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# Five-year antimicrobial resistance trends and facility antibiogram at Dodoma Regional Referral Hospital, Tanzania: a retrospective study (2018–2023)

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## Abstract

**Background:**

Antimicrobial resistance (AMR) represents an escalating public health crisis, disproportionately affecting low- and middle-income countries where empirical prescribing and limited diagnostic capacity drive inappropriate therapy. No published longitudinal antibiogram data exist for Dodoma Regional Referral Hospital, leaving clinicians reliant on uninformed empirical prescribing. This study characterized AMR patterns and antibiogram trends among bacterial isolates at Dodoma Regional Referral Hospital (DRRH), Tanzania.

**Methods:**

A hospital-based retrospective study was conducted using Laboratory records covering 363 culture-positive bacterial isolates from January 2018 to May 2023 were extracted using a structured checklist and analyzed following Clinical and Laboratory Standards Institute guidelines (CLSI) guidelines. Antimicrobial Susceptibility Testing (AST) followed CLSI data were analyzed using SPSS version 25, with chi-square to identify significant resistance associations at 0.05 significance level.

**Results:**

Among 363 bacterial isolates generating 591 resistance events, Staphylococcus aureus (41.6%) and Escherichia coli (32.8%) predominated. Resistance burden peaked in 2022 (26.2%) and 2020 (20.6%). Among Gram-negative isolates, ceftazidime resistance was disproportionately elevated in blood p = 0.01), while ciprofloxacin resistance predominated in urine (p = 0.02). Enterobacter spp. showed significantly higher ceftriaxone resistance than expected (p =0.02), whereas E. coli contributed 52 resistant isolates each for gentamicin and ciprofloxacin. Meropenem retained near-complete activity (99.5%).

Among Gram-positive isolates, clindamycin resistance was most strongly specimen-associated ($\chi^2 = 13.71$; $p < 0.01$), with gentamicin ($\chi^2 = 8.06$; $p = 0.02$) and cefoxitin ($\chi^2 = 5.66$; $p = 0.03$) resistance also significantly specimen-dependent. Ciprofloxacin resistance remained persistently elevated across all years, peaking at 29.5% in 2020.

**Conclusion:**

Significant, specimen- and organism-dependent AMR was demonstrated across common pathogens at DRRH. Ciprofloxacin and gentamicin resistance warrant prioritization in facility stewardship protocols, while carbapenem preservation should be actively monitored. Additionally, these findings underscore the urgent need for continuous surveillance and facility-specific antibiograms to guide empirical therapy and reinforce stewardship programs in Tanzania.


## Background

Antimicrobial resistance (AMR) represents one of the gravest public health threats of the 21st century(1). An estimated 4.95 million deaths were associated with bacterial AMR globally in 2019, including 1.27 million deaths directly attributable to resistant infections (2), surpassing HIV/AIDS and malaria as a cause of death. Projections warn that AMR could kill 10 million people annually by 2050(2), while current excess inpatient healthcare expenditure attributable to AMR is estimated at $66.4 billion per year, driven by 25.4 million AMR-related hospital admissions annually, 3.5% of all global admissions(3). Six leading pathogens, E. coli, S. aureus, K. pneumoniae, S. pneumoniae, A. baumannii, and P. aeruginosa, collectively accounted for 929,000 attributable AMR deaths, with MRSA alone responsible for over 100,000 deaths in 2019(2).

The burden falls most heavily on vulnerable populations and low-income settings(4). In the WHO African region, over 1.05 million deaths were associated with AMR and 250,000 were directly attributable to resistant infections in 2019, exceeding deaths from both HIV/AIDS (639,554) and malaria (594,348)(4). Sub-Saharan Africa recorded the highest AMR mortality rate globally at 23.5 deaths per 100,000 population, with western sub-Saharan Africa reaching 27.3 deaths per 100,000(5). Economically, patients with resistant infections cost more than twice as much to treat, exceeding US$20,000 per case versus US$10,000 for susceptible infections, with an average excess of 7.4 inpatient days and a nearly 50% higher readmission rate(2, 6). The World Bank estimates AMR could generate US$1 trillion in additional healthcare costs and GDP losses of up to US$3.4 trillion per year by 2030(7). Within this regional burden, Tanzania, a lower-middle-income country with high infectious disease prevalence, faces compounded challenges from limited diagnostic infrastructure and reliance on empirical prescribing.

