

Antimicrobial Resistance and Empirical Antibiotic Prescribing Among Cancer Patients at a Tertiary Referral Hospital in Rwanda, 2019–2024

Brandon Niyibizi Asuman

University of Freiburg

Damas Dukundane

King Faisal Hospital

Marrigje Jacoba Kreuger

King Faisal Hospital

Simon Ganal

University Medical Center Freiburg

Katarina Stete

University Medical Center Freiburg

Hajo Grundmann

University Medical Center Freiburg

Vanessa M. Eichel

vanessa.eichel@uniklinik-freiburg.de

University Medical Center Freiburg

Research Article

Keywords: Antimicrobial resistance, Oncology, Cancer, ESKAPEE, Urinary tract infection, Empirical antibiotic therapy, Antimicrobial stewardship, WHO AWaRe, sub-Saharan Africa, Rwanda

Posted Date: July 2nd, 2026

DOI: <https://doi.org/10.21203/rs.3.rs-10068762/v1>

License:   This work is licensed under a Creative Commons Attribution 4.0 International License. [Read Full License](#)

Additional Declarations: No competing interests reported.

Version of Record: A version of this preprint was published at BMC Infectious Diseases on October 21st, 2026. See the published version at <https://doi.org/10.1186/s12879-026-14689-2>.

Abstract

Background.

Antimicrobial resistance (AMR) increasingly threatens infection management in cancer patients, yet population-specific data from sub-Saharan African oncology settings remain scarce. We aimed to characterise bacterial profiles, antimicrobial resistance patterns, and empirical antibiotic prescribing among oncology patients with culture-confirmed infections at a tertiary referral hospital in Rwanda.

Methods.

We conducted a retrospective record-based study of 297 culture-confirmed infection episodes occurring in 286 oncology patients (11 patients contributed two episodes each) at King Faisal Hospital, Kigali, between January 2019 and December 2024. Antimicrobial susceptibility testing followed institutional standard operating procedures using disc diffusion and the BD Phoenix automated system, with results interpreted according to CLSI breakpoints in force at the time of testing. Multidrug resistance (MDR) was defined per Magiorakos et al. (2012) as non-susceptibility to at least one agent in three or more antimicrobial categories. We described isolate distributions and resistance patterns for all 297 episodes. Empirical prescribing was assessed in the subset of episodes with empirical therapy documented in the electronic medical record (105/297; 35.4%), predominantly inpatient encounters (100/105; 95.2%), against the WHO AWaRe (Access, Watch, Reserve) classification and the 2022 Rwanda Standard Treatment Guidelines. Predictors of MDR were examined by multivariable logistic regression among bacterial isolates ($n = 254$), with a sensitivity analysis restricted to the first bacterial episode per patient ($n = 246$).

Results.

Urinary tract infections (UTIs) predominated (172/297; 57.9%), followed by skin and soft tissue infections (48/297; 16.2%) and bloodstream infections (45/297; 15.2%). *Escherichia coli* (101/297; 34.0%), *Klebsiella* spp. (32/297; 10.8%), and *Enterococcus* species (25/297; 8.4%) were the most frequent isolates. ESKAPEE pathogens (*E. coli*, *K. pneumoniae*, *P. aeruginosa*, *Acinetobacter* spp., *Enterobacter* spp., *Enterococcus* spp., and *S. aureus* including MRSA) comprised 201 of 297 isolates (67.7%). Ceftriaxone resistance was high among gram-negative organisms (*E. coli* 64.4%; *Enterobacter* spp. 75.0%; *Klebsiella* spp. 55.6%). Carbapenem resistance in *Acinetobacter* spp. was 61.5% (8/13), although the small denominator warrants cautious interpretation. In multivariable logistic regression, infection type was the only independent predictor of MDR: compared with UTI (reference), bloodstream infection (aOR 0.29, 95% CI 0.11–0.81) and skin and soft tissue infection (aOR 0.30, 95% CI 0.11–0.81) were associated with significantly lower odds of resistance. The sensitivity analysis (first-episode-only) yielded essentially identical estimates. Among the 105 episodes (35.4%) with documented empirical regimens, predominantly inpatient encounters, adherence to national guidelines varied significantly by infection type ($p = 0.001$) and was lowest for UTIs (2.3%); outpatient empirical prescribing was systematically under-captured in the electronic medical record and therefore could not be evaluated.

Conclusions.

In this Rwandan oncology population, multidrug resistance was common, particularly among UTI pathogens. Ceftriaxone, the most frequently prescribed empirical agent, showed limited in vitro activity against the prevailing isolates. Revision of empirical antibiotic protocols based on locally stratified antibiograms is therefore indicated. Antimicrobial stewardship aligned with WHO AWaRe principles, infection prevention measures targeted at ESKAPEE pathogens, structured electronic medical record capture of empirical prescribing (especially in the outpatient setting), and integration of oncology-unit data into national AMR surveillance are further priorities.

Plain Language Summary

Antibiotic resistance is rising worldwide, and cancer patients are particularly vulnerable because their immune system is weakened by both their disease and its treatment. Most studies on this problem come from wealthy countries; very little is known about cancer patients in sub-Saharan Africa. We reviewed the medical records of 286 cancer patients treated at a large hospital in Kigali, Rwanda, who had a confirmed bacterial infection between 2019 and 2024 (297 infection episodes in total). Urinary tract infections were by far the most common, and the bacteria causing them were often resistant to ceftriaxone, the antibiotic most commonly used as first-line treatment at the hospital. Resistant bacteria from the WHO priority list (the so-called "ESKAPEE" group) accounted for two thirds of all infections.

Among the inpatient cases for whom the first-line antibiotic was recorded in the medical record, the choice frequently differed from what national Rwandan guidelines recommend; for outpatient cases, this information was rarely captured in the electronic record at all. Our findings suggest that hospitals treating cancer patients in Rwanda need to update which antibiotics are used as first choice based on the actual resistance profile in their own patients, strengthen infection-prevention measures, improve documentation of antibiotic prescribing (particularly for outpatients), and ensure that data from cancer wards feed into the national surveillance system for antibiotic resistance.

Background

Antimicrobial resistance (AMR) is recognised by the World Health Organization and the US Centers for Disease Control and Prevention as one of the foremost threats to global public health [1]. Antibiotic misuse, overuse, and limited diagnostic capacity are key drivers of rising resistance [2], and recent projections suggest that AMR could be associated with around 10 million additional deaths annually by 2050 in the absence of substantial intervention [3].

Bacterial infections are a leading cause of morbidity and mortality among cancer patients [4]. Increased susceptibility reflects immunosuppression from the malignancy itself and from systemic anti-cancer therapy, radiotherapy, surgery, and indwelling devices such as urinary and central venous catheters. Cancer patients face a threefold higher risk of infection-related death compared with patients without cancer [4]. Antibiotics play a critical prophylactic and therapeutic role for patients undergoing surgery [5], stem cell transplantation [6], and systemic anti-cancer therapy- or radiation-induced neutropenia [7]. The spectrum of infections varies with cancer type, neutropenic status, and treatment regimen [8], but gram-negative organisms are consistently reported as predominant pathogens [9]. Bloodstream infections are frequently caused by *Escherichia coli*, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa*, with rising resistance to commonly used agents [10].

