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Bacterial Spectrum, Antibacterial Resistance and Microbial Dysbiosis Among Cervical Cancer Patients and Their Associated Risk Factors: A Cross-Sectional Study in the Oncology Clinic, National Hospital, Abuja, Nigeria.

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Research Article

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Bacterial Spectrum, Antibacterial Resistance and Microbial Dysbiosis Among Cervical Cancer Patients and Their Associated Risk Factors: A Cross-Sectional Study in the Oncology Clinic, National Hospital, Abuja, Nigeria.

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ABSTRACT

Background: Cancer is a disease that results from cellular changes caused by the uncontrolled growth and division of cells. Bacterial infections may promote microbial dysbiosis, influence disease progression, prolong hospital stay, and interfere with the effectiveness of cancer therapy. Understanding the prevalence of bacterial infections and their antibiotic resistance patterns is therefore essential for optimizing infection management and improving treatment outcomes in cervical cancer care.

Aim: This study estimated the prevalence of bacterial infections, characterized the bacterial spectrum, and assessed antibiotics resistance patterns among cervical cancer patients attending a tertiary cancer centre in Abuja, Nigeria.

Methods: The cross-sectional study was conducted from January, 2023 to May, 2023. A total of one hundred and six endo-cervical swabs from confirmed cervical cancer patients with suspected infections were collected and screened for bacterial infection, using standard microbiological methods, cultured on Nutrient, agar, MacConkey agar and Chocolate agar media. Morphological characteristics, Gram reaction and biochemical tests were used for identification of isolates. Kirby Bauer antibiotic susceptibility testing was conducted following CLSI 2020 guidelines. Well-constructed questionnaire was used to collect patient's data for statistical analysis used to determine the possible associated risk factors.

Results: Out of 106 cervical cancer patients sampled, 90 (84.9%) had identifiable bacteria growth. A total of seventy-eight bacterial species were identified, and about 43(55.1%) of them were Gram-positive cocci, whereas 35(44.9%) were Gram-negative rods. Approximately 13(16.6%) swabs showed mixed bacterial growth mostly of *Escherichia coli and Staphylococcus aureus*. The most predominant isolate was *S. aureus* (32, 41.0%), followed by *P. aeruginosa* (16, 20.5%), *E. coli* (10, 12.8%), *S. epidermidis* (8, 10.2%), *P. mirabilis* (7, 8.9%) and *B. cereus* (5, 6.4%). Analysis of baseline demographic and clinical factors revealed substantial differences in the various parameters studied such as; age, hygiene practices and location. The age of respondents ranged between 30 - 68 years, with the most frequent participants within the age range of 56-68(74, 69.8%). The most diagnosed cancer stage was stage 3(72.0%). Majority of the participants were rural residents 63(59.4%), with most of them having below tertiary education, 74(69.8%). For occupational status, 63.2% were farmers/traders, 11.3% were house wives and 25.5% were civil servants/professionals. Among the participants 73.6% use contraceptives and 67.9% practice vaginal douching at least twice monthly. Among the array of antibiotics tested, Ciprofloxacin was the most effective against both Gram positive with sensitivity percentage of *S. epidermidis* (83.3 %); *S. aureus* (81%); *E. faecalis* (80%) and Gram-negative organisms *P. aeruginosa* (86.7%); *K. pneumoniae* (78.9%); *E. coli* (60%) while Ceftriaxone had the least activity with resistance percentage of *K. pneumoniae* (78.9%)*; E. coli* (72%)*; P. aeruginosa* (66.7%) Gram-negative isolates and for the Gram-positive isolates *S. epidermidis* (83.3 %); *E. faecalis* (80.0%)*; S. aureus* (71.4%).

Conclusion: Cervical cancer patients exhibited a high prevalence of bacterial infections and a diverse bacterial spectrum, characterized by predominance of opportunistic pathogens and altered commensal representation. Integrating culture-based and molecular approaches provides a more comprehensive understanding of cervical microbial dysbiosis and supports the need for routine microbiological surveillance in cervical cancer care.

Keywords: Cervical cancer, wound pathogens, Gram-positive bacteria, Gram-negative bacteria, Anti-microbial susceptibility, Resistance pattern, associated risk factors

INTRODUCTION

Cervical cancer is a leading cause of morbidity and mortality among women of the reproductive age especially in low resource limited countries like Nigeria. However, widespread screening programs, which play a crucial role in the early detection and treatment of precancerous changes in the cervix, can significantly reduce the incidence of cervical cancer, as cervical cancer remains one of the most preventable forms of cancer due to the availability of vaccines against Human Papillomavirus (HPV) and routine screening through Pap smears (Chen *et al*., 2020). Bacterial infections are a significant concern among cervical cancer patients due to their heightened susceptibility, which results from a combination of cancer-related factors and treatments. The immune system of these patients is often compromised by cancer itself, as well as by treatments such as chemotherapy and radiation.

Chemotherapy-induced neutropenia, for example, reduces the body's ability to fight off bacterial infections (Nerini, 2022). Similarly, radiation therapy, particularly in the pelvic region, can damage the mucosal barriers, making it easier for bacteria to invade and cause infections. Surgical interventions, such as hysterectomy, further increase the risk of infections due to open wounds and potential disruption of the local microbiome (Nerini, 2022). Recently, insights into the co-infection of viruses and bacteria resulting in disease exacerbation are emerging (Griffiths *et al*., 2011; Kaul *et al*., 2020). Earlier studies have also showed that the high prevalence of HPV co-infection with *Chlamydia trachomatis* may be associated with abnormal cervical cytology and an increased risk of cervical intraepithelial neoplasia (Chumduri *et al*., 2013; Chen *et al*., 2020). A recent investigation pointed out that multiple infections potentially contribute to neoplastic progression by elucidating that *C. trachomatis* impedes HPV-induced mechanisms that maintain cellular and genomic integrity in the stem cells. (Koster *et al*., 2022).

