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Comparative Antibiotic Resistance Profiles and Molecular Characterization of Uropathogens in Cancer and Non-Cancer Patients with Urinary Tract Infections Attending National Hospital Abuja, Nigeria

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ABSTRACT
Cancer patients are generally known to be vulnerable to infections, among which is urinary tract infection (UTI), mostly found in urinary related cancers. This study aimed at comparing bacterial profiles, antibiotic resistance patterns, and molecular characteristics of uropathogens isolated from cancer and non-cancer patients attending the National Hospital Abuja. A total of 200 urine samples were collected for this study, 100 samples each from cancer and noncancer patients. Culture, Gram staining, biochemical assays, and MALDI-TOF method were used in identifing the bacteria isolates. Kirby-Bauer disk diffusion method was used for the antimicrobial susceptibility testing. While, PCR was used to detect the blaCTX-M, sul1, and tetA resistance genes. A phylogenetic tree was generated from sequenced genes. Out of the 200 samples investigated in this study, 55 (27.5%) yielded bacterial growth. *Pseudomonas aeruginosa* (25%) and *Klebsiella pneumoniae* (19%) were the most isolated in cancer-positive patients, while *Escherichia coli* (30%) and *Proteus mirabilis* (18%) were the most prevalent isolates in cancer-negative patients. Isolates from cancer-positive patients showed high resistance rates for Amoxicillin (90%) and Nitrofurantoin (65%). PCR analysis revealed the presence of blaCTX-M in 40% of isolates, sul1 in 35%, and tetA in 30%. Gel electrophoresis showed sharp DNA bands at 550 bp (blaCTX-M), 432 bp (sul1), and 210 bp (tetA). Phylogenetic analysis showed the dominace of local *Pseudomonas aeruginosa* and *Klebsiella pneumoniae* isolates with globally known multidrug-resistant strains. High levels of multidrug resistance were observed among bacteria isolated from cancer patients, which has also showed high prevelence of resistant genes.

Keywords:
Cancer Patients,
Urinary Tract Infection,
Antibiotic Resistance,
Molecular diagnostics.

INTRODUCTION

Cancer patients are prone to infections and have been a global public health challenge due to their compromised immune systems and some of their treatments and invasive procedures. The risk of urinary tract infections (UTIs), especially among urinary tract-related cancers such as cervical cancer and bladder cancer, is exacerbated because of frequent hospital visits, catheter use, and prolonged antibiotic exposure (Garcia-Clemente *et al*., 2021).The molecular profiling of UTIs in cancer positive patients is not largely explored, therefore the burden of UTIs, among cancer patients, is of high concern in Nigeria and other sub-Saharan countries.

Even though, studies indicate that non-traditional pathogens such as *Pseudomonas aeruginosa* and *Klebsiella pneumoniae* predominate in cancer patients as a result of frequent hospitalizations, invasive procedures, and antibiotic exposure (Flores-Mireles et al., 2019), yet *Escherichia coli* is still the most common uropathogen in the general cases of UTIs (Hooton *et al*., 2019; Johnson *et al*., 2020).

This study aimed at investigating the profile, prevalence, antibiotic resistance patterns, and molecular profile of bacteria that cause UTIs in individuals with and without cancer.

This will reveal vital information about the distribution of resistance genes and the phylogenetic links of isolates using molecular methods like PCR and MALDI-TOF. The result from this study will improve antibiotic stewardship in clinical practice and increase focus on infection control measures by comparing these profiles across cancer-positive and cancer-negative patients attending National Hospital Abuja, Nigeria. This result will indicate the important of molecular diagnostics and precision antimicrobial therapy particularly in oncology care (Rolston, 2021).

MATERIALS AND METHODS

Study Design and Ethical Approval

A cross-sectional comparative study was conducted between August 2024 and March 2025 at National Hospital Abuja, Nigeria. Ethical approval was obtained from the Health Research Ethics Committee of National Hospital Abuja (Ref: NHREC/NHA/2024/034). Patients consent was also gotten in written before samples were collected from participants.

Study Population and Sample Size

The sample size for this study was determined using the formula below.

$n = Z^2 P (1 – P) / d^2$ (Daniel, 1999; Naing *et al*., 2016)

Where: Z = 1.96 (95% confidence level), P = 0.1 (10.2% prevalence from a similar study by Zayyan *et al*., 2017), d = 0.05 (precision).

Substituting these values into the above formula the sample size (n) is taken to be 187 numbers of samples which was approximated to 200 samples for this study. This included 100 samples each from cancer-positive (prostate, cervical, or bladder cancer) and cancer-negative UTI patients respectively.

Sample Collection and Processing

Using sterile universal containers, midstream urine samples (10–20 mL) were collected from both categories of patients, after which they were taken to the microbiology laboratory within 45 minutes of collection. The samples were then inoculated on Brilliance UTI clarity agar and incubated at 37°C for 24 hours. Colony counts ≥10 CFU/mL were considered significant bacteriuria (Hooton *et al*., 2019).