Multidrug-resistant (MDR) pathogens have become increasingly prevalent in oncology settings [11], with implications for prognosis and treatment planning [12]. Resistant ESKAPE/ESKAPEE pathogens (*Enterococcus* spp., *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter* spp., *Pseudomonas aeruginosa*, *Enterobacter* spp., and *Escherichia coli*), methicillin-resistant *S. aureus* (MRSA), carbapenem-resistant Enterobacterales (CRE), and extended-spectrum β -lactamase (ESBL)-producing Enterobacterales feature prominently in this population [13]. A previous study at Kigali University Teaching Hospital reported third-generation cephalosporin resistance of 31.4% in *E. coli* and 58.7% in *Klebsiella* isolates, with 82% of *S. aureus* isolates classified as MRSA [14]. The WHO AWaRe (Access, Watch, Reserve) classification [15] and the 2022 Rwanda Standard Treatment Guidelines [16] provide frameworks for appropriate empirical prescribing, but adherence remains suboptimal across low- and middle-income countries (LMICs) including Rwanda [17, 18].

Despite the heightened vulnerability of cancer patients to drug-resistant infection, oncology-specific empirical treatment guidance is rare in LMIC settings, and the evidence base from sub-Saharan African oncology populations is particularly limited [19, 20]. To our knowledge, no published study has described bacterial profiles, antimicrobial resistance patterns, or the appropriateness of empirical antibiotic prescribing among cancer patients in Rwanda. We therefore aimed to characterise these features and to compare empirical prescribing with both international and national guideline recommendations.

Methods

Study design and setting

We conducted a retrospective record-based study of bacterial isolates and antimicrobial resistance among cancer patients with culture-confirmed infections at King Faisal Hospital, Kigali, Rwanda, between January 2019 and December 2024. King Faisal Hospital is a 160-bed tertiary referral and teaching hospital affiliated with Africa Health Sciences University. The hospital is currently expanding to 600 beds and houses one of the three major cancer-care facilities in Rwanda, providing comprehensive oncology services including systemic anti-cancer therapy, surgical oncology, and palliative care [21]. Reporting follows the Strengthening the Reporting of Observational Studies in Epidemiology (STROBE) guidelines for cross-sectional studies.

Study population and case definition

Eligible cases were pseudonymised electronic medical records (EMR) of cancer patients with at least one culture-confirmed infection during the study period. A total of 297 infection episodes from 286 unique patients were included; 11 patients contributed two infection episodes each, separated in time and managed as distinct clinical events. Infections were classified by site as urinary tract infection

(UTI), bloodstream infection (BSI), skin and soft tissue infection (SSTI), respiratory tract infection (RTI), or gastrointestinal/other infection on the basis of the clinical record and culture source.

Microbiological methods

Microbiological processing and antimicrobial susceptibility testing (AST) were performed during the study period in accordance with hospital standard operating procedures. Blood samples were inoculated into BD BACTEC bottles (Becton-Dickinson, Franklin Lakes, NJ, USA) and incubated at 37°C in the BACTEC automated system; bottles flagged as positive were subcultured on solid media. Other clinical samples were directly inoculated onto blood agar, MacConkey agar, and Sabouraud-dextrose agar plates and incubated at 37°C. Plates were examined after 18–24 hours; exudate cultures were monitored daily for up to 72 hours. Recovered isolates were identified using the BD Phoenix automated microbiology system or analytical profile index (API) biochemical tests, and AST was performed by disc diffusion or the BD Phoenix system. AST results were interpreted according to Clinical and Laboratory Standards Institute (CLSI) breakpoints in force at the time of testing; we did not retrospectively reclassify historical results against updated breakpoints, and acknowledge this as a potential source of temporal variation.

Operational definitions

Multidrug resistance (MDR) was defined according to Magiorakos et al. as acquired non-susceptibility to at least one agent in three or more antimicrobial categories [22]. *ESKAPEE* pathogens were operationally defined to include *E. coli*, *K. pneumoniae*, *P. aeruginosa*, *Acinetobacter* spp. (species-level identification was not consistently available and *Acinetobacter baumannii* specifically could not be distinguished from related species), *Enterobacter* spp., *Enterococcus* spp., and *S. aureus* (including MRSA). Empirical antibiotic prescribing was defined as the antibiotic regimen initiated before the availability of culture and susceptibility results. The empirical-therapy variable was extracted from the electronic medical record (EMR) as documented at the time of care; an empirical regimen was recorded for 105 of 297 episodes (35.4%). The asymmetry of EMR capture was striking: among inpatient episodes, 100 of 192 (52.1%) had a documented empirical regimen, whereas only 5 of 105 outpatient episodes (4.8%) did so. Outpatient empirical prescribing was therefore systematically under-captured in the EMR, although clinical practice strongly suggests that antibiotics were administered at the point of care in most such encounters. Adherence analyses were accordingly confined to the 105 episodes with documented therapy and should be interpreted as reflecting predominantly inpatient prescribing practice.

Data collection

A structured data collection tool implemented in KoBoToolbox captured demographic, clinical, and microbiological variables, including age, sex, cancer type and stage, treatment setting (inpatient versus outpatient), infection type, sample type, organism identification, and complete antimicrobial susceptibility profiles. Data abstraction was performed from pseudonymised EMR by one trained reviewer (BNA), with cross-verification of 15% of records by a second reviewer at three-day intervals during data collection; discrepancies were resolved by discussion and, where needed, adjudicated by the clinical supervisor (MJK). The data collection tool was pilot-tested on 20 records before full implementation. All isolates were processed using identical microbiology protocols and no systematic differences in measurement methods between groups were identified.

Statistical analysis

Continuous variables were summarised using medians and interquartile ranges (IQR); categorical variables were expressed as frequencies and percentages. Antimicrobial susceptibility patterns were cross-tabulated by bacterial species. Associations between patient characteristics and antimicrobial resistance were examined using chi-squared tests; the Mann–Whitney U test was used for age. Adherence to WHO AWaRe and to the 2022 Rwanda Standard Treatment Guidelines [15, 16] was compared across infection types using chi-squared tests, restricted to the 105 episodes with documented empirical therapy (Table 6). To assess the independence of observed associations, multivariable logistic regression was performed with MDR as the binary outcome, restricted to bacterial isolates ($n = 254$) and including standardised age, sex, treatment setting, gram-stain category, and infection type as simultaneous covariates. UTI was used as the infection-type reference because it was both the largest category (172/254 bacterial episodes; 67.7%) and the clinical focus of the analysis. Cancer stage was excluded from the regression because of missing values in 49 patients (16.5%). Adjusted odds ratios (aOR) with 95% confidence intervals (CI) are reported. To address potential within-patient clustering due to 11 patients contributing two episodes each, a sensitivity analysis restricted to the first bacterial episode per patient ($n = 246$) was performed; results were essentially

unchanged (see Results). All analyses were performed using SPSS version 29 (IBM Corp., Armonk, NY, USA) and verified in R; a two-sided p-value of < 0.05 was considered statistically significant.

Table 6

Adherence to WHO AWaRe and Rwanda Standard Treatment Guidelines by infection type among oncology patients with empirical therapy documented in the electronic medical record, King Faisal Hospital, Kigali, Rwanda, 2019–2024 (n = 105; predominantly inpatient).