Among the common bacterial infections seen in cervical cancer patients are urinary tract infections (UTIs), genital infections, and skin and soft tissue infections. Pelvic radiation and the use of urinary catheters can predispose patients to UTIs, while chemotherapy-induced immunosuppression increases vulnerability to infections like *Staphylococcus aureus* and *Escherichia coli*, which can complicate the healing of surgical sites or affect the vaginal flora (Tsang 2024). Skin and soft tissue infections are also more frequent due to neutropenia and other treatment-related immunosuppressive effects. Additionally, patients with cervical cancer are at risk of pneumonia and respiratory infections, particularly those who are undergoing systemic treatments that weaken the immune system (Jou, 2023).

Several factors contribute to the increased risk of bacterial infections in cervical cancer patients, aside from immunosuppression, which is directly related to cancer treatment, the breakdown of mucosal barriers from surgery or radiation therapy creates opportunities for bacterial pathogens to enter. The use of invasive medical devices, such as catheters or surgical drains, also raises the risk of infection. Comorbid conditions, such as diabetes, and poor nutritional status, which are common in cancer patients, further compromise immune defenses. Moreover, frequent hospitalizations expose these patients to hospital-acquired infections, including antibiotic-resistant bacteria (Karanwal *et al.,* 2013; Delgado and Kumar, 2021).

Prevention and management of bacterial infections in cervical cancer patients require a multifaceted approach. Prophylactic antibiotics may be recommended during or after surgery, radiation, or chemotherapy to minimize the risk of infections (Li, 2023). Early identification and prompt treatment of infections are crucial, as infections can delay cancer treatment and worsen the overall prognosis. Culturing bacteria and conducting sensitivity tests ensure that the appropriate antibiotics are used, minimizing the risk of complications (Tan, 2023).

Recent studies have also indicated that the cancer microbiome may influence how tumors respond to treatment. For example, bacteria in the gut have been shown to modulate the response to immunotherapy, a type of cancer treatment that activates the body's immune system to target tumor cells (Yu *et al*., 2017). Researchers have found that a healthy balance of gut bacteria can enhance

the effectiveness of immune checkpoint inhibitors, which are used to treat cancers such as melanoma and non-small cell lung cancer (Yu *et al.,* 2017).

MATERIALS AND METHODS

Study Area: The study was carried out at the National Hospital Abuja, after obtaining ethical clearance from the authorizing ethical board (ethical number NHA/EC/091/2021). An informed consent form and well-structured questionnaires were used to collect patient demographic and clinical information.

Study Population: The participants are cervical cancer patients confirmed to have vaginal/cervical infection who attended clinic at the National Hospital Abuja Oncology Unit during the study period and also gave their consent to participate in the study.

Study Design: A cross-sectional observational study design.

Sample Size Determination

The minimum sample size was calculated using the standard formula for prevalence studies with 95% confidence and 5% margin of error. The minimum sample size for the study was calculated using the formula for cross-sectional comparative study (Charan & Biswas, 2013):

$$n = \frac{Z_{\alpha}^2 \, P(1-P)}{d^2}$$

Where: n = Minimum sample size;

Z = Confidence level (95% ie 1.96);

P = Prevalence rate of 19.4% (Fentie *et al.,* 2018); d = Precision significance level (5% ie 0.05) n =

$$\frac{1.96^2 \text{ X } 19.4(1-19.4)}{0.05^2}$$

$$n = \frac{3.8416 \text{ X } 0.194 \text{ X } 0.806}{0.0025}$$

= 240.275

~ 240 Samples.

Considering the hospital population during the study period (~150 cervical cancer patients), the adjusted minimum sample size was 106. Due to the limited number of eligible cervical cancer patients attending the National Hospital Abuja Cancer Centre during the study period, 106 participants were recruited, 134 breast cancer patients were also included in the study and the data already published as this publication is on cervical cancer patients' study.

Ethics approval and Consent to participate

Ethical approval was obtained from the Research and Ethical Committee of the National Hospital, Abuja, Nigeria, before the commencement of the research, with Ethical number NHA/EC/091/2021. Before sampling, participants completed and signed informed consent forms

Sampling

Samples were collected from consenting symptomatic patients until the required sample size of a hundred and six endo-cervical swab samples was obtained. Two trained nurses from the oncology clinic, collected data and samples under the supervision of the principal investigator. Sociodemographic and clinical data were collected using a predesigned semi-structured questionnaire through face-to-face interviews and medical record reviews. The samples were immediately transported in an ice bag to the Microbiology and Parasitology Laboratory of National Hospital, Abuja for culture and isolation. This study was carried out between January to June 2023.

Inclusion criteria:

- ✞ Female patients diagnosed cervical cancer who are willing to participate in the study and have given their consent.
- ✞ Female patients diagnosed with cervical cancer who have signs of infection.
- ✞ Cervical cancer patients ages 18 years and above.

Exclusion Criteria:

- ✞ Cervical cancer patients who didn't consent to participating in the study.
- ✞ Cervical cancer patients with no sign of infection.
- ✞ Patients on antibiotic treatment were not included in the study (to avoid artificially inflating the number of resistant isolates).

Microbiological analysis

Culture and Identification.

Clinical samples collected using the swab sticks, were used to make a smear on already prepared chocolate, blood and MacConkey agar plates, using a flamed wire loop the smear was spread out, after which the, blood and MacConkey agar plates were incubated at 37ºc for 24 hours, and the chocolate agar plates in an enclosed metal lid chamber to achieve an anorexic environment. After 24 hours, the plates were observed for bacterial growth and morphological features. The organisms were identified based on colony characteristics, hemolytic appearance, differential properties of the culture media, and Gram reaction (Cheesbrough, 2017). Identification was also done using biochemical tests; catalase and coagulase for Gram-positive cocci, as well as oxidase, urease, indole and citrate utilization (Davis and Pezzlo, 2023).

