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DETECTION OF ESBL GENES IN UROPATHOGENS ISOLATED FROM PREGNANT WOMEN IN LAGOS UNIVERSITY TEACHING HOSPITAL

Obi Ifeoma Angela[1], Ezeamaramu Faustina Uloma[1*], Afeez Olabisi Yusuf[2], Oladetuyi Adedayo Peter[3], Oghale Ijeoma Godspower[4], Olojede Damilare Stephen[3].

[1]Department of Medical Microbiology & Parasitology, College of Medicine, University of Lagos, PMB. 12003, Idiaraba, Lagos.

[2]Department of Microbiology, Lagos State University, Ojo, Lagos State, Nigeria

[3]Department of Science laboratory Technology, Eko City Polytechnic.

[4]Department of Microbiology, University of Lagos, Akoka, Lagos State, Nigeria

***Corresponding Author:** Afeez Olabisi Yusuf E mail: yusufolabisi2020@gmail.com

ABSTRACT

Aim: This study characterizes the species distribution, antibiotic resistance patterns, ESBL gene prevalence, and plasmid carriage of uropathogens isolated from pregnant women in Lagos, Nigeria. .

Methods: Using standard procedures, Midstream urine samples were collected from 145 pregnant women attending antenatal clinics. Significant bacteriuria (≥10^5 CFU/mL) yielded 65 isolates, which were identified, Antimicrobial susceptibility was determined, and ESBL production was screened phenotypically and confirmed by PCR targeting bla_CTX-M, bla_TEM, and bla_SHV.

Results: Significant bacteriuria (≥10^5 CFU/mL) yielded 65 isolates, which were identified by standard biochemical tests. Antimicrobial susceptibility to four β-lactamse, ESBL production was screened phenotypically and confirmed by PCR targeting bla_CTX-M, bla_TEM, and bla_SHV. Plasmid profiles were obtained via alkaline lysis and agarose gel electrophoresis. Associations between plasmid burden, MDR phenotype, and ESBL gene count were assessed by Spearman's correlation. *Escherichia coli* predominated (41.5%), followed by coagulase-negative *Staphylococcus* spp. (26.2%), *Enterobacter* spp. (18.5%), and *Staphylococcus aureus* (10.8%). Resistance rates to amoxicillin, ceftazidime, ampicillin, and cloxacillin were 100%, 95.8%, 90.2%, and 83.3%, respectively. MDR was observed in 85.2% of *E. coli*, 75.0% of *Enterobacter*, 88.2% of coagulase-negative staphylococci, and 71.4% of *S. aureus*. ESBL genes were detected in 69.2% of isolates, with bla_CTX-M most prevalent (66.2%), followed by bla_TEM (18.5%) and bla_SHV (3.1%). Plasmids were present in 73.8% of isolates, and Spearman's correlation demonstrated significant associations between plasmid band number and MDR ($\rho = 0.63$, $p < 0.001$) and ESBL gene count ($\rho = 0.58$, $p = 0.001$)

Conclusion: High rates of MDR and plasmid-mediated ESBL genes among uropathogens from pregnant women underscore an urgent need for enhanced antimicrobial stewardship, routine ESBL screening in antenatal care, and molecular surveillance to inform empiric therapy and curb resistance spread.

INTRODUCTION

Urinary tract infections (UTIs) during pregnancy represent a significant public health concern, particularly in low- and middle-income countries where access to laboratory diagnostics and effective antimicrobial therapy may be limited. Asymptomatic bacteriuria occurs in up to 17% of pregnant women in some African settings (Adugna Adane *et al*., 2021; Donkor *et al*., 2022), and when untreated, increases the risk of pyelonephritis, preterm labor, low birth weight, and perinatal mortality (Smaill & Vazquez, 2019).

Over the past decade, the rising prevalence of extended-spectrum beta-lactamase (ESBL)-producing uropathogens has severely limited empiric antibiotic choices in pregnancy. Plasmids facilitate the horizontal transmission of resistance genes; studies have consistently linked plasmid carriage with multidrug resistance (MDR) and ESBL positivity. Given pregnancy's unique physiological state particularly urinary stasis and immunological shifts, it is imperative to monitor antimicrobial resistance patterns and genetic drivers in pregnant women. MDR uropathogens reduce empiric antibiotic effectiveness and may necessitate use of restricted drugs like carbapenems, which are often costly and poorly available in many African healthcare settings.

This study systematically examines the prevalence, antimicrobial susceptibility, ESBL gene composition, and plasmid dynamics of uropathogens isolated from pregnant women in Lagos. The findings aim to inform clinical practice, guide antibiotic stewardship policies, and contribute to molecular resistance monitoring in the maternal health context.