Infection type	WHO AWaRe N (%)	p-value	National guidelines N (%)	p-value
Bloodstream infection	22 (78.6)	0.616	9 (32.1)	0.001**
Respiratory tract infection	6 (75.0)		4 (50.0)	
Skin and soft tissue infection	15 (65.2)		4 (17.4)	
Urinary tract infection	28 (65.1)		1 (2.3)	
<i>Adherence was defined as the selection of an empirical antibiotic consistent with the recommended agent(s) for the identified infection site according to each guideline framework. Percentages are calculated within infection type. The analysis is restricted to the 105 of 297 episodes (35.4%) with an empirical regimen documented in the EMR; because 100 of these 105 documented regimens were prescribed for inpatients, these adherence estimates should be interpreted as reflecting predominantly inpatient practice. ** p < 0.01 by chi-squared test.</i>				

Ethics

All ethical aspects were conducted in accordance with the Declaration of Helsinki. Ethical approval was obtained from the Institutional Review Board of King Faisal Hospital (protocol KFH/2025/291/IRB) and the Ethics Committee of the University of Freiburg (reference EK-Freiburg 25-1122-S2). The requirement for written informed consent was waived given the retrospective, pseudonymised nature of the dataset.

Results

Patient and clinical characteristics

The study included 297 culture-confirmed infection episodes in 286 unique cancer patients, of whom 173 (58.2%) were male and 124 (41.8%) were female. Among men, the 60–69-year age group was the largest subgroup, whereas women showed a more balanced distribution across age categories (Table 1). The majority of episodes occurred in inpatients (192/297; 64.6%). Solid organ malignancies accounted for 88.2% of cases and haematological malignancies for 11.8%. Prostate cancer was the most common diagnosis (22.9%), followed by colorectal cancer (14.5%), reflecting the cancer epidemiology of Rwanda where prostate cancer is the leading malignancy in men [23]. Stage IV disease accounted for the largest share of episodes (53.2%), indicating that many patients had advanced metastatic cancer at the time of infection.

Table 1
Demographic and clinical characteristics of cancer patients with culture-confirmed infection, King Faisal Hospital, Kigali, Rwanda, 2019–2024.

Category	Variable	Frequency	Percentage (%)
Treatment setting (n = 297)	Inpatient	192	64.6
	Outpatient	105	35.4
Underlying cancer type (n = 297)	Solid organ malignancy	262	88.2
	Haematological malignancy	35	11.8
Specific cancer type (n = 297)	Prostate	68	22.9
	Colorectal	43	14.5
	Brain and nervous system	24	8.1
	Breast	23	7.7
	Stomach	22	7.4
	Leukaemia	19	6.4
	Head and neck	14	4.7
	Urinary bladder	12	4.0
	Lymphoma	12	4.0
	Ovarian	6	2.0
	Liver	6	2.0
	Other ($\leq 1.7\%$ each)	48	16.2
Cancer stage (n = 248)	Stage I	6	2.4
	Stage II	39	15.7
	Stage III	71	28.6
	Stage IV	132	53.2

Infection types and microbiology

Urinary tract infections were the most common infection type (172/297; 57.9%), followed by skin and soft tissue infections (48/297; 16.2%) and bloodstream infections (45/297; 15.2%) (Fig. 1; Table 2).

Table 2

Distribution of isolated microorganisms by clinical sample type among cancer patients, King Faisal Hospital, Kigali, Rwanda, 2019–2024.

Gram type	Organism	Total N (%)	Urine N (%)	Blood N (%)	Pus N (%)	Tracheal aspirate N (%)	Body fluid N (%)	Sputum N (%)	Other N (%)
Gram-negative rods	<i>Escherichia coli</i>	101 (34.0)	81 (80.2)	7 (6.9)	11 (10.9)	–	1 (1.0)	1 (1.0)	–
	<i>Klebsiella</i> spp.	32 (10.8)	15 (46.9)	9 (28.1)	4 (12.5)	–	–	1 (3.1)	3 (9.4)
	<i>Pseudomonas aeruginosa</i>	19 (6.4)	6 (31.6)	5 (26.3)	4 (21.1)	3 (15.8)	1 (5.3)	–	–
	<i>Acinetobacter</i> spp.	13 (4.4)	5 (38.5)	–	–	5 (38.5)	2 (15.4)	1 (7.7)	–
	<i>Proteus</i> spp.	10 (3.4)	6 (60.0)	1 (10.0)	2 (20.0)	1 (10.0)	–	–	–
	<i>Enterobacter</i> spp.	8 (2.7)	3 (37.5)	3 (37.5)	1 (12.5)	–	1 (12.5)	–	–
	Other gram-negative rods [‡]	15 (5.1)	8 (53.3)	3 (20.0)	2 (13.3)	1 (6.7)	1 (6.7)	–	–
Gram-positive cocci	<i>Enterococcus</i> spp.	25 (8.4)	16 (64.0)	4 (16.0)	2 (8.0)	–	3 (12.0)	–	–
	<i>Streptococcus</i> spp.	11 (3.7)	3 (27.3)	2 (18.2)	2 (18.2)	–	–	1 (9.1)	3 (27.3)
	<i>Staphylococcus aureus</i> (incl. MRSA)	11 (3.7)	1 (9.1)	2 (18.2)	3 (27.3)	1 (9.1)	1 (9.1)	1 (9.1)	2 (18.2)
	Coagulase-negative staphylococci	9 (3.0)	5 (55.6)	3 (33.3)	1 (11.1)	–	–	–	–
Yeast cells	<i>Candida albicans</i>	40 (13.5)	22 (55.0)	5 (12.5)	4 (10.0)	1 (2.5)	2 (5.0)	4 (10.0)	2 (5.0)
	Other yeasts	3 (1.0)	–	–	–	–	–	–	3 (100)
Total		297 (100)							
ESKAPEE pathogens[‡]		201 (67.7)	122 (60.7)	30 (14.9)	24 (11.9)	9 (4.5)	10 (5.0)	4 (2.0)	2 (1.0)
[‡] Other gram-negative rods comprised <i>Providencia</i> spp. (n = 4), <i>Pseudomonas</i> spp. (non-aeruginosa, n = 4), <i>Serratia</i> spp. (n = 2), <i>Morganella morganii</i> (n = 2), <i>Salmonella</i> spp. (n = 1), <i>Stenotrophomonas maltophilia</i> (n = 1), and one unspciated gram-negative bacillus. [§] ESKAPEE pathogens were defined as <i>E. coli</i> , <i>K. pneumoniae</i> , <i>P. aeruginosa</i> , <i>Acinetobacter</i> spp., <i>Enterobacter</i> spp., <i>Enterococcus</i> spp., and <i>S. aureus</i> (including MRSA). Species-level identification for <i>Acinetobacter</i> was not consistently available.									

Gram-negative bacilli dominated the microbial profile (198/297; 66.7%), followed by gram-positive cocci (56/297; 18.9%) and *Candida albicans* (40/297; 13.5%). *Escherichia coli* was the single most common pathogen (101/297; 34.0%), with most isolates (81/101; 80.2%) recovered from urine. *Klebsiella* spp. (combining *K. pneumoniae* and other *Klebsiella* spp.) were the second most common gram-negative group (32/297; 10.8%). Among gram-positive organisms, *Enterococcus* spp. were most prevalent (25/297; 8.4%) and were also predominantly recovered from urine (16/25; 64.0%). Overall, ESKAPEE pathogens (as defined in Methods) accounted for 201 of 297 isolates (67.7%), of which 122 (60.7%) were recovered from urine specimens.

Predictors of antimicrobial resistance

Age, sex, cancer stage, and gram-stain classification were not significantly associated with MDR in unadjusted analyses (Table 3). Outpatient status showed a significant unadjusted association with resistance (41.7% versus 22.2% among non-resistant cases; p = 0.041). Infection type showed the strongest unadjusted association (p = 0.006); UTIs accounted for 63.8% of all MDR cases.