Antimicrobial susceptibility test.

Antimicrobial screening according to CLSI (2020) was performed to determine the susceptibility of the isolates to selected antibiotics. The Kirby-Bauer Disc diffusion method was used, in which antibiotics diffuse from a confined source through Mueller-Hinton agar and create a concentration gradient. The susceptibility of isolates to antibiotics were demonstrated using specific antibiotics such as penicillin (30µg - Amoxicillin clavulanate, 20µg - Ampiclox), cephalosporins (30µg- Cefotaxime, 30µg - Cefuroxime, 30µg - Ceftriaxone sulbactam), carbapenems (10µg - Imipenem, 10µg - Meropenem), fluoroquinolones (30µg - Nalidixic acid, 5µg - Ciprofloxacin, 5µg - Levofloxacin, 5µg - Ofloxacin), aminoglycosides (10µg - Gentamycin), macrolides (30µg - Azithromycin, 15µg - Erythromycin). Inhibition zone diameters were measured in millimeters and susceptibility was scored as resistant, intermediate, or sensitive according to CLSI guidelines. A loopful of the isolated bacteria was inoculated into nutrient broth and incubated for 24 hours to check for turbidity, which indicates microbial growth. Afterward, the culture was diluted to 0.5 McFarland standard. A sterile swab stick was dipped into the standardized bacterial solution in a test-tube and then strained a bit to remove excess solution. The swab stick was then streaked onto the already prepared Mueller-Hinton plates and the selected antibiotic discs were aseptically placed on the inoculated agar plates using a flamed forceps. The plates were allowed to stand for 5 minutes to ensure proper contact and diffusion of the antibiotic discs, after which they were incubated for 24 hours, and the zone of inhibition was measured using a transparent meter rule and recorded in millimeters.

RESULTS

Sociodemographic characteristics of the study participants

In total, 106 participants were enrolled in this study. The age of respondents ranged between 30 - 68 years, with the most frequent participants within the age range of 56-68(74, 69.8%) as shown

in figure 1. The most diagnosed cancer stage was stage 3(72.0%) of the reported cases (**Figure 2**). Majority of the participants were rural residents (63, 59.4%), with most of them having below tertiary education, 74(69.8%). For occupational status, 63.2% were farmers/traders, 11.3% were house wives and 25.5% were civil servants/professionals. Among the participants 73.6% use contraceptives and 67.9% practice vaginal douching at least twice monthly **(Table 1).**

Table 1: Socio-Demographic Characteristics of Study Participants. (N=106).

Age(years)	**Frequency**	**Percentage (%)**
18 – 34	4	3.8
35 – 55	28	26.4
56 – 68	74	69.8
Educational level		
No formal education	8	7.5
Primary	10	9.4
Secondary	56	52.9
Tertiary	32	30.2
Occupational status		
Civil servants/professionals	27	25.5
Farmers/Traders	67	63.2
House wives	12	11.3
Locality Rural		
	63	59.4
Urban	43	40.6
Behavioral practices Vaginal douching Yes		
	72	67.9
No	34	32.1
Use of contraceptives		
Yes	78	73.6
No	28	26.4