Bacterial Identification

Colonies with distinct morphology were sub cultured and identified based on; Gram staining, Biochemical tests (catalase, oxidase, citrate, urease, TSI, indole) and Matrix-Assisted Laser Desorption Ionization-Time of Flight (MALDI-TOF) Mass Spectrometry.

Antimicrobial Susceptibility Testing (AST)

The AST was performed using the Kirby-Bauer disk diffusion method in accordance with CLSI (2023) guidelines. The antibiotics used were Amoxicillin (10 µg), Trimethoprim (5 µg), Nitrofurantoin (300 µg) and Imipenem (10 µg) (which are the common antibiotics used for the treatment of UTIs in the Hospital). Zones of inhibition were interpreted and categorized as Susceptible, Intermediate, or Resistant.

Molecular Detection of Resistance Genes

Genomic DNA was extracted using a commercial spin column kit (Zymo Research, USA). BlaCTX-M (550 bp), Sul1 (432 bp) and TetA (210 bp) were detected and amplified using PCR. Agarose gel (1.5%) electrophoresis stained with ethidium bromide used to visualize the PCR products which was then compared against a 100 bp DNA ladder (Li *et al.*, 2022).

Gene Sequencing and Phylogenetic Analysis

Representative PCR amplicons were purified and sequenced using Sanger sequencing. Sequence alignment and similarity searches were conducted using NCBI BLAST. Phylogenetic trees were constructed using MEGA 11 software with the Neighbor-Joining method and 1,000 bootstrap replicates (Davin-Regli & Pagès, 2015; Tamura et al., 2021).

Data Analysis

Data were analyzed using SPSS v25. Categorical variables were compared using Chi-square tests. Logistic regression was used to assess predictors of UTI. Significance was set at $p < 0.05$.

RESULTS AND DISCUSSION

Bacterial Growth and Distribution

Out of the 200 samples that were collected for this study only fifty-five (55) (27.5%) yielded significant bacterial growth. The most frequent isolates among cancer-positive patients were *Pseudomonas aeruginosa* (25%), *Klebsiella pneumoniae* (19%), and *Acinetobacter baumannii* (11%). On the other hand, *Escherichia coli* (30%) and *Proteus mirabilis* (18%) were the most dominant bacteria isolated from cancer-negative patients (Foxman, 2024).

Table 1: Bacterial Isolates in Cancer-Positive and Cancer-Negative Patients

Bacteria	Cancer-Positive (%)	Cancer-Negative (%)
Pseudomonas aeruginosa	25	7
Klebsiella pneumoniae	19	5
Escherichia coli	11	30
*Proteus mirabili*s	8	18
Others (eg Acinebacter)	12	5

Antimicrobial Susceptibility Profiles

The AST result revealed that isolates from cancer-positive patients showed higher resistance to Amoxicillin (90%) and Nitrofurantoin (65%) compare with those of the cancer-negative patients. Meanwhile, isolates from both cancer positive and cancer negative presented low resistance to Imipenem (<10%).

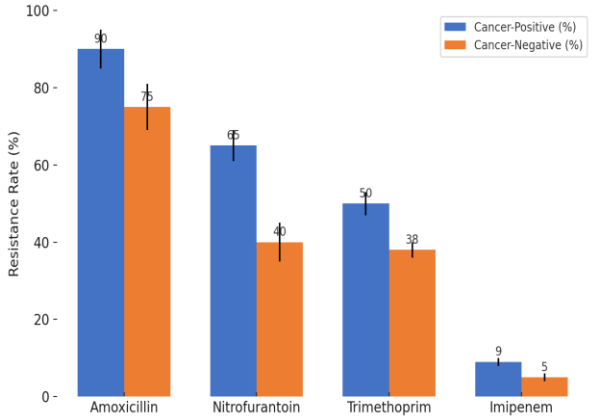

Fig. 1. Resistance rates of Isolates from Cancer and Non-cancer Patients

Molecular Characterization

The presence of BlaCTX-M, Sul1, TetA were revealed in 40%, 35% and 30% respectively in of isolates. The sharp bands were shown in Gel electrophoresis at the expected base pair positions.

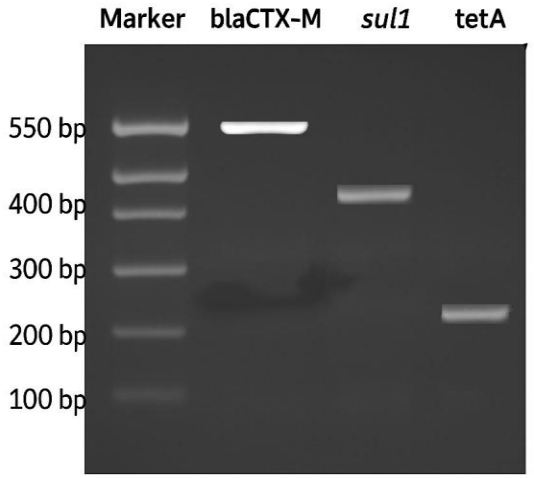

Fig. 2. Agarose Gel Showing Bands for blaCTX-M (550 bp), sul1 (432 bp), tetA (210 bp)

Phylogenetic Analysis

Sequencing and tree construction showed that the *Pseudomonas aeruginosa* and *K. pneumoniae* strains clustered with multidrug-resistant global reference strains, suggesting potential nosocomial or community-acquired transmission (Bray *et al*., 2018).