Table 3
Variables associated with multidrug resistance (MDR) among cancer patients with bacterial infection, King Faisal Hospital, Kigali, Rwanda, 2019–2024.

Feature	Category	MDR (n = 218)	Non-MDR (n = 36)	Unadj. p	aOR (95% CI)	Adj. p
Age, median (IQR)	—	59 (21)	59 (22)	0.556	1.03 (0.72–1.49)	0.869
Sex	Female	80 (36.7%)	18 (50.0%)	0.182	0.68 (0.32–1.45)	0.323
	Male (ref)	138 (63.3%)	18 (50.0%)		Ref.	
Treatment setting	Outpatient	91 (41.7%)	8 (22.2%)	0.041*	1.42 (0.56–3.63)	0.461
	Inpatient (ref)	127 (58.3%)	28 (77.8%)		Ref.	
Cancer stage	I (ref)	3 (1.6%)	2 (7.4%)	0.135	— [‡]	
	II	30 (16.1%)	4 (14.8%)		— [‡]	
	III	48 (25.8%)	10 (37.0%)		— [‡]	
	IV	105 (56.5%)	11 (40.7%)		— [‡]	
Infection type	UTI (ref)	139 (63.8%)	11 (30.6%)	0.006**	Ref.	
	BSI	30 (13.8%)	10 (27.8%)		0.29 (0.11–0.81)	0.019*
	RTI	13 (6.0%)	3 (8.3%)		0.45 (0.10–1.99)	0.283
	SSTI	30 (13.8%)	10 (27.8%)		0.30 (0.11–0.81)	0.018*
	GI/other	6 (2.8%)	2 (5.6%)		0.25 (0.05–1.43)	0.117
Gram stain	Gram-positive	43 (19.7%)	10 (27.8%)	0.379	1.16 (0.51–2.65)	0.723
	Gram-negative (ref)	175 (80.3%)	26 (72.2%)		Ref.	
Continuous variables are presented as median (interquartile range); categorical variables are presented as frequency (%). Unadj. p = unadjusted p-value (chi-squared test for categorical variables; Mann–Whitney U test for age). aOR = adjusted odds ratio from multivariable logistic regression (n = 254 bacterial isolates), adjusted simultaneously for age (standardised), sex, treatment setting, gram-stain category, and infection type. Ref. = reference category (aOR = 1.00 by definition). Adj. p = adjusted p-value from the regression model. [‡] Cancer stage was excluded from the regression model owing to 49 missing values (16.5%). * p < 0.05; ** p < 0.01. A sensitivity analysis restricted to the first bacterial episode per patient (n = 246) yielded essentially identical estimates (see Results).						

In multivariable logistic regression (n = 254 bacterial isolates), infection type was the only independent predictor of MDR after mutual adjustment. Compared with UTI (reference), bloodstream infection (aOR 0.29, 95% CI 0.11–0.81, p = 0.019) and skin and soft tissue infection (aOR 0.30, 95% CI 0.11–0.81, p = 0.018) were associated with significantly lower odds of resistance, confirming that UTIs carry a disproportionate MDR burden in this cohort. Age, sex, gram stain, and treatment setting were not independently associated with MDR after adjustment. The unadjusted association between outpatient status and MDR was fully attenuated after adjustment for infection type (adjusted p = 0.461), indicating confounding by infection type rather than a direct effect of care setting. A sensitivity analysis restricted to the first bacterial episode per patient (n = 246) yielded essentially identical estimates (BSI versus UTI: aOR 0.28, 95% CI 0.10–0.79, p = 0.016; SSTI versus UTI: aOR 0.29, 95% CI 0.10–0.80, p = 0.015), suggesting that the findings are not driven by within-patient clustering.

Resistance patterns

Resistance among WHO priority pathogens was substantial (see Additional file 1 for the full breakdown by priority category). Within the WHO *critical-priority* group, carbapenem-resistant *Acinetobacter* was identified in 61.5% (8/13) of isolates (the small denominator results in wide uncertainty around this estimate); carbapenem-resistant *Pseudomonas* in 26.1% (6/23), and carbapenem-resistant

Enterobacterales in 6.9% (11/159). Among *high-priority* pathogens, MRSA was identified in 36.4% (4/11) of *S. aureus* isolates and no vancomycin-resistant enterococci were detected (0/25).

Among gram-negative bacilli (Table 4), ceftriaxone resistance was high: *E. coli* 64.4%, *Enterobacter* spp. 75.0%, *Providencia* spp. 75.0%, and *Klebsiella* spp. 55.6%. Trimethoprim–sulfamethoxazole resistance was similarly high, particularly in *E. coli* (67.3%). Fluoroquinolone resistance ranged from 20.0% in *Proteus* spp. to 75.0% in *Providencia* spp. Carbapenem resistance was most pronounced in *Acinetobacter* spp. (meropenem 61.5%; imipenem 53.8%), with clinically relevant meropenem resistance also observed in *Pseudomonas aeruginosa* (31.6%).

Table 4

Antibiotic resistance patterns among gram-negative rods isolated from cancer patients, King Faisal Hospital, Kigali, Rwanda, 2019–2024. Values are number of resistant isolates (% of tested) unless otherwise indicated.

Antibiotic agent	<i>E. coli</i>	<i>Klebsiella</i> spp.	<i>P. aeruginosa</i>	<i>Acinetobacter</i>	<i>Proteus</i>	<i>Enterobacter</i>	Other GNR	<i>Providencia</i>	<i>Salmonella</i>
Ceftriaxone	65 (64.4)	20 (55.6)	R ^a	7 (53.8)	4 (40.0)	6 (75.0)	2 (33.3)	3 (75.0)	1 (100)
TMP/SMX (co-trimoxazole)	68 (67.3)	19 (52.8)	R ^a	4 (30.8)	4 (40.0)	4 (50.0)	4 (66.7)	3 (75.0)	1 (100)
Cefuroxime	59 (58.4)	19 (52.8)	R ^a	R ^a	5 (50.0)	4 (50.0)	4 (100)	–	1 (100)
Ampicillin	65 (64.4)	R ^a	R ^a	R ^a	3 (30.0)	R ^a	4 (66.7)	R ^a	–
Levofloxacin	45 (44.6)	12 (33.3)	7 (36.8)	6 (46.2)	2 (20.0)	2 (25.0)	3 (50.0)	3 (75.0)	–
Amoxicillin–clavulanate	41 (40.6)	17 (47.2)	R ^a	R ^a	2 (20.0)	R ^a	3 (50.0)	R ^a	–
Ciprofloxacin	30 (29.7)	10 (27.8)	7 (36.8)	9 (69.2)	2 (20.0)	3 (37.5)	2 (33.3)	3 (75.0)	–
Cefepime	33 (32.7)	12 (33.3)	2 (10.5)	5 (38.5)	3 (30.0)	3 (37.5)	2 (33.3)	3 (75.0)	1 (100)
Gentamicin	34 (33.7)	14 (38.9)	2 (10.5)	5 (38.5)	1 (10.0)	2 (25.0)	4 (66.7)	R ^a	1 (100)
Cefotaxime	24 (23.8)	12 (33.3)	R ^a	2 (15.4)	1 (10.0)	4 (50.0)	4 (66.7)	3 (75.0)	1 (100)
Amoxicillin	27 (26.7)	R ^a	R ^a	R ^a	1 (10.0)	R ^a	2 (33.3)	R ^a	–
Piperacillin–tazobactam	24 (23.8)	10 (27.8)	3 (15.8)	3 (23.1)	1 (10.0)	3 (37.5)	1 (16.7)	3 (75.0)	–
Aztreonam	24 (23.8)	7 (19.4)	3 (15.8)	R ^a	–	3 (37.5)	1 (16.7)	–	1 (100)
Nitrofurantoin	21 (20.8)	3 (8.3)	R ^a	–	R ^a	–	–	R ^a	–
Amikacin	9 (8.9)	3 (8.3)	6 (31.6)	5 (38.5)	–	1 (12.5)	1 (16.7)	–	–
Norfloxacin	23 (22.8)	3 (8.3)	6 (31.6)	8 (61.5)	–	1 (12.5)	–	–	–
Meropenem	1 (1.0)	2 (5.6)	6 (31.6)	8 (61.5)	–	1 (12.5)	–	–	–
Imipenem	2 (2.0)	1 (2.8)	5 (26.3)	7 (53.8)	–	–	–	–	–
Ceftazidime	12 (11.9)	6 (16.7)	6 (31.6)	3 (23.1)	–	–	–	–	–