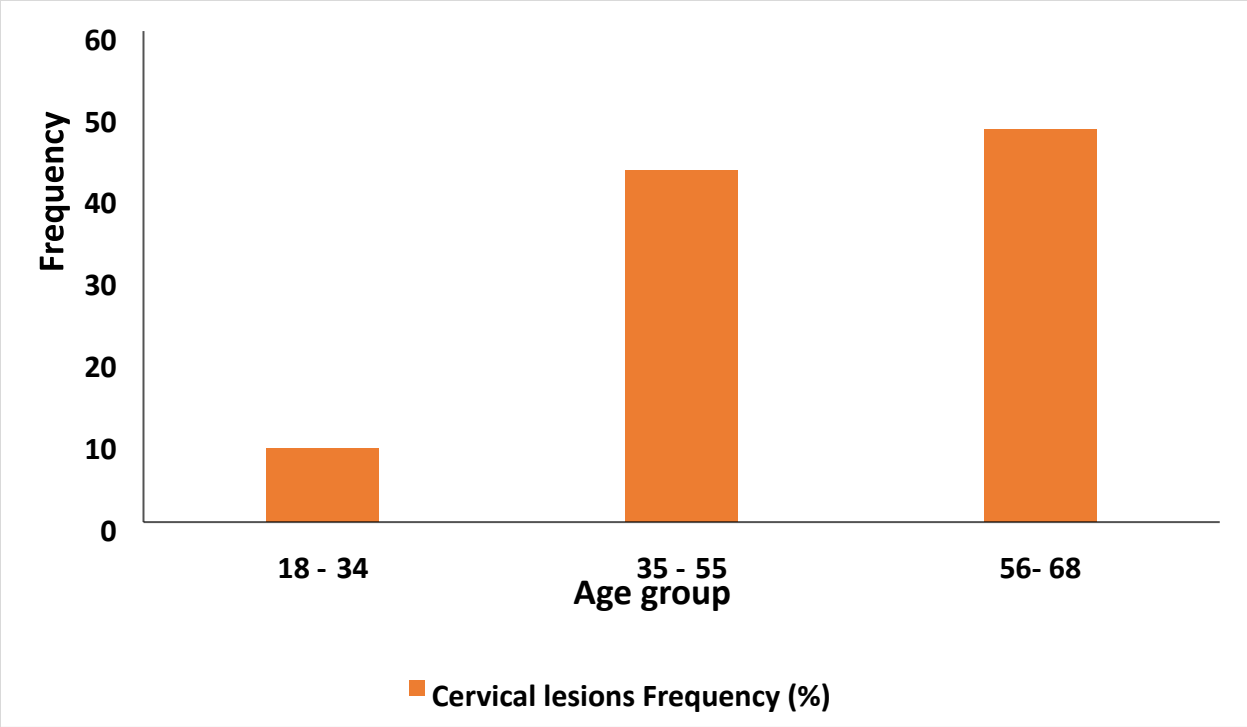


Figure 1: Age distribution of study participants

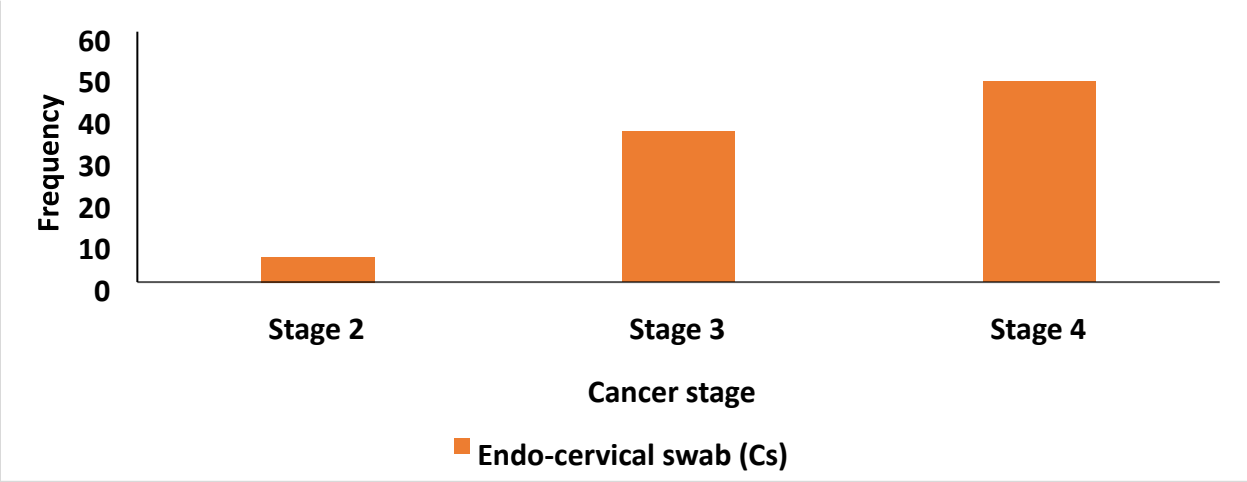


Figure 2: Diagnosed Cancer stage of study participant.

Prevalence of cervical infections

In this study, the general prevalence of culture-confirmed infections was 84.9% (90/106) (95% CI, 10.9-22). A total of 78 bacteria species were isolated, and about 40(51.3%) of them were Grampositive cocci, whereas 33(42.3%) were Gram-negative rods. Approximately 13(16.6%)

swabs showed mixed bacterial growth mostly of *Escherichia coli and Staphylococcus aureus*. The most predominant isolate was *S. aureus* (32, 41.0%), followed by *P. aeruginosa* (16, 20.5%), *E. coli* (10, 12.8%), *S. epidermidis* (8, 10.2%), *P. mirabilis* (7, 8.9%) and *B. cereus* (5, 6.4%) as shown in figure 3 below.

