



Identification of Virulence Genes and Antibiotic Resistance Patterns of *Escherichia coli* in Samples from Patients Referred to Medical Centers of Mazandaran University of Medical Sciences in 2022

Mahdieh Mousivand¹, Elnaz Akbari Alaei¹, Mohammadreza Khosravi Largani¹, Sara Ghandi¹, Hamidreza Goli², Mehrdad Gholami^{3*}

¹Department of Medicine, Faculty of Medicine, Mazandaran University of Medical sciences, Sari, Iran

²Department of Medical Bacteriology and Virology, School of Medicine, Molecular and Cell Biology Research Center, Hemoglobinopathy Institute, Mazandaran University of Medical Sciences, Sari, Iran

³Department of Medical Bacteriology and Virology, School of Medicine, Antimicrobial Resistance Research Center, Communicable Diseases Institute, Mazandaran University of Medical Sciences, Sari, Iran

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*Corresponding Author:

Dept. of Medical Bacteriology and Virology, School of Medicine, Antimicrobial Resistance Research Center, Communicable Diseases Institute, Mazandaran University of Medical Sciences, Sari, Iran

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ABSTRACT

Introduction: Urinary tract infections (UTIs), commonly caused by *Escherichia coli*, are widespread. The virulence factors of *E. coli* enhance its ability to adhere, establish infection, and resist antimicrobial resistance. This study aimed to investigate the presence of virulence genes and antibiotic resistance patterns in *E. coli* strains obtained from patients at hospitals affiliated with Mazandaran University of Medical Sciences.

Methods and Materials: In this descriptive cross-sectional study, we collected and analyzed 100 positive clinical specimens (urine cultures) containing *E. coli* obtained from patients with UTIs. We assessed the antimicrobial susceptibility profile of the *E. coli* isolates using the Kirby-Bauer disk diffusion method on Mueller-Hinton agar media, following the guidelines of the Clinical and Laboratory Standards Institute (CLSI). Additionally, we employed PCR with specific primers to identify three virulence genes: *papC*, *fimH*, and *afa*. Statistical data were analyzed using SPSS version 16 software and descriptive statistical tests.

Results: Among 100 patients diagnosed with UTI, 82 isolates were found in females (82%) and 18 isolates in males (18%). The highest incidence of UTIs was observed in the youngest age group (0-25 years) at 42%, followed by the age groups 25-50 years (22%) and 50-75 years (21%). The lowest incidence was recorded in the oldest age group (75-95 years) at 15%. All samples demonstrated sensitivity to tobramycin and amikacin antibiotics. Subsequently, imipenem, ceftazidime, and gentamicin exhibited the highest sensitivity against *E. coli*, with the rates of 99%, 98.80%, and 94.60%, respectively. The prevalence of *fimH*, *papC*, and *afa* genes in *E. coli* isolates was 73%, 39%, and 8%, respectively. Additionally, ampicillin displayed the lowest sensitivity among all antibiotics tested.

Conclusion and Discussion: The current study revealed that among patient isolates, the *fimH*, *papC*, and *afa* virulence genes were the most prevalent. Moreover, women exhibited a higher frequency of virulence factors compared to men. All samples demonstrated sensitivity to tobramycin and amikacin antibiotics while displaying the highest resistance to ampicillin.

Keywords: *Escherichia coli*, Urinary tract infections, Virulence factors