

Prevalence of Integrations and Multi-Drug-Resistance Among *E. coli* Isolates

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ABSTRACT

Introduction: *Escherichia coli* (*E. coli*) is a common bacterium found in clinical, environmental, and food sources. It contributes to major infections such as urinary tract infections and sepsis. Its ability to acquire and disseminate antibiotic resistance genes is because it's a type of intestinal organism that can easily contribute significant rise in the emergence of multidrug-resistant (MDR) strains, expanding a global health challenge. Along with other virulence factors, the integron is one of the genetic elements that are not mobile by themselves but are present on plasmids and transposons, making it prone to the dissemination of multidrug resistance in bacteria like *E. coli*. Moreover, these genes are associated with enhanced biofilm formation, promoting bacterial persistence, protection from host defenses, and increased antimicrobial tolerance. It also contributes to extended-spectrum beta-lactamase (ESBLs) transmission of multidrug resistance (MDR) in gram-negative bacteria through integron-like mobile genetic elements.

Objectives: This investigation aimed to evaluate the distribution of integrations associated with *int1* genes in *E. coli* isolates and to relate the possible association among the antibiogram profile and integron genes.

Methodology: 42 clinical isolates of *E. coli* were collected from local clinical pathological settings of Karachi, Pakistan. Identification was done by means of standard conventional methods, using selective and differential media and biochemical tests. DNA was extracted via the boiling method. Molecular screening was evaluated by polymerase chain reaction (PCR) with region-specific primers of the integron-encoded integrase gene *int1*, which are known to act as virulence factors. Antibiotic susceptibility testing (AST) was done using the Kirby-Bauer disk diffusion method with reference to CLSI guidelines. Statistical analysis assessed correlations between integron presence and resistance patterns.

Results: The current investigation showed a high prevalence of drug resistance among study strains of *E. coli*. It was observed that imipenem and piperacillin showed the highest resistance of 51%, meropenem and ciprofloxacin 45%, cefepime 39%, gentamycin 36% and 21% was observed in ceftazidime, gentamycin, and sulfamethoxazole. However, the class 1 integrations *int1* genes were detected in 40% of isolates. The findings revealed a significant association between the dissemination of drug resistance and *int1* genes.

Conclusion: The rising prevalence of integron genes among study strains of *E. coli* underscores their pivotal role in disseminating antibiotic resistance and fostering the threat of developing ESBL strains. Molecular detection of integrations is essential for continuous monitoring and control of resistant bacterial strains. Responsible antibiotic use and regular surveillance are crucial to curb the spread of multidrug-resistant bacteria.

Keywords: Integrations, ESBL, Antibiotic Resistance, PCR, Horizontal Gene Transfer.

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