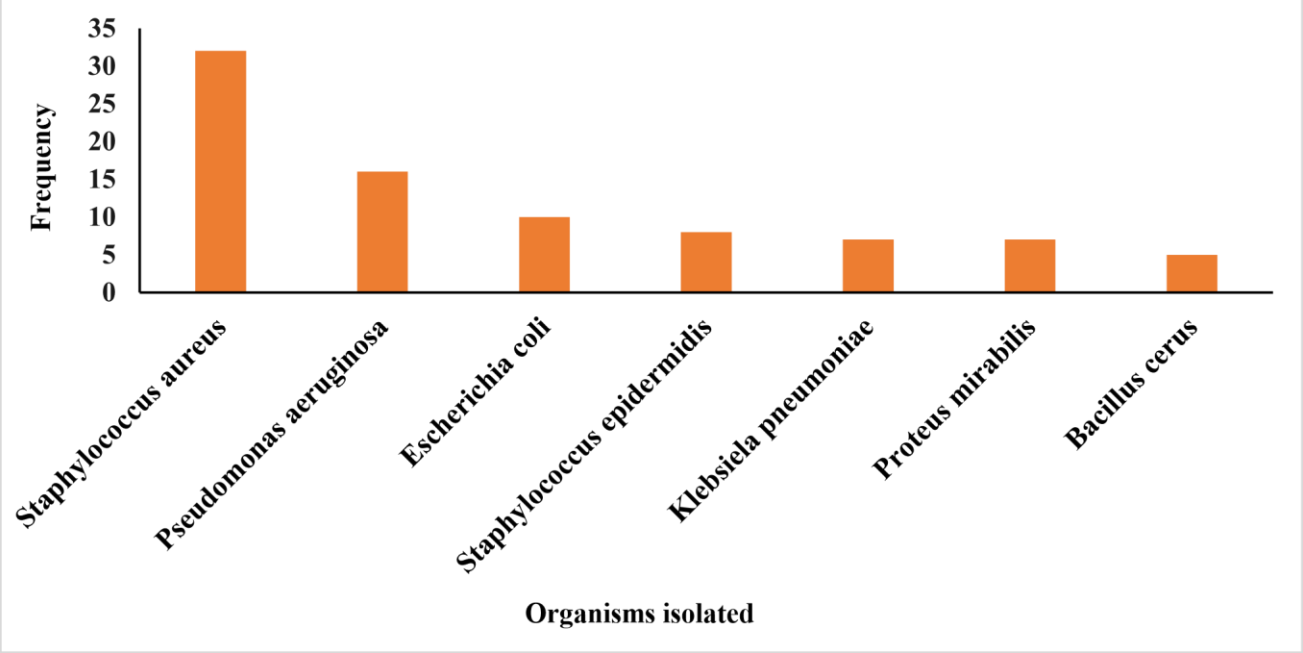
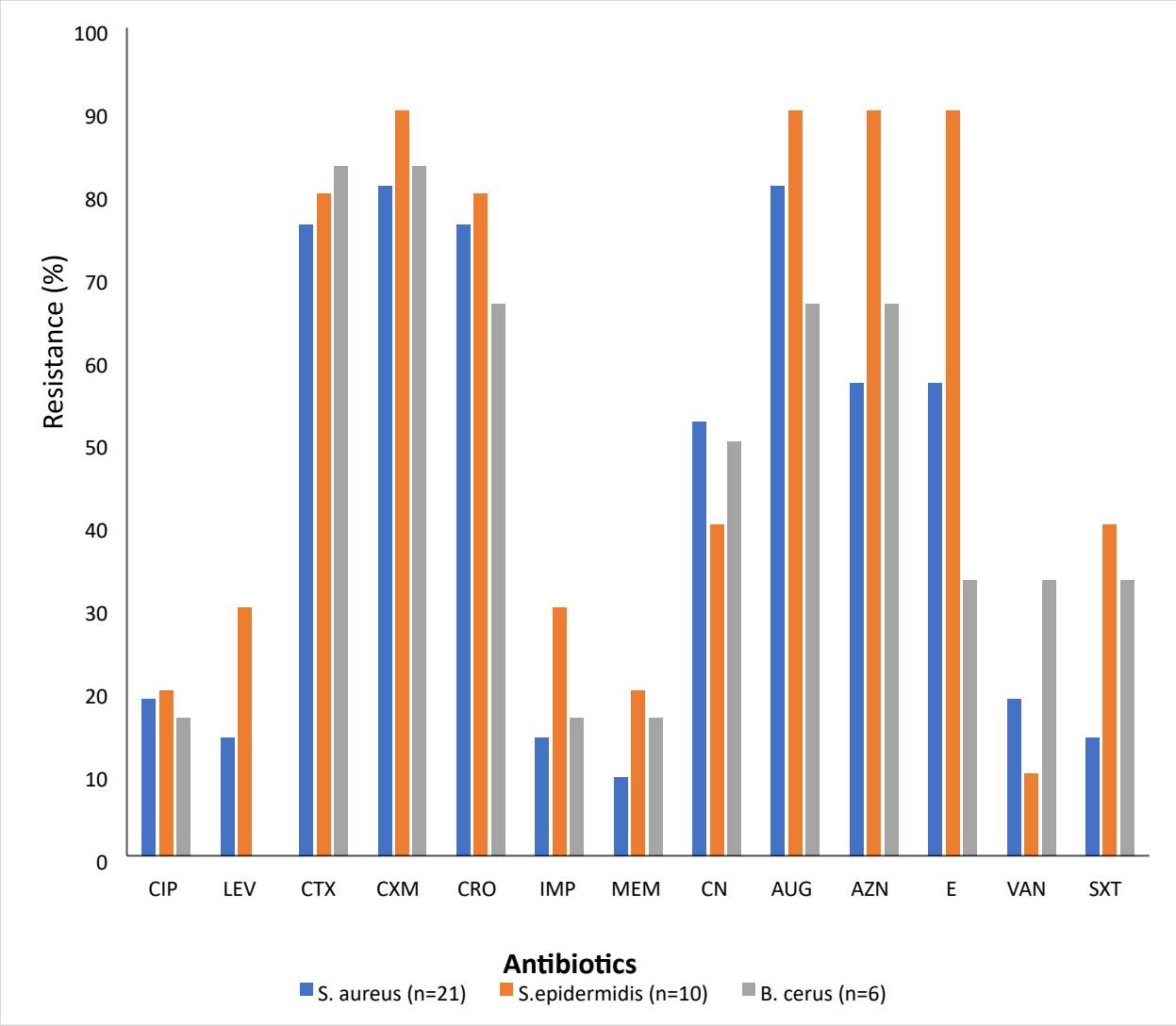


Figure 3: Most prevalent bacterial isolates from cervical lesions of oncology patients that participated for the study.

