

# Jordan University of Science and Technology

## Antimicrobial Resistance, Virulence Factors, and Pathotypes of *Escherichia coli* Isolated from Drinking Water Sources in Jordan

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**Abstract:** The study investigated the prevalence of potentially pathogenic and drug resistant *Escherichia coli* among drinking water sources in Jordan. A total of 109 confirmed *E. coli* isolates were analyzed. Antimicrobial susceptibility testing was done using the Kirby Bauer disk diffusion method. Phenotypic identification of extended spectrum beta-lactamase (ESBL) and carbapenemase production was done using the double disk synergy test and the modified Hodge test, respectively. Isolates' plasmid profiles were determined by gel electrophoresis. PCR was used for detection of virulence and resistance genes. Overall, 22.0% of the isolates were potentially intestinal pathogenic *E. coli* (IPEC); namely enteroaggregative *E. coli* (16.5%), enteropathogenic *E. coli* (2.8%), enteroinvasive *E. coli* (1.8%), and enterohemorrhagic *E. coli* (0.9%). A third of the isolates were multi-drug resistant. The highest rates of antimicrobials resistance were observed against ampicillin (93.6%) and sulfamethoxazole/trimethoprim (41.3%). All isolates were susceptible to imipenem, meropenem, doripenem and tigecycline. The prevalence of ESBL and carbapenemase producers was 54.1% and 2.8%, respectively. *bla*VIM was the most prevalent resistance gene (68.8%), followed by *bla*CTX (50.5%), *bla*TEM (45.9%), *bla*NDM (11%), *bla*KPC (4.6%), and *bla*SHV (0.9%). Fifty-eight (53.2%) isolates contained one or more plasmid ranging from 1.0 to 8.0 kbp. Overall, high prevalence of potentially pathogenic and resistant isolates was observed