^a R indicates intrinsic resistance and is not reported as a percentage. TMP/SMX, trimethoprim–sulfamethoxazole; GNR, gram-negative rods.

Among gram-positive cocci (Table 5), trimethoprim–sulfamethoxazole resistance was high in *S. aureus* (63.6%). Erythromycin resistance affected 44.0% of *Enterococcus* isolates and more than one third of *S. aureus* isolates. Chloramphenicol retained good in vitro activity across gram-positive isolates, with resistance rates of 8.0% in *Enterococcus* spp. and 9.1% in *S. aureus*.

Table 5

Antibiotic resistance patterns among gram-positive cocci isolated from cancer patients, King Faisal Hospital, Kigali, Rwanda, 2019–2024. Values are number of resistant isolates (% of tested).

Antibiotic agent	<i>Enterococcus</i> spp. N (%)	<i>Staphylococcus aureus</i> (incl. MRSA) N (%)	<i>Streptococcus</i> spp. (incl. α -HS) N (%)
TMP/SMX	R ¹⁰⁰	7 (63.6)	5 (45.5)
Erythromycin	11 (44.0)	4 (36.4)	2 (18.2)
Ampicillin	4 (16.0)	6 (54.5)	2 (18.2)
Clindamycin	R ¹⁰⁰	1 (9.1)	1 (9.1)
Oxacillin	–	4 (36.4)	–
Doxycycline	9 (36.0)	1 (9.1)	–
Gentamicin	R ¹⁰⁰	1 (9.1)	3 (27.3)
Tetracyclines	5 (20.0)	1 (9.1)	1 (9.1)
Cefazolin	R ¹⁰⁰	–	2 (18.2)
Cefuroxime	R ¹⁰⁰	–	1 (9.1)
Penicillins (combined)	5 (20.0)	3 (27.3)	–
Ofloxacin	R ¹⁰⁰	2 (18.2)	2 (18.2)
Cephalexin	R ¹⁰⁰	–	2 (18.2)
Chloramphenicol	2 (8.0)	1 (9.1)	2 (18.2)
Norfloxacin	4 (16.0)	–	1 (9.1)
Ciprofloxacin	2 (8.0)	3 (27.3)	1 (9.1)
Nitrofurantoin	3 (12.0)	–	–
Amoxicillin–clavulanate	1 (4.0)	1 (9.1)	1 (9.1)
Levofloxacin	1 (4.0)	–	1 (9.1)

¹⁰⁰ R indicates intrinsic resistance and is not reported as a percentage. TMP/SMX, trimethoprim–sulfamethoxazole; α -HS, alpha-haemolytic streptococci; MRSA, methicillin-resistant *S. aureus*.

Empirical treatment and guideline adherence

A documented empirical antibiotic regimen was available in the EMR for 105 of 297 episodes (35.4%). EMR capture was markedly asymmetric: 52.1% of inpatient episodes (100/192) had a documented regimen, compared with only 4.8% of outpatient episodes (5/105); outpatient empirical therapy was therefore systematically under-captured, although clinical practice suggests antibiotics were administered in most such encounters. A total of 19 different antibiotic agents were prescribed empirically in the 105 documented episodes; the complete distribution by WHO AWaRe category is provided in Additional file 2. Watch-group antibiotics predominated; ceftriaxone was the most frequently prescribed agent (54/105; 51.4%), followed by meropenem (14/105; 13.3%) and ciprofloxacin (6/105; 5.7%). Access-group antibiotics accounted for a notable proportion, with metronidazole (12/105; 11.4%) the most commonly prescribed, followed by amoxicillin–clavulanate (7.6%). Use of Reserve-group agents was minimal (polymyxin B, 1.0%).

Within this predominantly inpatient subset, adherence to both WHO AWaRe and the 2022 Rwanda Standard Treatment Guidelines was assessed; adherence was defined as the selection of an empirical antibiotic consistent with the recommended agent(s) for the identified infection site. The two frameworks differ substantially: while the WHO AWaRe classification broadly endorses Watch-category agents such as ceftriaxone for common infections, the Rwanda national guidelines specify narrower, pathogen-directed first-line choices. WHO AWaRe-based adherence ranged from 65.1% for UTIs to 78.6% for BSIs (Table 6). Adherence to national guidelines was substantially lower across all infection types: 32.1% for BSIs, 50.0% for RTIs, 17.4% for SSTIs, and only 2.3% for UTIs. The association between infection type and national-guideline adherence was statistically significant ($p = 0.001$). Laboratory turnaround time had a median of 2 days (IQR 2 days), with 75% of results available within 4 days of sampling.

Discussion

This retrospective study of 297 infection episodes among cancer patients at a tertiary referral hospital in Rwanda describes a substantial burden of antimicrobial resistance with direct clinical implications. UTIs were the predominant infection diagnosis (57.9%) and showed a high proportion of MDR isolates (63.8% of all MDR cases). *E. coli* was the single most common pathogen (34.0%), and ESKAPEE organisms comprised 67.7% of all isolates. Ceftriaxone resistance was high across multiple Enterobacterales (*E. coli* 64.4%, *Enterobacter* spp. 75.0%, *Klebsiella* spp. 55.6%), and carbapenem resistance in *Acinetobacter* spp. reached 61.5% in a small subset of isolates. Empirical prescribing frequently diverged from national guidance ($p = 0.001$). In multivariable analysis, infection type was the only independent predictor of MDR, with UTIs carrying the highest resistance burden. An unadjusted association between outpatient status and MDR was fully explained by confounding with infection type, and the sensitivity analysis indicated that the findings were not driven by within-patient clustering.