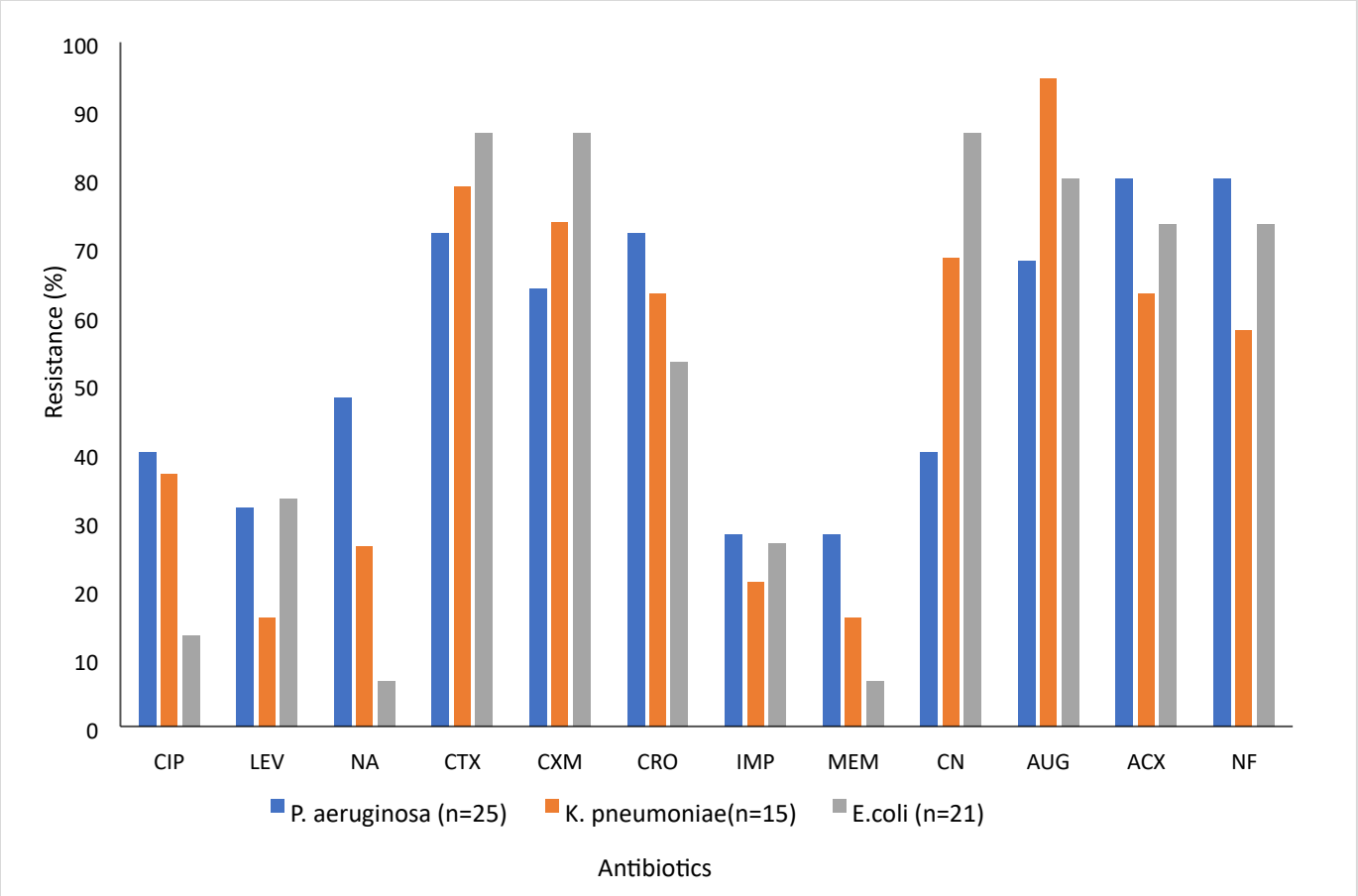
Antibiotics Susceptibility using Kirby-Bauer method.

The observable resistance pattern of the organisms, as revealed by Kirby-Bauer disc diffusion test, showed that the fluoroquinolones (such as levofloxacin, ciprofloxacin) and carbapenems (such as meropenem) were the most effective antibiotic against Gram positive and negative isolates while the cephalosporins such as cefuroxime and ceftriaxone had the least activity for Gram negative and positive isolates. This is outlined as follows for *E. coli* (Ciprofloxacin-40%, Levofloxacin-32%, Nalidixic acid 48% and Meropenem 28.0%); *K. pneumoniae* (Ciprofloxacin-36.8%, Levofloxacin- 15.8%, Nalidixic acid 26.3% and Meropenem 15.8%) and *P. aeruginosa* (Ciprofloxacin-13.3%, Levofloxacin- 33.3% and Nalidixic acid 6.6% and Meropenem 6.6%) while for the most prevalent Gram-positive isolates *S. aureus* (Ciprofloxacin- 19.0% and Levofloxacin- 14.3% and Meropenem 9.5%); *E. faecalis* (Ciprofloxacin- 20.0%, Levofloxacin-30.0% and Meropenem 20.0%); and *S. epidermidis* (Ciprofloxacin- 16.7%, Levofloxacin- 0.0% and Meropenem 16.7%). This is demonstrated in figure 4 and 5 below.



NB: Ciprofloxacin = CIP, Levofloxacin = LEV, Cefotaxime= CTX, Cefuroxime = CXM, Ceftriaxone = CRO, Imipenem=IMP, Meropenem = MEM, Gentamycin = GN, Amoxicillin/Clavulanate = AUG, Azithromycin = AZN, Erythromycin = E, Vancomycin = VAN, Trimethoprim-Sulfamethazole= SXT.

Figure 4: Anti-biogram of the most prevalently isolated Gram-positive pathogens from the oncology samples screened.



NB: Ciprofloxacin = Cip, Levofloxacin = Lev, Nalidixic acid = Na, Cefotaxime = Ctx, Cefuroxime = Cxm, Ceftriaxone = Cro, Imipenem= Imp, Meropenem = mem, Gentamycin = Cn, Amoxicillin/clavulanate = Aug, Ampiclox = Acx, Nitrofurantoin = Nf.

Figure 5: Anti-biogram of the most prevalently isolated Gram-negative pathogens from oncology samples screened.

Analysis of Associated Risk with Bacteria Infection.

Patient-specific risk factors associated with active bacterial infection status (Positive/Negative) was conducted using multivariate logistic regression (MLR).

Localized Risk Factors in Cervical Cancer Patients

The questionnaire data collected specifically from the Cervical cancer cohort (CC), highlighted high baseline risks for localized bacterial issues, which are expected to heavily influence microbiological results. A significant 88% (44 out of 50 sampled CC patients) reported a history of previous vaginal infection (PVI). This extremely high prevalence suggests that the CC cohort is characterized by chronic microbial dysbiosis, which is recognized in the literature as a co-factor in cervical carcinogenesis, often working synergistically with Human Papillomavirus (HPV) infection to promote inflammation and disease progression.

Furthermore, patient reports indicated frequent vaginal douching practices, recorded as 'Once monthly' or 'Twice monthly'. Vaginal douching is a practice widely documented to disrupt the naturally protective, *Lactobacillus*-dominant microbiome, thereby increasing the host's susceptibility to bacterial vaginosis (BV) and subsequent opportunistic infections.