Despite global, African, and national responses, including the WHO Global Action Plan on AMR, the GLASS surveillance framework, and Tanzania's second National Action Plan on AMR (2023–2028), the problem persists due to deep structural gaps(8). As of 2023, 26 of 46

WHO African region countries have no national system for monitoring antimicrobial consumption, and only 5 countries regularly monitor consumption in a representative sample of facilities(9). In Tanzania, only 35.9% of surveyed health facilities had implemented any antimicrobial stewardship program, only 17.9% conducted microorganism susceptibility testing, and merely 15.4% had a hospital antibiotic policy document(10). Compounding this, across six Tanzanian referral hospitals, 62.3% of inpatients were prescribed antibiotics empirically, and only 2 of 591 patients received antibiotics guided by culture and susceptibility testing results(11).

Failure to address AMR jeopardizes the 2030 SDGs across multiple goals. AMR could push 28.3 million people into extreme poverty by 2050, reduce global economic output by 1–3% by 2030, and cost up to US$3.4 trillion annually(12). SDG 1, SDG 2, SDG 3, and SDG 8 are all directly threatened, as AMR escalates healthcare costs, reduces agricultural productivity, undermines universal health coverage, and depresses labor supply(13).

Dodoma Regional Referral Hospital generates a substantial volume of microbiological data that has not been systematically analyzed to reveal longitudinal resistance trends, a gap that leaves clinicians reliant on uninformed empirical prescribing. Few sentinel sites in Tanzania have the trained staff capacity to produce and share antibiograms with clinical and AMR teams(14). This five-year retrospective study (2018–2023) therefore addresses a critical evidence gap, generating institution-specific antibiogram trends to guide empirical treatment protocols, support antimicrobial stewardship at Dodoma Regional Referral Hospital, and contribute locally grounded data to Tanzania's national and global AMR response.

## Methods

# 3.1. Study design and setting

A hospital-based retrospective study was conducted using laboratory records from January 2018 to May 2023 at Dodoma Regional Referral Hospital (DRRH) in Dodoma, Tanzania. DRRH is a regional referral and teaching hospital with approximately 420 beds, serving about 150,000 patients annually, including referrals from surrounding district and primary healthcare facilities.

# 3.2. Study population

All culture-positive bacterial isolates processed at the DRRH laboratory during the study period were included; isolates with complete susceptibility results were retained, while duplicates, contaminated cultures, and incomplete records were excluded. Duplicate isolates were defined as repeated recovery of the same organism from the same patient within a 30-day period; only the first isolate per patient-episode was included in resistance calculations.

# 3.3. Data collection

Data were extracted from the laboratory information system using a structured checklist, capturing the date of antimicrobial susceptibility testing (AST), specimen type (blood, urine, sputum, others), bacterial species (Gram positive or negative), and susceptibility results (resistant or sensitive). All specimens were processed according to Clinical and Laboratory Standards Institute guidelines (CLSI M100, 30th edition, 2020), with quality control performed using *E. coli* ATCC 25922 and *S. aureus* ATCC 25923 reference strains.

Antibiotics tested were based on the Standard Treatment Guidelines and National Essential Medicines List (STG/NEMLIT). For Gram-negative isolates, these included ceftriaxone (30 µg), cefotaxime (30 µg), ceftazidime (30 µg), meropenem (10 µg), gentamicin (10 µg), ciprofloxacin (5 µg), and ampicillin (10 µg). For Gram-positive isolates, cefoxitin (30 µg), erythromycin (15 µg), gentamicin (10 µg), ciprofloxacin (5 µg), clindamycin (2 µg), and co-trimoxazole (1.25/23.75 µg) were tested. Vancomycin resistance was confirmed using MIC methods with a breakpoint of ≥ 16 µg/mL (resistant) per CLSI guidelines. Isolates with intermediate MIC values (4–8 µg/mL) were classified separately as vancomycin-intermediate S. aureus (VISA).

# 3.4. Data analysis

Data were analyzed using IBM SPSS Statistics version 25. Categorical variables (specimen type: blood, urine, sputum; bacterial species: Escherichia coli, Enterobacter spp., Klebsiella oxytoca, Klebsiella pneumoniae, Acinetobacter spp., Staphylococcus aureus; antimicrobial susceptibility results: resistant, sensitive) were summarized using frequencies and percentages. Antimicrobial susceptibility was recorded as a binary outcome (resistant or sensitive) for each antibiotic. Resistance rates per antibiotic were calculated as the proportion of resistant isolates among the total number tested for each antibiotic. In addition, antimicrobial resistance per isolate was assessed by determining the number of antibiotics (or antimicrobial classes) to which each isolate was resistant, used for classification of multidrug resistance (MDR).

