

Molecular Epidemiology of Antimicrobial Resistance in *Escherichia coli* Isolates from Clinical Specimens

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Citation: Amira Abdulrahman Al-Shammari, Hiba Kareem Al-Musawi, Ahmed Fadhil Al-Khateeb (2025). Molecular Epidemiology of Antimicrobial Resistance in *Escherichia coli* Isolates from Clinical Specimens. *Psychiatry*, 17(10), 51-53. <https://doi.org/10.5281/zenodo.19095316>

ABSTRACT

A total of 49 different clinical samples (urine n=30, stool n=10, and blood n=8) were collected from patient admitted to the Al-Sadder medical City in Al-Najaf Governorate-Iraq. The results demonstrated that 49 specimens (100%) were diagnosed as *E. coli* by cultural, biochemical characteristics and Vitek2[®] system. Polymerase Chain Reaction has been used to detect of some genes which coding antimicrobial resistance in *E. coli* isolates. Regarding genes that responsible for ESBL enzymes (*bla_{CTX-M}*, *bla_{OXA}* and *bla_{TEM}*), the current results proved that *bla_{TEM}* genes have highest rate (97.95%) followed by *bla_{TEM}* and *bla_{OXA}* (93.75%) for each.

Keywords: *Escherichia coli*, *bla_{CTX-M}*, *bla_{OXA}*, *bla_{TEM}*, by product, Iraq.

INTRODUCTION

Antimicrobial resistance (AMR) is when a microbe *Extended spectrum beta lactamases Primers* evolves to become more or fully resistant to antimicrobials Primers used were supplied from Bioneer and were listed which previously could treat it¹. When a bacterial strain in Table (1).

resistant to three or more different antimicrobial classes defined as MDR bacteria².

Since meat and its byproducts are important sources of human deals, it should be free of contamination and hazard³. Thus *E. coli* and the other member of *Enterobacteriaceae* are important reservoirs of transferable antibiotic resistance⁴. *E. coli* may use various biochemical pathways to escape the lethal action of drugs: (i) decreased intracellular accumulation of the antibiotic by an alteration of outer membrane permeability, diminished transport across the inner membrane, or active efflux; (ii) alteration of the target by mutation or enzymatic modification; (iii) enzymatic detoxification of the drug; and (iv) by passing of the drug target. The coexistence of several of these mechanisms in the same host can lead to multidrug resistance (MDR)⁵.

Antibiotic resistance in MRSA is determined by the *mecA* gene, which encodes an altered penicillin binding protein (PBP-2a), that reduces the binding affinity for methicillin and other β -lactam antibiotics⁶.

MATERIALS AND METHODS

DNA extraction

Three to five pure and fresh colonies of *E. coli* were inoculated from MacConkey agar plate into 300 μ l of distilled water. Then cells were lysed by heating at 100 °C for 20 minutes (in water bath), and then immediately the cells were placed in ice for 30 minutes, and the other cellular components were removed by centrifugation at 8500 rpm for 10 min. Finally the supernatant was used as the DNA template⁷.

PCR amplification

The reaction mixture contains Go Taq[®] Green Master Mix, X2 which is premixed ready-to-use solution containing bacteriology derived TaqDNA polymerase dNTP, MgCl₂, and reaction buffers at optimal concentrations and its recommended for any amplification reaction that to be visualized by agarose gel electrophoresis and ethidium bromide staining.

Agarose gel electrophoresis

Agarose gel was prepared by dissolving 1.5 gm of agarose powder in 100 ml of TBE buffer (pH 8) in boiling water bath, allowed to cool to 50°C, then ethidium bromide (at concentration of 0.5 mg/ml) was added. A tape was placed across the end of the gel tray; the comb was fixed at one end of the tray for making wells used for loading DNA samples⁸.

RESULTS AND DISCUSSION

CTX-M-type enzymes were the most common type of ESBL in *E. coli* isolates compared with SHV and TEM enzymes¹². Since then, an increase in the CTX-M β lactamases has been seen in many countries in Europe and Asia¹³. The *bla_{CTX-M}* was reported the most prevalent *blagene* in Korea¹⁴.

Results showed that *ermC* was detected in 6 (50%), another high detection show moderate prevalence 35.9%¹⁵, while another study found that 3.9% of staphylococci isolates carried *ermC*¹⁶.