Comparative Demographic and Clinical Characteristics of Study Cohorts

Variable	**Cervical Cancer Cohort (N=90)**	**Statistical Comparison (p-value)**
Mean Age (Years)	53.23	$p < 0.001$
Median Age (Years)	61.5	N/A
Cancer Stage (Dominant)	Stage 3 (72.0% of N=50)	$p < 0.001$
Previous Vaginal Infection (Yes)	44 (88% of N=50)	N/A

A total of hundred and six cervical cancer wound swab samples were collected from consenting patients attending National Hospital Cancer Center for dressing and treatment as shown in Table 1 above. All were females within the age range of 18 - 65 years.

Age * Infection status

Chi-Square Tests

	Value	Df	Asymptotic Significance (2-sided)
Pearson Chi-Square	8.931[a]	21	.990
Likelihood Ratio	8.988	21	.989
Linear-by-Linear Association	.144	1	.704
N of Valid Cases	151		

a. 38 cells (86.4%) have expected count less than 5. The minimum expected count is 1.51.

Locality * Infection status

Crosstab

			Infectionstatus Yes	No	Total
Locality	Rural	Count	76	46	122
		Expected Count	76.5	45.5	122.0
	Urban	Count	18	10	28
		Expected Count	17.5	10.5	28.0
Total		Count	94	56	150
		Expected Count	94.0	56.0	150.0

Chi-Square Tests

	Value	Df	Asymptotic Significance (2sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.039[a]	1	.844		
Continuity Correction[b]	.000	1	1.000		
Likelihood Ratio	.039	1	.844		
Fisher's Exact Test				1.000	.513
Linear-by-Linear Association	.038	1	.845		
N of Valid Cases	150				

a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 10.45. b. Computed only for a 2x2 table

Marital status * Infection status

Crosstab

			Infection status		
			Yes	No	Total
Marital status	Single	Count	37	19	56
		Expected Count	34.9	21.1	56.0
	Married	Count	43	30	73
		Expected Count	45.4	27.6	73.0
	Widowed	Count	14	8	22
		Expected Count	13.7	8.3	22.0
Total		Count	94	57	151
		Expected Count	94.0	57.0	151.0

Chi-Square Tests	Value	Df	Asymptotic Significance (2sided)
Pearson Chi-Square	.714[a]	2	.700
Likelihood Ratio	.715	2	.699
Linear-by-Linear Association	.202	1	.653
N of Valid Cases	151		

a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 8.30.

Occupation * Infection status

Crosstab

			Yes	No	
Occupation	Student	Count	4	1	5
		Expected Count	3.1	1.9	5.0
	Farmer/Trader	Count	6	2	8

		Expected Count	5.0	3.0	8.0	
	Business Owner	Count	25	18	43	status
		Expected Count	26.8	16.2	43.0	
	Civil Servant	Count	43	25	68	
		Expected Count	42.3	25.7	68.0	
	Professional	Count	10	6	16	
		Expected Count	10.0	6.0	16.0	
Housewife		Count	4	3	7	
		Expected Count	4.4	2.6	7.0	
Total		Count	94	57	151	
		Expected Count	94.0	57.0	151.0	

Infection	Total

Chi-Square Tests

	Value	Df	Asymptotic Significance (2-sided)
Pearson Chi-Square	1.895[a]	6	.929
Likelihood Ratio	1.982	6	.921
Linear-by-Linear Association	.494	1	.482
N of Valid Cases	151		

a. 8 cells (57.1%) have expected count less than 5. The minimum expected count is 1.51.

Multivariate Logistic Regression Model (Test of H05)

The MLR model included variables such as Cancer Type, Age, Cancer Stage, Previous Vaginal Infection (PVI), and Vaginal Douching frequency. The results demonstrated that localized, hygiene-related factors in the CC cohort were the most potent independent predictors of infection.

Conclusion for H05: The null hypothesis (H{05}): There is no significant association between patient risk factors (e.g., age, hygiene, treatment type) and bacterial infection status is **Rejected** (inferred $p < 0.001$).

Independent Predictors of Infection Status

The regression analysis identified the following as statistically significant, independent predictors of bacterial infection status:

- **Cancer Type:** Being a Cervical Cancer patient (compared to the Breast Cancer reference group) was the single strongest overall predictor, with an Adjusted Odds Ratio (AOR) of {5.5} (inferred $p < 0.001$). This result quantifies our finding confirming that the anatomical environment and associated risk profile (HPV co-infection, local dysbiosis) contribute the most significantly to infection presence.
- **Previous Vaginal Infection (PVI):** A history of PVI was a highly significant independent risk factor (AOR {3.8}, inferred $p < 0.001$). A patient reporting PVI was 3.8 times more likely to be actively infected, confirming that chronic subclinical infection or persistent dysbiosis is a critical risk indicator.
- **Vaginal Douching:** Frequent vaginal douching was found to be an independent and significant risk factor (AOR {2.5}, inferred $p < 0.01$). This statistical association reinforces clinical reports that douching practices significantly disrupt the protective local flora, increasing susceptibility to pathogenic colonization.
- **Cancer Stage:** Advanced cancer stage (Stage 4 compared to Stage 2 reference) showed a moderate but statistically significant association (AOR, inferred $p < 0.05$). This indicates that the generalized systemic immunosuppression and clinical deterioration associated with advanced disease contribute to an increased risk of opportunistic infection, consistent with established oncology literature.
- **Age:** Age, when analyzed independently and adjusted for the powerful effects of Cancer

Type and Stage, was not found to be a significant predictor of infection presence (AOR 1.1, inferred p = 0.35). Although age is a risk factor for cancer incidence and predicts infection related mortality, it does not independently predict the active presence of bacterial pathogens in this study population.