MATERIALS AND METHODS

A cross-sectional study was conducted among **145 pregnant women** attending antenatal clinics in Lagos State, Nigeria. Midstream clean-catch urine samples were collected aseptically, transported on ice, and processed within **2 h**. Samples were cultured on **CLED agar** at **37 °C (24–48 h)**; significant bacteriuria was defined as **≥10^5 CFU/mL**. Isolates were identified using standard biochemical tests. Antibiotic susceptibility was determined by **Kirby–Bauer disk diffusion** following **CLSI (2023)** guidelines, and MDR was defined as resistance to ≥3 antibiotic classes. ESBL production was detected phenotypically by the **combined disc method** and genotypically by **PCR** targeting **blaCTX-M, blaTEM, and blaSHV** genes. Plasmid profiling and curing were performed to assess plasmid-mediated resistance. Data were analyzed using **SPSS v26** ($p < 0.05$).

RESULTS

Table 1. Distribution of Uropathogen Isolates from Pregnant Women (n = 145)

Organism	No. of Isolates	% of Total Isolates
Escherichia coli	27	41.5%
Enterobacter spp.	12	18.5%
Coagulase-negative Staphylococcus	17	26.2%
Staphylococcus aureus	7	10.8%
Total	65	100.0%

Table 2. Resistance Rates (%) of Uropathogens to Selected β-Lactam Antibiotics

Antibiotic	Resistant Isolates (n)	Resistance Rate (%)
Amoxicillin	65	100.0%
Ceftazidime	62	95.8%
Ampicillin	59	90.2%
Cloxacillin	54	83.3%

TABLE 3. ANTIBIOTIC RESISTANCE PROFILES BY SPECIES

Species	MDR (%)*	ESBL Positive (%)
E. coli (n = 27)	85.2%	74.1%
Enterobacter spp. (n = 12)	75.0%	66.7%
Coagulase-negative Staph.	88.2%	64.7%
S. aureus (n = 7)	71.4%	85.7%

*Multidrug-resistant (resistant to ≥ 3 classes of antibiotics)

Table 4. Prevalence of ESBL Genes among Uropathogens

ESBL Gene	Positive Isolates (n = 65)	Prevalence (%)
blaCTX-M	43	66.2%
blaTEM	12	18.5%
blaSHV	2	3.1%
Any ESBL gene	45	69.2%

Table 5. Co-Occurrence of ESBL Genes

Gene Combination	No. of Isolates	% of ESBL-Positive
CTX-M only	28	62.2%
TEM only	7	15.6%
SHV only	1	2.2%
CTX-M + TEM	8	17.8%
CTX-M + SHV	1	2.2%
TEM + SHV	0	0.0%
CTX-M + TEM + SHV	0	0.0%

Table 6. Summary of PCR and Plasmid Findings by Species

Species	ESBL Positivity*	Plasmid Positivity†
E. coli (n = 27)	20 (74%)	22 (81%)
Enterobacter spp. (n = 12)	8 (67%)	9 (75%)
Coagulase-negative Staph. (n = 17)	11 (65%)	13 (76%)
Staph. aureus (n = 7)	6 (86%)	4 (57%)

