

## Molecular mechanism of antibiotic resistance in multi drug resistance *E.coli* isolated from diabetes mellitus patients in Northern Sudan

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### Abstract

*Escherichia coli* poses a (MDR) resistance the emergence of multi drug patient (DM) among diabetes mellitus especially significant threat to public health who are highly susceptible to bacterial infections, this study investigate the molecular mechanism under lying anti biotic resistance in MDR *E.coli* isolate from diabetes mellitus patient in Northern Sudan .Resistance genes include ,*bla TEM*, *blaCTX-M*, *tetA*, and *aadA* were detecting using (PCR) and sequencing .the study highlights the role of plasmid –mediated resistance and provides insights in to the genetic basis of antibiotic resistance in clinical settings. These findings underscore the need for stringent infection control measures and targeted antibiotic stewardship programs.

**Keywords:** *E.coli*, (MDR)Multidrug Resistance , diabetes, Northern Sudan.

### INTRODUCTION

Antibiotic resistance is global health concern, with *Escherichia coli* being one of the most common pathogens responsible of multidrug resistance (MDR). Diabetes mellitus (DM) patients are particularly vulnerable to infections due to immune dysfunction, making them a key population for studying MDR *E.coli* (Livermore ,D.M .2003)

This study aim to elucidate the molecular mechanism of resistance in MDR *E.coli* isolates focusing on the detection of gene resistance and plasmid –mediated mechanisms understanding these mechanisms is critical for developing effective treatment strategies and controlling the spread of resistance.

### METHODS

#### Study design and samples collections

Across sectional study was conducted in Dongola Northern Sudan from January to June 2024. A total of 150 urine and wound samples were collected from diabetic patients attending primary health care facilitates.

Standard microbiology techniques were used to isolate *E.coli*, Antibiotic susceptibility was assessed using disc diffusion methods as per CLSI guidelines, minimum inhibitory concentration (MICs) were determined for cephalosporins,

aminoglycosides ,fluoroquinolones,and tetracyclines using broth micro dilution. MDR was defined as resistance to three or more antibiotic classes.

### **Molecular detection of resistance genes**

DNA extraction was performed using commercial bacteria DNA kit, polymerase chain reaction (PCR) was conducted to detect the presence of Beta –lactamase genes :bla TEM,blaCTX-M, and blaSHV. Aminoglycoside resistance genes .aadA and aphA. Tetracycline resistance genes tetA and tetB.Efflux pump genes acrAB and tolC. Sequencing of amplified products was carried out to confirm gene identities.

### **Plasmid analysis**

Plasmid DNA was extracted using alkaline lysis method and conjugations experiments performed were to assess plasmid transferability.

## **RESULTS**

Out of 150 isolates 68(45.3%) were identified as MDR. high resistance rate were observed for ampicillin (87.2%) ceftriaxone and tetracycline (76.5%,62.3%) while lower resistance rates were noted for imipenem (5.9%) .

### **Detection of resistance genes**

Beta –lactamase: the bla TEM gene was present in 56(82.4%)MDR isolates followed by ,blaCTX-M, in 48(70.6%) isolates tetracycline : the tetA gene was detected in 34(50.0%)isolates while tetB was found in 18 (26.5%). Aminoglycosides the aadA gene was identified in 42(61.8%) isolates.

Plasmid – mediated resistance was confirmed in 60% of MDR isolates with conjugation experiments indicating successful transfer of resistance genes in 35% of cases.

### **Phylogenetic groups**

Most of MDR isolates belong to phylogenetic group B2(40%) and D (30%) which are associated with high virulence and resistance traits.

## **DISCUSSIONS**

This study highlights the prevalence of key resistance genes such as blaCTX-M and tetA in MDR E.coli isolates from diabetic patients .The frequency of plasmid-mediated resistance underscores the role of horizontal gene transfer in the dissemination of resistance .The finding align with global reports on the predominance of bla CTX-M in clinical isolates and the rising prevalence of amonoglycoside resistance gene (**Poirel, L, et al 2007., Jacoby, G,A 2009, Magiorakos, A,P., etal 2012**)

Association of MDR E.coli with phylogenetic group B2 and D suggest a dual threat of resistance and virulence complicating treatment outcomes for diabetic patients (**Clermont, O ., et al 2000**) . Theses results call for improved infection control policies ,regular surveillance of resistance patterns ,and judicious use of antibiotics.

## CONCLUSION

MDR Ecoli isolates from diabetic patients in Northern Sudan exhibit a high prevalence of resistance genes primary bla TEM,blaCTX-M, and .aadA .The role of plasmid-mediated resistance in gene transfer necessitates stricter antimicrobial stewardship .Future research should focus on developing therapeutic approaches to compact MDR infections in vulnerable populations.

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