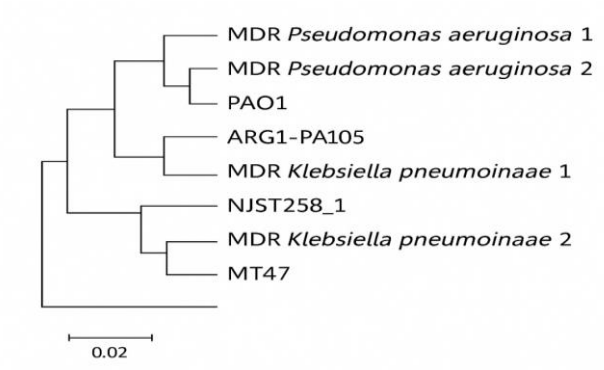

Fig.3. Phytogenetic Tree of MDR isolates, *pseudomonas aeruginosa and Klebsiella pneumonie* clustered with known Global MDR Strains

This study provides a comperative analysis of uropathogens in cancer and non-cancer patients attending National Hospital Abuja. The findings indicate that the overall UTI prevalence among participants was 27.5%. Among cancer-positive patients, Pseudomonas aeruginosa (25%) and Klebsiella pneumoniae (19%) were the most dominant isolates, whereas Escherichia coli (30%) and Proteus mirabilis (18%) were most prevalent

among cancer-negative patients. These results highlight the microbial differences between immunocompromised and immunocompetent patients.

The observed predominance of *P. aeruginosa* and *K. pneumoniae* among cancer-positive patients may be attributed to frequent hospitalizations, prolonged antibiotic usage, and the immunosuppressed state of oncology patients. These organisms are known for their adaptability in nosocomial environments and ability to develop resistance (Flores-Mireles *et al*., 2019; Garcia-Clemente *et al*., 2021). On the contrary, the high frequency of E. coli among cancer-negative patients aligns with global epidemiological data identifying it as the leading cause of community-acquired UTIs (Hooton *et al.*, 2020; Johnson *et al*., 2020, Grace *et al.*, 2025). Grace et al (2025) also reported 29% prevalance from 385 urine sample screened in their study.

Antimicrobial susceptibility testing revealed high resistance rates among isolates from cancer-positive patients, particularly to Amoxicillin (90%) and Nitrofurantoin (65%). This can be explained by repeated empirical treatment, which often leads to selective pressure and the emergence of resistant strains (WHO, 2021). Imipenem maintained low resistance levels (<10%) in both groups, reaffirming its role as a reserve antibiotic, albeit with caution due to the threat of carbapenem resistance (Livermore, 2002).

Molecular analyses detected blaCTX-M, sul1, and tetA genes in 40%, 35%, and 30% of isolates, respectively. These genes are associated with extended-spectrum β-lactamase (ESBL) production and resistance to sulfonamides and tetracyclines. The presence of these genes in a significant proportion of isolates suggests horizontal gene transfer via plasmids, a trend consistent with global surveillance reports (Davin-Regli & Pagès, 2015). Similar findings were reported by Okeke (2022), who identified blaCTX-M genes in multidrug-resistant uropathogens from cancer patients in Nigeria.

Phylogenetic tree analysis further confirmed that local strains of P. aeruginosa and K. pneumoniae are genetically related to globally circulating multidrug-resistant strains. This suggests potential clonal dissemination or shared resistance evolution pathways, reinforcing the need for stringent infection control and molecular surveillance strategies (Tamura *et al.*, 2021; Okeke, 2022).

The findings in this study shows more Gram negative isolate from cancer patients exhibing more resistance to the antibiotic used, which is contrary to the study conducted by Grace *et al.* (2025) which reported a slightly different resistance patterns among Gram-positive isolates in patients with prolonged hospital stays in St. Lukes Hospital Anua, Uyo, Akwa Ibom State. However, this study emphasized the dominance enterobacters especially in immunocompromised populations, validating the report of increased resistance gene prevalence in cancer patients.

In conclusion, the elevated resistance levels, predominance of non-traditional uropathogens, and detection of resistance genes in cancer-positive patients underscore the need for molecular diagnostics in routine clinical practice. These findings reinforce the relevance of tailored antimicrobial therapy and advocate for the revision of treatment protocols, especially in oncology care settings.

CONCLUSION

The findings in this study established that cancer patients in National Hospital Abuja, Nigeria are proportionately affected by multidrug-resistant uropathogens compared to cancer-negative patients. The study also revealed that *P. aeruginosa* and *K. pneumoniae are most* dominance coupled with high resistance to common antibiotics and the presence of resistance genes, hence, calls for urgent revisit of the conventional treatment protocols.

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