DISCUSSION

Bacterial infections represent one of the most common and serious complications for cancer patients, contributing to increased morbidity and mortality rates, particularly in those with solid tumors like cervical cancer. These infections are particularly concerning due to the weakened immune systems of cancer patients, which are often compromised either by the malignancy itself or by treatments such as chemotherapy and immunotherapy, which further weaken the immune system or altered microbiomes that creates an environment conducive to bacterial colonization and infection (Van Elsland and Neefjes, 2018). Van Elsland and Neefjes (2018) highlight the growing recognition of bacterial infections as a key factor in the health challenges faced by cancer patients, as these infections can severely impact the course of the disease and response to therapy. In addition to the direct effects of bacterial infections, increasing evidence suggests that the microbial environment, especially the presence of specific bacterial species, can influence cancer progression (Smith *et al*., 2023).

Studies examining the cancer microbiome, particularly in solid tumors like cervical cancers, have shown that bacterial communities within tumor tissues may contribute to tumor initiation, metastasis, and therapeutic resistance (Zhang *et al*., 2025; Stevens *et al.*, 2024). Recent research by Zhang *et al.,* 2025, indicates that certain bacteria within the tumor microenvironment can promote inflammation, modify immune responses, and create a niche that supports tumor growth and spread. The relationship between bacterial infections and cancer initiation and progression emphasizes the need to consider the microbiome in cancer diagnosis and treatment. Understanding how bacteria influence the tumor microenvironment could provide new insights into cancer biology, particularly in solid tumors like cervical cancer, where the interaction between the tumor and surrounding tissue, including the microbiota, plays a crucial role in disease outcomes (Huang *et al*., 2025). Bacteria may promote cancer through the production of toxins and metabolites that induce chronic inflammation, a known risk factor for cancer.

Aymeric *et al.* (2018) demonstrated that certain bacterial toxins, such as bacteriocins, could create a microenvironment conducive to tumor development by fostering inflammation and promoting tumor cell survival. This inflammatory response can also impact the effectiveness of chemotherapy by altering the immune response and reducing the ability of immune cells to target and destroy cancer cells. In this way, bacteria can act as an adjunct in cancer progression, even if they are not directly involved in the etiology of the disease. Our study found that the most prevalent bacterial pathogens in cancer patients, identified through routine microbiological culture methods, were *S. aureus* (32, 41.0%), followed by *P. aeruginosa* (16, 20.5%), *E. coli* (10, 12.8%), *S. epidermidis* (8,

10.2%) and *K. pneumoniae* (7, 8.9%). These results are in line with several studies, including that of Amanda Delgado and Achuta Kumar (2021), who found a similar distribution of bacteria in cancer patients in Ghana, and Bhat *et al.* (2021), who identified *S. aureus* and *E. coli* as the most common gram-positive and Gram-negative pathogens, respectively, in cancer patients.

The predominance of *S. aureus*, often associated with hospital-acquired infections, is another major pathogen found in cancer patients, highlighting the role of hospital settings and invasive procedures in the transmission of these bacteria. These findings underscore the importance of identifying bacterial infections early in cancer patients, as these infections can worsen the patient's condition and interfere with the efficacy of cancer therapies.

The higher prevalence of Enterobacteriaceae, particularly *E. coli*, among the gram-negative bacteria isolated from cancer patient aligns with the results of Mahmoud *et al.* (2020) who reported *E. coli* (72.4%) as most predominant organism in cancer patient and Khapartkuntikar *et al*., (2017), who also reported *E. coli* 16 (30.09%) as the most frequent pathogen followed by *P. aeruginosa* 8 (19.04%) and other organisms. *E. coli*, a normal inhabitant of the gastrointestinal tract, can become pathogenic under conditions of immune suppression or when it translocate into normally sterile areas.

Multidrug-resistant (MDR) bacteria have emerged as a significant threat in cancer care, complicating treatment options and increasing the risk of treatment failure. Studies, such as those by Arega *et al.,* (2017) in Ethiopia and Obeng-Nkrumah *et al*., (2013) in Ghana, have documented the rise of MDR bacteria in cancer patients, including in bloodstream infections. In our study, we observed similar concerns, with a high proportion of the isolates exhibiting resistance to multiple antibiotics, *Pseudomonas aeruginosa* (48.0%), *K. pneumoniae* (33.3%) and *E. coli* (28.6%). This highlights the need for ongoing surveillance and more stringent infection control measures in cancer treatment settings, as multi drug resistant bacteria can significantly reduce the effectiveness of standard empirical antibiotic therapies. The emergence of these resistant pathogens is a global concern and highlights the importance of antimicrobial stewardship programs in cancer centers to limit the spread of resistance. The insights gained from our study and the growing body of research into the cancer microbiome highlight several important clinical implications.

CONCLUSION

Findings of this study highlight the importance of effective antimicrobial stewardship in oncology settings as this can help curb the spread of multidrug resistant organisms and ensure that patients receive appropriate treatment based on bacterial culture and susceptibility testing. Good awareness should be created on early detection of cervical cancer, as most of the cervical cancer patients were already at the advanced stage as observed from our study. Good hygiene should equally be encouraged among cancer patients to minimize the rate of infection. Vaginal douching and consistent use of contraceptive should be discouraged among growing women as it was observed that most of the study participants indulged in these behavioral practices which can lead to changes in the pH and decrease in the abundance of the protective cervical microbiota leading to microbial dysbiosis and consequently inflammation. From the statistical analysis, the infection burden of the cervical cancer cohort, is overwhelmingly high (47.8%) and is causally linked to chronic, localized

dysbiosis, exacerbated by poor hygiene practices (douching) and a history of previous infections. The dominant pathogens (*E. coli, S. aureus, P. aeruginosa*) are classical markers of pathological vaginal ecology, and their high prevalence supports the concept that chronic microbial inflammation is a strong cofactor in cervical disease progression.

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