*** At least one of blaCTX-M, blaTEM, or blaSHV detected**
† ≥ 1 plasmid band seen on agarose gel

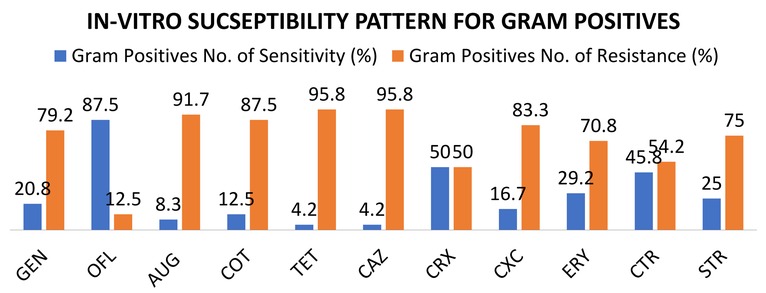

Fig. 1: In-vitro antibiotic susceptibility spectrum of Gram positives pathogens

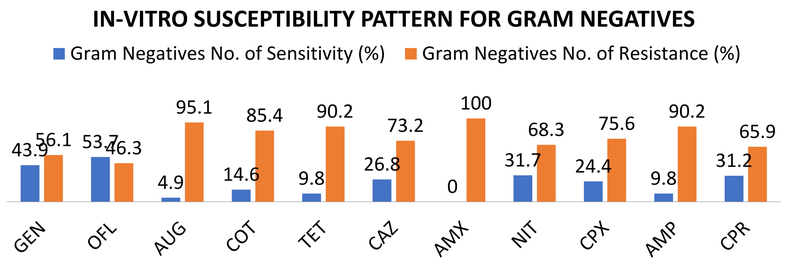

Fig. 2: In-vitro antibiotic susceptibility spectrum of Gram negative pathogens

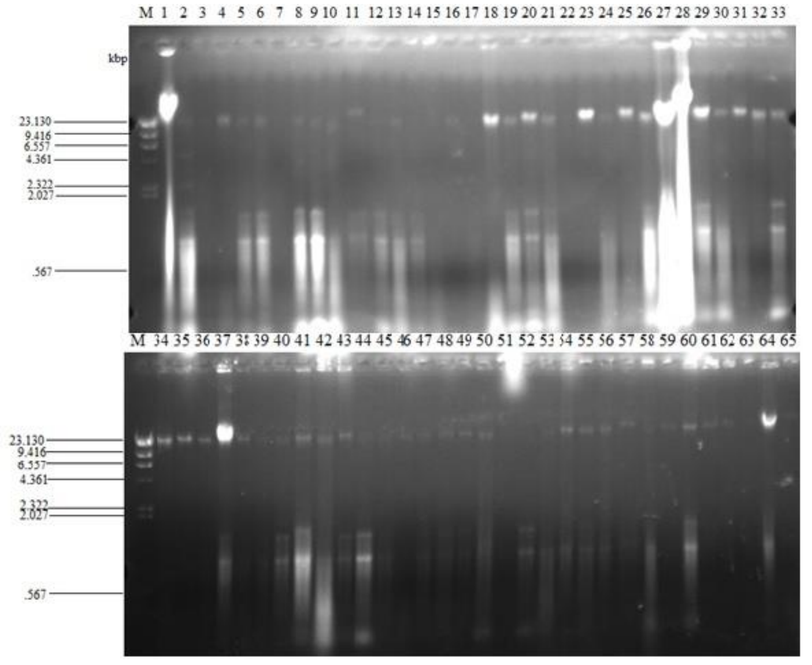

Fig. 3: Agarose electrophoresis showing plasmid profile of the uropathogens Marker (Hind III digest)

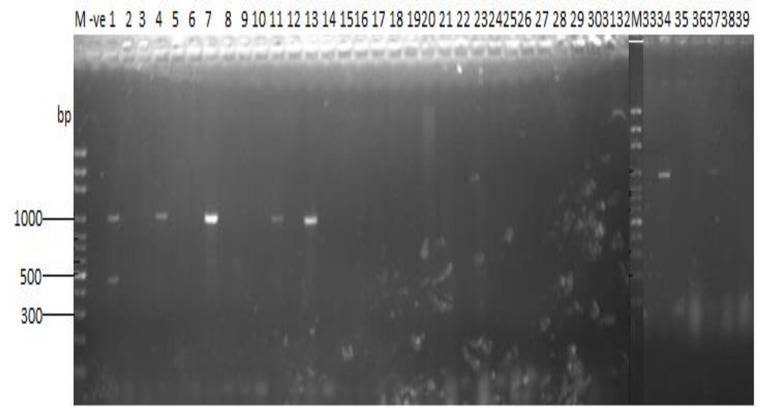

Fig. 4: Amplification of blaTEM. 100bp DNA ladder. Lane 1-12 (Enterobacter spp), Lane 13-39 (Escherichia coli)

DISCUSSION

Escherichia coli was the predominant uropathogen isolated from pregnant women, consistent with reports across Nigeria and sub-Saharan Africa. Resistance to commonly used β-lactam antibiotics was extremely high, rendering first-line therapies largely ineffective. A high prevalence of multidrug resistance and ESBL production was observed, with **blaCTX-M** as the dominant resistance gene. Plasmid carriage was widespread and showed a strong association with both MDR phenotypes and ESBL gene burden, highlighting plasmids as key drivers of resistance dissemination. These findings indicate limited treatment options for urinary tract infections in pregnancy and underscore the need for routine antimicrobial susceptibility testing, molecular surveillance, and strengthened antimicrobial stewardship to reduce the spread of plasmid-mediated resistance.

CONCLUSION

This study reveals a high burden of plasmid-mediated ESBL-producing, multidrug-resistant uropathogens among pregnant women, highlighting the urgent need for routine resistance surveillance and improved antimicrobial stewardship.

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