The predominance of gram-negative organisms (66.7%) is consistent with previous reports from Rwanda and with oncology-based series in other LMICs and high-income settings, in which rising ESBL- and carbapenem-resistant phenotypes are increasingly reported among immunocompromised hosts. The large share of ESKAPEE pathogens points to an elevated risk of difficult-to-treat infections in oncology populations. Comparison with earlier Rwandan data must, however, be made cautiously, because our cohort comprises a specific oncology subgroup whereas earlier figures derive from all medical-ward cultures at a different hospital. Third-generation cephalosporin resistance in *E. coli* reached 64.4% in our cohort, higher than the 31.4% reported by Ntirenganya and colleagues at Kigali University Teaching Hospital in 2015 [14], while the *Klebsiella* spp. figure (55.6%) is comparable to the 58.7% reported a decade ago. Notably, recent hospital-wide King Faisal Hospital data from 2024 and 2025 indicate *E. coli* ceftriaxone resistance of approximately 40–45%, suggesting that the higher resistance observed in the present study reflects the oncology subgroup studied rather than a uniform hospital-wide increase over time. Sutherland and colleagues likewise described widespread resistance in a Rwandan referral hospital in 2019 [24]. The high ceftriaxone resistance we observed is also consistent with regional studies from Uganda, Ethiopia, and Zimbabwe [27–29] and calls into question the use of third-generation cephalosporins as first-line empirical therapy in settings with high ESBL prevalence [20, 30]. The 2022 Rwanda Standard Treatment Guidelines recommend ceftriaxone as first-line therapy for several common infections, including hospital-acquired UTIs and BSIs [16]; the resistance rates observed here therefore directly undermine the national empirical prescribing framework for the oncology population studied.

The substantial carbapenem non-susceptibility observed in *Acinetobacter* spp. (8/13 isolates; 61.5%) raises serious therapeutic and infection-control concerns given the limited effective alternatives and the toxicity and costs of available last-resort drugs such as polymyxins. The small denominator ($n = 13$) limits the precision of this estimate, with a wide 95% confidence interval (approximately 33–85%), and the finding should be confirmed in larger samples, ideally through coordinated multi-centre surveillance.

The apparent unadjusted association between outpatient status and MDR ($p = 0.041$) was fully explained by confounding with infection type (adjusted $p = 0.461$): UTIs were disproportionately frequent among outpatients and disproportionately likely to be MDR. This contrasts with a recent multi-country African study in which inpatients carried higher adjusted odds of resistance (adjusted OR 1.24, $p < 0.0001$) [31], and illustrates the importance of multivariable methods when interpreting setting-based associations in oncology AMR data.

Clinical and public health implications

Empirical antibiotic protocols require urgent revision. Because ceftriaxone, the single most frequently prescribed empirical agent in our cohort (51.4%), was inactive in vitro against the majority of *E. coli* (64.4%), *Klebsiella* spp. (55.6%), and *Enterobacter* (75.0%) isolates, continued empirical reliance on third-generation cephalosporins for hospital-managed oncology UTIs is unlikely to achieve adequate microbiological coverage. Empirical regimens should be revised on the basis of locally stratified antibiograms that account for treatment setting, recent antibiotic exposure, and catheterisation status, with carbapenem-sparing alternatives such as piperacillin–tazobactam (*E. coli* resistance 23.8% in our data) considered as first-line for hospitalised oncology UTI pending culture confirmation.

Antimicrobial stewardship should align with WHO AWaRe principles. The high reliance on Watch-group agents and the markedly low adherence to national guidance, particularly for UTIs (2.3%), identify concrete targets for stewardship intervention: prescribing audits with feedback, clinical decision-support integration in the EMR, formulary restrictions on key broad-spectrum agents, and prescriber education specifically tailored to oncology contexts.

UTI management pathways in oncology require optimisation. Given the preponderance of UTIs in our cohort and their disproportionate MDR burden, targeted measures are warranted. These include minimisation of unnecessary urinary catheter use, aseptic insertion and

maintenance technique, mandatory pre-treatment urine culture, and susceptibility-guided intravenous-to-oral step-down, all of which could reduce both selection pressure and clinical morbidity.

Infection prevention and control should target ESKAPEE pathogens. The high proportion of ESKAPEE organisms (67.7%), and the carbapenem non-susceptibility observed in *Acinetobacter* spp. in particular, call for intensified transmission-based (horizontal) measures applied uniformly to all patients. These include strict hand hygiene observance across the WHO Five Moments for Hand Hygiene, enhanced cleaning of high-touch surfaces in oncology wards, and systematic implementation of catheter and central-line care bundles. Pathogen-specific (vertical) strategies such as active surveillance cultures and contact precautions for confirmed MDR carriers warrant consideration in this high-risk population.

Electronic medical record capture of empirical prescribing must be improved. Empirical regimens were recorded in the EMR for only 4.8% of outpatient encounters in this cohort, compared with 52.1% of inpatient encounters. This gap represents a major blind spot for stewardship and surveillance. Standardised structured fields for empirical antibiotic indication, agent, dose, and duration should be introduced for both inpatient and outpatient encounters, ideally with prompts triggered at the point of prescribing. Reliable EMR capture is a prerequisite for any meaningful audit of community-level prescribing practice in this population.

Microbiology capacity and surveillance integration must be strengthened. Consistent susceptibility testing with internal and external quality assurance, timely reporting, and integration of oncology-unit isolate data into national AMR surveillance will enable more responsive, evidence-based updates to national prescribing guidance, and will help close the persistent LMIC oncology data gap.

Limitations

Several limitations should be considered when interpreting these findings. First, the retrospective, single-centre design and reliance on culture-positive cases drawn from electronic medical records may underrepresent culture-negative infections and may not always distinguish true infection from asymptomatic colonisation, particularly for urine and respiratory samples. Differentiation in this study relied on documented clinical features in combination with positive culture; standardised symptom-based criteria were not consistently available in the source records. Second, because we sampled only culture-positive infection episodes, we cannot estimate the incidence of bacterial infection or AMR in the oncology population at large, nor identify patient-level risk factors for developing a resistant rather than a susceptible infection; our findings characterise the resistance profile among culture-confirmed infections, but should not be interpreted as population-level risk estimates. Third, documentation of empirical antibiotic therapy in the EMR was incomplete and markedly asymmetric: an empirical regimen was recorded for 52.1% of inpatient episodes (100/192) but for only 4.8% of outpatient episodes (5/105), despite a strong clinical likelihood that antibiotics were administered at the point of care. As a result, the adherence analyses presented here should be interpreted as reflecting predominantly inpatient prescribing practice, and the true patterns of outpatient empirical therapy in this cohort could not be evaluated. Improved structured EMR capture of empirical prescribing for both inpatients and outpatients is therefore a prerequisite for any thorough future stewardship assessment in this setting. Fourth, data on prior outpatient antibiotic exposure, indwelling-device duration, and clinical outcomes (mortality attributable to resistant infection, length of stay, delays in cancer therapy) were incomplete and warrant prospective collection. Fifth, CLSI breakpoints in force at the time of testing were used as recorded, without retrospective reclassification against updated breakpoints; changes in breakpoint definitions over the 6-year study period, particularly for carbapenems and polymyxins, could have introduced temporal variation in resistance categorisation. Finally, eleven patients contributed two infection episodes each; while a sensitivity analysis restricted to the first episode per patient confirmed the stability of the main multivariable findings, residual within-patient clustering cannot be entirely excluded.

Prospective, multi-centre cohort studies enrolling consecutive oncology admissions at presentation, regardless of subsequent infection status, are required to quantify the true incidence of resistant infection and to identify patient-level and treatment-related risk factors. Molecular epidemiological investigations into resistance mechanisms (ESBL genotypes, carbapenemases, plasmid-mediated transfer) would further inform targeted infection prevention and containment strategies. Despite these limitations, our study provides a contemporary snapshot of AMR in an oncology population in Rwanda through December 2024 and offers concrete data for empirical prescribing and stewardship in this setting.

