keywords: Escherichia coli O157:H7; Urinary Tract Infections; Shiga Toxin 1; Shiga Toxin 2.