Table 1: Target genes, amplification sizes and cycling conditions.

Gene name	Initial denaturation	Cycles	Denaturation	Primer annealing	Elongation	Final elongation	References
<i>bla</i> _{TEM}	94°C / 30 sec	35	94°C / 30 sec	45°C / 1 min	72°C / 1 min	72°C / 10 min (then 4°C → ∞	9
<i>bla</i> _{CTX-M}	94°C / 30 sec	35	94°C / 30 sec	60°C / 1 min	72°C / 1 min	72°C / 10 min (then 4°C → ∞	10
<i>bla</i> _{OXA}	94°C / 5 min	30	94°C / 50 sec	55°C / 50 sec	72°C / 1min	72°C / 10 min (then 4°C → ∞	11

Table 2: Prevalence of extended spectrum beta lactamases genes of *E. coli* according to infections site (n=48).

Genes	Urine Total Isolates (n=30)	Stool Total Isolates (n=10)	Blood Total Isolates (n=8)	Total (48)
<i>bla</i> _{CTX-M}	29 (96.66%)	9 (90%)	7 (87.5%)	45 (93.75%)
<i>bla</i> _{OXA}	29 (96.66%)	9 (90%)	7 (87.5%)	45 (93.75%)
<i>bla</i> _{TEM}	30 (61.22%)	10 (20.40%)	8 (16.32%)	48 (97.95%)

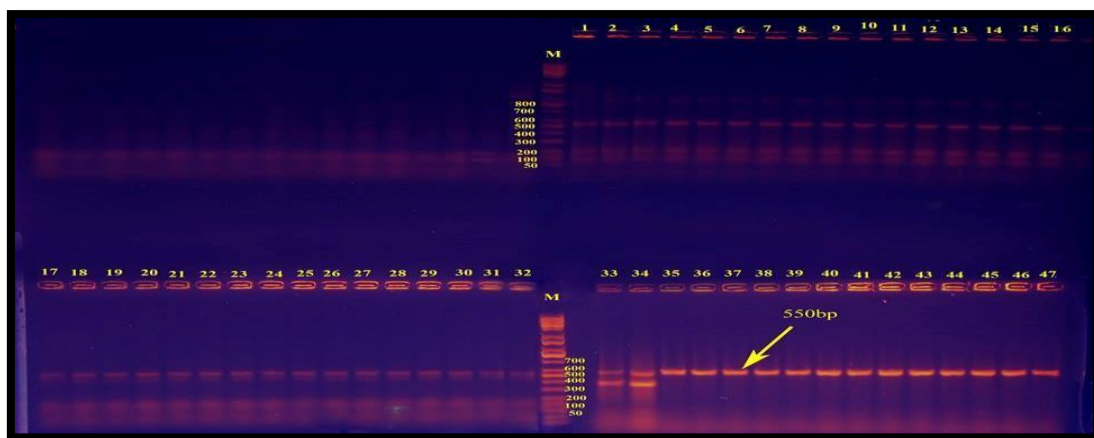


Photo 1: Ethidium bromide-stained agarose gel electrophoresis of monoplex PCR amplified products from extracted total DNA of 49 *E. coli* isolates isolated from different clinical specimens. Lane: (1 to 47 isolates) amplified with diagnostic *bla*_{CTX-M} gene, show positive results at 550 bp . The electrophoresis was performed at 80 volt for 95 minutes. (L): DNA molecular size marker (50 bp ladder).

On the other hand, TEM-1, which is responsible for most of the ampicillin resistance in; 94% of *E. coli* strains isolated in Spain, 89% of *E. coli* strains isolated in Hong Kong, and in 78% of *E. coli* strains isolated in London¹⁷. The OXA enzymes are regarded as OXA-type ESBLs and have been discovered mainly in *P. aeruginosa* in specimens from Turkey and France¹⁸.

Pyridoxine (V B6) significantly increased growth of *Cymbopogon citrates* L. plants, especially in plants treated with 200 mg/l¹⁹. Similar results were recorded by²⁰ on *Antirrhinum majus* plant, and on corn plant^{21,22}.
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CONCLUSION

Our findings showed that there was relationship between phenotypic and genotypic detection of antimicrobial resistance in *E. coli*.

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