Conclusions

In this cohort of Rwandan cancer patients with culture-confirmed infection, multidrug resistance was common, particularly among UTI pathogens and ESKAPEE organisms. Ceftriaxone, the most frequently prescribed empirical agent, showed limited in vitro activity against the prevailing isolates. Immediate priorities include revision of empirical UTI regimens for hospitalised oncology patients away from third-generation cephalosporins, mandatory pre-treatment cultures, infection-prevention measures targeted at ESKAPEE pathogens, structured

EMR capture of empirical prescribing for both inpatients and outpatients, and integration of King Faisal Hospital oncology data into the Rwandan AMR surveillance system. Such measures are needed to preserve effective therapeutic options for cancer patients and to limit the further expansion of antimicrobial resistance in this vulnerable population.

Abbreviations

AMR	antimicrobial resistance
aOR	adjusted odds ratio
AST	antimicrobial susceptibility testing
AWaRe	Access, Watch, Reserve
BSI	bloodstream infection
CI	confidence interval
CLSI	Clinical and Laboratory Standards Institute
CRE	carbapenem-resistant Enterobacterales
EMR	electronic medical records
ESBL	extended-spectrum β -lactamase
ESKAPEE	Enterococcus, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter spp., Pseudomonas aeruginosa, Enterobacter spp., Escherichia coli
GI	gastrointestinal
IQR	interquartile range
IRB	Institutional Review Board
KFH	King Faisal Hospital
LMIC	low- and middle-income country
MDR	multidrug resistance/resistant
MRSA	methicillin-resistant Staphylococcus aureus
RTI	respiratory tract infection
SSTI	skin and soft tissue infection
STROBE	Strengthening the Reporting of Observational Studies in Epidemiology
TMP/SMX	trimethoprim–sulfamethoxazole
UTI	urinary tract infection

Declarations

Ethics approval and consent to participate

Ethical approval was obtained from the Institutional Review Board of King Faisal Hospital (protocol KFH/2025/291/IRB) and the Ethics Committee of the University of Freiburg (reference EK-Freiburg 25-1122-S2). Given the retrospective, pseudonymised nature of the dataset, the requirement for individual written informed consent was waived by both ethics committees.

Consent for publication

Not applicable. No individually identifying information is presented in this manuscript.

Availability of data and materials

The pseudonymised dataset supporting the findings of this study is not publicly available because of restrictions imposed by the King Faisal Hospital Institutional Review Board, but is available from the corresponding author on reasonable request and subject to applicable data-sharing agreements.

Competing interests

The authors declare that they have no competing interests.

Funding

This study received no specific grant from any funding agency in the public, commercial, or not-for-profit sectors. B.N. Asuman was supported by a personal scholarship from the German Academic Exchange Service (DAAD) covering travel costs associated with this project; the DAAD had no role in study design, data collection, analysis, interpretation, or manuscript preparation.

Authors' contributions

B.N.A. conceptualised the study, collected and analysed the data, and drafted the manuscript. D.D. contributed to study design, facilitated clinical data access, and critically reviewed the manuscript. M.J.K. supervised microbiological data collection and interpretation and reviewed the manuscript. K.S. and S.G. contributed to data interpretation and manuscript revision. H.J.G. contributed to conceptualising the study and to manuscript revision. V.M.E. conceptualised and supervised the study, contributed to data interpretation, and critically revised the manuscript. All authors read and approved the final version of the manuscript.

Acknowledgements

We thank the staff of the King Faisal Hospital oncology unit and microbiology laboratory for their support of this work, and the German Academic Exchange Service (DAAD) for supporting B.N. Asuman through a personal scholarship.

References

1. Centers for Disease Control and Prevention. Antibiotic resistance threats in the United States, 2019. Atlanta: Centers for Disease Control and Prevention; 2019.
2. Murray CJL, Ikuta KS, Sharara F, Swetschinski LR, Robles Aguilar G, Gray A, et al. Global burden of bacterial antimicrobial resistance in 2019: a systematic analysis. *Lancet*. 2022;399:629–55.
3. Naghavi M, Vollset SE, Ikuta KS, Swetschinski LR, Gray AP, Wool EE, et al. Global burden of bacterial antimicrobial resistance 1990–2021: a systematic analysis with forecasts to 2050. *Lancet*. 2024;404:1199–226.
4. Zembower TR. Epidemiology of infections in cancer patients. In: Stosor V, Zembower TR, editors. *Infectious complications in cancer patients*. Cancer treatment and research. Volume 161. Cham: Springer; 2014. pp. 43–89.
5. Park SY, Kim MS, Eom JS, Lee JS, Rho YS. Risk factors and etiology of surgical site infection after radical neck dissection in patients with head and neck cancer. *Korean J Intern Med*. 2015;31:162–9.

