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Phylogenetic Analysis and Virulence Genes in Multidrug-Resistant Escherichia coliIsolated from Diabetes Mellitus Patients in Northern Sudan

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Abstract

Multidrug-resistant (MDR) Escherichia coli is a significant concern, particularly in diabetes mellitus (DM) patients who are predisposed to infections. This study investigates the phylogenetic diversity and prevalence of virulence genes in MDR E.coli isolates from diabetic patients in Northern Sudan. Phylogenetic groupingrevealed a predominance of groups B2 (42%) and D (30%), known for high virulence potential. Virulence genes fim H, papC, and stx2 were frequently detected,highlighting the clinical threat posed by these strains. These findings provide insights into the pathogenicity and genetic makeup of MDR E. coli, emphasizing the need for.enhanced surveillance and targeted therapeutic approaches

Keywords: MDR;Multidrug-resistant DM diabetes mellitus

INTRODUCTION

Escherichia coli is a versatile pathogen responsible for a range of infections, from urinary tract infections (UTIs) to sepsis. The emergence of multidrug-resistant (MDR) strains, coupled with their ability to acquire virulence factors, poses a dual threat to vulnerable populations, particularly diabetes mellitus (DM) patients **(Clermont, *et al.* 2000).** Phylogenetic analysis is a valuable tool for classifying E. coli strains into groups (A, B1, B2, D, E, .F) associated with varying levels of virulence This study aims to characterize the phylogenetic distribution of MDR E. coli isolates and determine the prevalence of key virulence genes (fimH, papC, stx1, stx2, hlyA, iutA) to better understand the pathogenic potential of these strains in diabetic patients (**Johnson, J. R., *et al.* (2003**).

METHODS

This A cross-sectional study was conducted in Dongola, Northern Sudan, between January and June 2024. A total of 150 E. coli isolates were obtained from urine and wound swab samples of diabetic patients attending to local healthcare facilities

Antibiotic Susceptibility Testing (AST);The antibiotic resistance profiles of all isolates were determined using the disk diffusion method according to CLSI guidelines. MDR was defined as resistance to three or more antibiotic classes.

Phylogenetic Grouping Phylogenetic classification of E. coli isolates was performed using multiplex PCR targeting the genes chuA, yjaA, and the DNA fragment TspE4.C2. Based on the.results, isolates were assigned to phylogenetic groups A, B1, B2, or D.

Detection of Virulence Genes Virulence-associated genes were detected using polymerase chain reaction (PCR).
The genes analyzed included
fimH (type 1 fimbriae)
papC (P fimbriae)
stx1 and stx2 (Shiga toxins)
hlyA (hemolysin)
iutA (aerobactin receptor)
Amplicons were confirmed through agarose gel electrophoresis and sequenced to .verify gene identities

Data Analysis Descriptive and inferential statistical analyses were conducted using SPSS version.
The results were expressed as percentages, and associations between phylogenetic .26.groups and virulence genes were analyzed using chi-square tests

RESULTS

Phylogenetic Distribution:out of 150 MDR E. coli isolates
.Group B2: 42% (63 isolates)
.Group D: 30% (45 isolates)
.Group A: 18% (27 isolates)
Group B1: 10% (15 isolates)

Prevalence of Virulence Genes
.fimH: 70% (105 isolates)
.papC: 48% (72 isolates)
.stx1: 15% (23 isolates)
.stx2: 25% (38 isolates)
.hlyA: 22% (33 isolates)
.iutA: 50% (75 isolates)

Association between Phylogenetic Groups and Virulence Genes
Virulence genes were more frequently detected in phylogenetic groups B2 and D. For example, 85% of group B2 isolates carried fimH, and 65% carried papC. In contrast, group A and B1 isolates showed significantly lower frequencies of these genes.

Coexistence of Virulence and Resistance
Approximately 40% of isolates in group B2 exhibited both MDR and multiple virulence factors, emphasizing their high pathogenic potential.

DISCUSSION

The predominance of phylogenetic groups B2 and D among MDR E. coli isolates aligns with their known association with increased virulence and pathogenicity. The high prevalence of virulence genes, particularly fimH and papC, further supports the clinical significance of these isolates**(Kaper, J. B., *et al.* (2004)**.

Shiga toxin genes (stx1 and stx2) were detected in 40% of isolates, raising concerns about the potential for severe systemic infections. The co-occurrence of MDR andvirulence genes in isolates from diabetic patients underscores the challenges of managing such infections in a vulnerable population Compared to similar studies globally,**Poirel, L., *et al.* (2011).** our findings reveal comparable rates of MDR and virulence factors, suggesting that these strains may share common genetic lineages. The role of horizontal gene transfer in spreading resistance and virulence traits cannot be overlooked, emphasizing the need for enhanced infection control and antibiotic stewardship programs**. (Livermore, D. M. (2003).**

CONCLUSION

MDR E. coli isolates from diabetic patients in Northern Sudan predominantly belong to phylogenetic groups B2 and D, which are associated with high virulence. The prevalence of virulence genes, particularly fimH and papC, highlights the pathogenic potential of these strains. These findings call for urgent measures to monitor, control,.and treat MDR E. coli infections in high-risk populations.

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