Associations between antimicrobial resistance and specimen type or bacterial species were assessed using the Chi-square ($\chi^2$) test or Fisher's exact test, as appropriate. Adjusted residuals were used to identify cells contributing to significant associations, with values ≥ |2| at $p < 0.05$ indicating statistical significance.

## Results

# 4.1. Distribution of Bacterial Isolates and Resistance Events

Of 17,680 clinical specimens processed during the study period, 363 (2.1%) were culture-positive and included in the analysis, yielding 591 discrete antibiotic resistance events. Staphylococcus aureus dominated the isolate profile (n = 151; 41.6%), followed by Escherichia coli (n = 119; 32.8%), Enterobacter spp. (n = 43; 11.8%), Klebsiella oxytoca (n = 35; 9.6%), Klebsiella pneumoniae (n = 10; 2.8%), and Acinetobacter baumannii (n = 5; 1.4%).

Table 1
Distribution of Antimicrobial Resistance by Bacterial Isolates and Antibiotic Class (2018–2023)

| **Bacterial Isolate** | **FOX** | **E** | **CRO** | **CXT** | **CN** | **CIP** | **DA** | **SXT** | **VA** | **CAZ** | **MEM** | **AMP** | **Total (n,%)** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Escherichia coli | N/A | N/A | 27 | 7 | 52 | 52 | N/A | N/A | N/A | 33 | 0 | 29 | 200 (33.8) |
| Enterobacter species | N/A | N/A | 21 | 4 | 13 | 13 | N/A | N/A | N/A | 15 | 0 | 12 | 78 (13.2) |
| Klebsiella pneumoniae | N/A | N/A | 4 | 0 | 4 | 3 | N/A | N/A | N/A | 3 | 0 | 4 | 18 (3.0) |
| Klebsiella oxytoca | N/A | N/A | 8 | 1 | 12 | 12 | N/A | N/A | N/A | 8 | 1 | 14 | 56 (9.5) |
| Acinetobacter baumannii | N/A | N/A | 1 | 0 | 1 | 0 | N/A | N/A | N/A | 2 | 0 | 2 | 6 (1.0) |
| Staphylococcus aureus | 6 | 26 | N/A | N/A | 71 | 61 | 26 | 15 | 28 | N/A | N/A | N/A | 233 (39.4) |
| **Total** | 6 | 26 | 61 | 12 | 153 | 141 | 26 | 15 | 28 | 61 | 1 | 61 | 591 (100.0) |

n = number of resistant AST outcomes; % = percentage of resistant isolates. FOX = cefoxitin; E = erythromycin; CRO = ceftriaxone; CXT = cefotaxime; CN = gentamicin; CIP = ciprofloxacin; DA = clindamycin; SXT = co-trimoxazole; VA = vancomycin; CAZ = ceftazidime; MEM = meropenem; AMP = ampicillin, N/A = not tested

Resistance was predominantly driven by Gram-negative organisms, which accounted for 358/591 (60.6%) of all resistant outcomes, largely contributed by Escherichia coli (200; 33.8%) and Enterobacter species (78; 13.2%), followed by Klebsiella oxytoca (56; 9.5%), Klebsiella pneumoniae (18; 3.0%), and Acinetobacter baumannii (6; 1.0%). In contrast, Gram-positive isolates, represented entirely by Staphylococcus aureus, accounted for 233/591 (39.4%) of resistance events.

Across antibiotic classes, the highest resistance burden was observed among aminoglycosides (gentamicin: 153/591; 25.9%) and fluoroquinolones (ciprofloxacin: 141/591; 23.9%), followed by third-generation cephalosporins (ceftriaxone and ceftazidime: each 61/591; 10.3%), and penicillins (ampicillin: 61/591; 10.3%), indicating reduced effectiveness of commonly used first- and second-line agents. Moderate resistance was observed for macrolides (erythromycin: 26/591; 4.4%), lincosamides (clindamycin: 26/591; 4.4%), folate pathway inhibitors (co-trimoxazole: 15/591; 2.5%), and glycopeptides (vancomycin: 28/591; 4.7%). Resistance to cefoxitin (6/591; 1.0%) indicates the presence of methicillin-resistant strains, while carbapenem resistance (meropenem: 1/591; 0.2%) remained minimal (Table 1).