6. Alonso CD, Marr KA. Clostridium difficile infection among hematopoietic stem cell transplant recipients: beyond colitis. *Curr Opin Infect Dis.* 2013;26:326–31.
7. Lustberg MB. Management of neutropenia in cancer patients. *Clin Adv Hematol Oncol.* 2012;10:825–6.
8. Vento S, Cainelli F. Infections in patients with cancer undergoing chemotherapy: aetiology, prevention, and treatment. *Lancet Oncol.* 2003;4:595–604.
9. Garg VK, Mishra S, Gupta N, Garg R, Sachidanand B, Vinod KS, et al. Microbial and antibiotic susceptibility profile among isolates of clinical samples of cancer patients admitted in the intensive care unit at regional tertiary care cancer center. *Indian J Crit Care Med.* 2019;23:67–72.
10. Mohamed N, Ghazal A, Ahmed AAH, Zaki A. Prevalence and determinants of antimicrobial resistance of pathogens isolated from cancer patients in an intensive care unit in Alexandria, Egypt. *J Egypt Public Health Assoc.* 2023;98:9.
11. Lopera C, Monzó P, Aiello TF, Garcia-Vidal C, Chumbita M, Puerta-Alcalde P, et al. Prevalence and impact of multidrug-resistant bacteria in solid cancer patients with bloodstream infection: a 25-year trend analysis. *Microbiol Spectr.* 2024;12:e02961–23.
12. Nanayakkara AK, Boucher HW, Fowler VG Jr, Jezek A, Outtersen K, Greenberg DE. Antibiotic resistance in the patient with cancer: escalating challenges and paths forward. *CA Cancer J Clin.* 2021;71:488–504.
13. Perdikouri EIA, Arvaniti K, Lathyris D, Koulourida V, Apostolidou-Kiouti F, Siskou E, et al. Infections due to multidrug-resistant bacteria in oncological patients: insights from a five-year epidemiological and clinical analysis. *Microorganisms.* 2019;7:277.
14. Ntirenganya C, Manzi O, Muvunyi CM, Ogbuagu O. High prevalence of antimicrobial resistance among common bacterial isolates in a tertiary healthcare facility in Rwanda. *Am J Trop Med Hyg.* 2015;92:865–70.
15. World Health Organization. The WHO AWaRe (Access, Watch, Reserve) antibiotic book. 1st ed. Geneva: World Health Organization; 2022.
16. Ministry of Health, Rwanda. Rwanda Standard Treatment Guidelines: the guideline for the use of antibiotics in Rwanda. Kigali: Ministry of Health; 2022.
17. Igizeneza A, Bitunguhari L, Masaisa F, Uwimana M, Sebatunzi O, Mvukiyehe JP, et al. Prescription practices and usage of antimicrobials in a tertiary teaching hospital in Rwanda: a call for antimicrobial stewardship. *Antibiot (Basel).* 2024;13:1032.
18. Jiang AM, Shi X, Liu N, Zhu H, Yang C, Bai H, et al. Nosocomial infections due to multidrug-resistant bacteria in cancer patients: a six-year retrospective study of an oncology center in Western China. *BMC Infect Dis.* 2020;20:452.
19. Tadesse BT, Ashley EA, Ongarello S, Havumaki J, Wiber M, Lester R, et al. Antimicrobial resistance in Africa: a systematic review. *BMC Infect Dis.* 2017;17:616.
20. Gahimbare L, Muvunyi CM, Guessennd NAK, Musabyimana JP, Ndayisaba GF, Niyonzima FN et al. Antimicrobial resistance in the World Health Organization African region: a systematic literature review 2016–2020. *Antibiotics (Basel).* 2024;13:659.
21. Rubagumya F, Costas-Chavarri A, Manirakiza A, Murenzi G, Uwizeye FR, Shyirambere C et al. State of cancer control in Rwanda: past, present, and future opportunities. *JCO Glob Oncol.* 2020;6:GO.20.00281.
22. Magiorakos AP, Srinivasan A, Carey RB, Carmeli Y, Falagas ME, Giske CG, et al. Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: an international expert proposal for interim standard definitions for acquired resistance. *Clin Microbiol Infect.* 2012;18:268–81.
23. Rwanda Biomedical Centre. National cancer control plan 2020–2024. Kigali: Rwanda Biomedical Centre; 2020.
24. Sutherland T, Mpirimbanyi C, Nziyomaze E, Niyibizi G, Niyonsenga Z, Nzarora B, et al. Widespread antimicrobial resistance among bacterial infections in a Rwandan referral hospital. *PLoS ONE.* 2019;14:e0221121.
25. Bosco MJ, Jonas B, Evelyn K, Pauline K. Urinary tract infection and antimicrobial resistance profile in patients attending Nemba District Hospital in Rwanda. *Asian J Med Sci.* 2020;11:101–5.
26. Habyarimana T, Murenzi D, Musoni E, Yadufashije C, Niyonzima FN. Bacteriological profile and antimicrobial susceptibility patterns of bloodstream infection at Kigali University Teaching Hospital. *Infect Drug Resist.* 2021;14:699–707.
27. Lubwama M, Phipps W, Najjuka CF, Kajumbula H, Ddungu H, Kambugu JB, et al. Bacteremia in febrile cancer patients in Uganda. *BMC Res Notes.* 2019;12:464.
28. Worku M, Belay G, Tigabu A. Bacterial profile and antimicrobial susceptibility patterns in cancer patients. *PLoS ONE.* 2022;17:e0266919.
29. Chinowaita F, Chaka W, Nyazika TK, Nziramasanga P, Mhangara M, Nkavulu L, et al. Sepsis in cancer patients residing in Zimbabwe: spectrum of bacterial and fungal aetiologies and their antimicrobial susceptibility patterns. *BMC Infect Dis.* 2020;20:161.

30. Ntim OK, Awere-Duodu A, Osman AH, Donkor ES. Antimicrobial resistance of bacterial pathogens isolated from cancer patients: a systematic review and meta-analysis. BMC Infect Dis. 2025;25:296.

31. Osen G, Kapoor G, Kalanxhi E, Oyston J, Klein EY. Antimicrobial resistance in Africa: a retrospective analysis of data from 14 countries, 2016–2019. PLoS Med. 2025;22:e1004638.

Figures

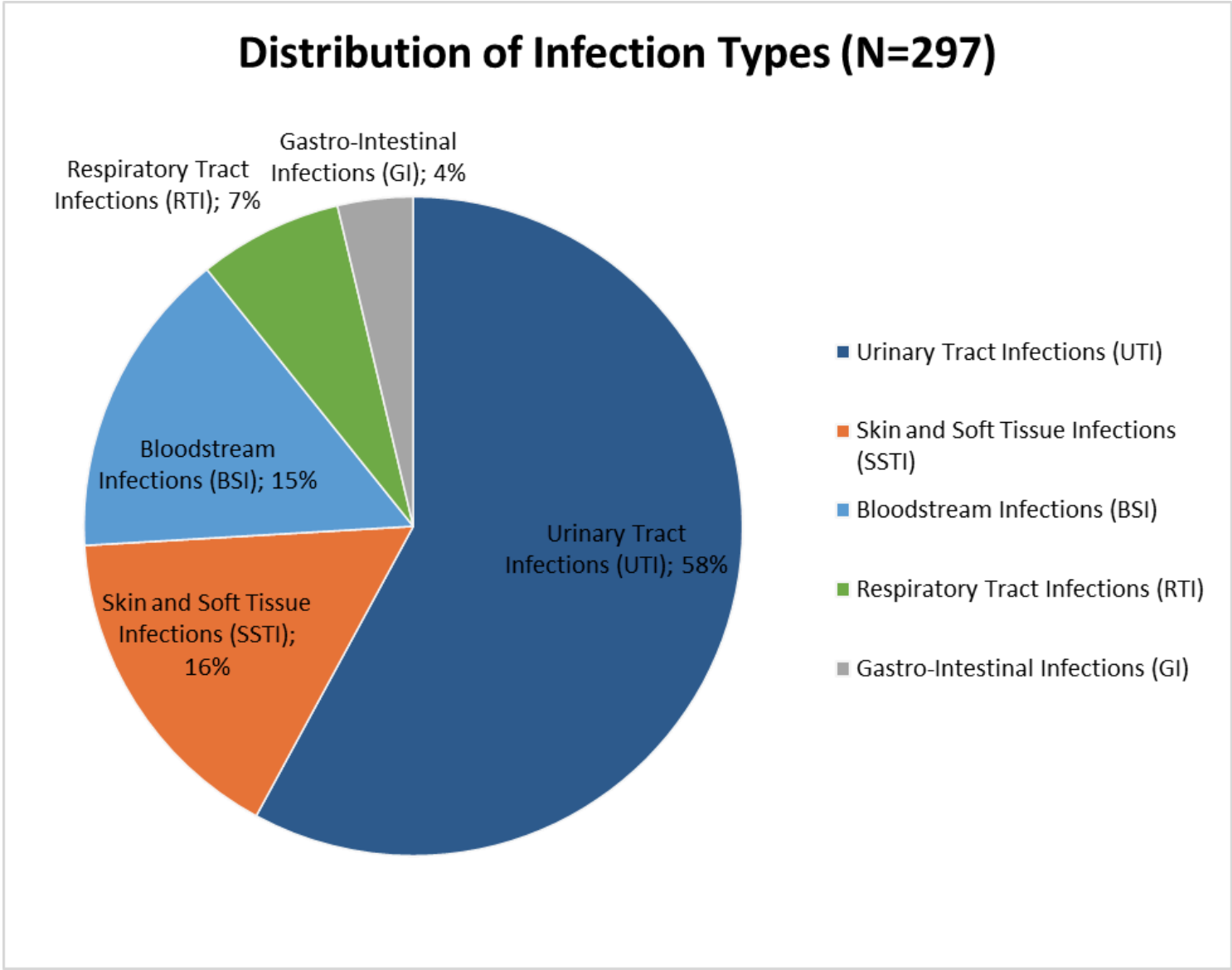


Figure 1

Distribution of infection types among cancer patients with culture-confirmed infections at King Faisal Hospital, Kigali, Rwanda, 2019–2024 (n = 297).

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- [AdditionalfilesBMC.docx](#)