# 4.2. Temporal Trends in Antimicrobial Resistance (2018–2023)

Resistance patterns demonstrated marked annual variability across the study period, with the overall burden peaking in 2022 (155; 26.2%), followed by 2020 (122; 20.6%), 2019 (105; 17.8%), 2023 (97; 16.4%), 2021 (84; 14.2%), and the lowest in 2018 (28; 4.7%), indicating a fluctuating but generally increasing trend in antimicrobial resistance over time. Across antibiotic classes, aminoglycoside resistance (gentamicin) was the most dominant overall (153/591; 25.9%), with highest contributions observed in 2020 (40; 32.8%), 2019 (33; 31.4%), and 2022 (32; 20.6%). Fluoroquinolone resistance (ciprofloxacin) followed closely (141/591; 23.9%), peaking in 2020 (36; 29.5%), 2022 (36; 23.2%), and 2023 (25; 25.8%), demonstrating sustained high resistance across recent years.

Moreover, third-generation cephalosporins showed consistent resistance pressure, with ceftriaxone (61/591; 10.3%) highest in 2023 (20; 20.6%) and 2020 (12; 9.8%), while ceftazidime (61/591; 10.3%) peaked in 2020 (24; 19.7%) and remained notable in 2022 (17; 11.0%). Penicillins (Ampicillin) resistance remained steady across years (61/591; 10.3%), reflecting persistent inefficacy of this agent in the study setting. Other antibiotic classes showed comparatively lower but clinically relevant resistance, including erythromycin (26; 4.4%), clindamycin (26; 4.4%), and co-trimoxazole (15; 2.5%), with variable yearly distribution. Vancomycin resistance (28; 4.7%) emerged from 2021 onwards, peaking in 2022 (14; 9.0%), while cefoxitin resistance (6; 1.0%) was sporadic but indicative of methicillin resistance. Carbapenem resistance (meropenem: 1; 0.2%) remained rare and confined to 2019, suggesting sustained preservation of last-line therapeutic efficacy (Table 2).

Table 2
Temporal trends in antimicrobial susceptibility testing (AST) resistance outcomes among clinical bacterial isolates across selected antibiotics, 2018–2023

| Year of AST | FOX | E | CRO | CXT | CN | CIP | DA | SXT | VA | CAZ | MEM | AMP | Total |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | n(%) | n(%) | n(%) | n(%) | n(%) | n(%) | n(%) | n(%) | n(%) | n(%) | n(%) | n(%) | n(%) |
| 2018 | 0 (0.0) | 1 (3.6) | 3 (10.7) | 0 (0.0) | 15 (53.6) | 3 (10.7) | 1 (3.6) | 0 (0.0) | 0 (0.0) | 1 (3.6) | 0 (0.0) | 4 (14.3) | 28 (4.7) |
| 2019 | 1 (1.0) | 9 (8.6) | 8 (7.6) | 1 (1.0) | 33 (31.4) | 28 (26.7) | 5 (4.8) | 0 (0.0) | 2 (1.9) | 2 (1.9) | 1 (1.0) | 15 (14.3) | 105 (17.8) |
| 2020 | 0 (0.0) | 3 (2.5) | 12 (9.8) | 2 (1.6) | 40 (32.8) | 36 (29.5) | 0 (0.0) | 0 (0.0) | 2 (1.6) | 24 (19.7) | 0 (0.0) | 3 (2.5) | 122 (20.6) |
| 2021 | 2 (2.4) | 9 (10.7) | 8 (9.5) | 1 (1.2) | 11 (13.1) | 13 (15.5) | 8 (9.5) | 6 (7.1) | 5 (6.0) | 11 (13.1) | 0 (0.0) | 10 (11.9) | 84 (14.2) |
| 2022 | 3 (1.9) | 3 (1.9) | 10 (6.5) | 7 (4.5) | 32 (20.6) | 36 (23.2) | 10 (6.5) | 2 (1.3) | 14 (9.0) | 17 (11.0) | 0 (0.0) | 21 (13.5) | 155 (26.2) |
| 2023 | 0 (0.0) | 1 (1.0) | 20 (20.6) | 1 (1.0) | 22 (22.7) | 25 (25.8) | 2 (2.1) | 7 (7.2) | 5 (5.2) | 6 (6.2) | 0 (0.0) | 8 (8.2) | 97 (16.4) |
| Total | 6 (1.0) | 26 (4.4) | 61 (10.3) | 12 (2.0) | 153 (25.9) | 141 (23.9) | 26 (4.4) | 15 (2.5) | 28 (4.7) | 61 (10.3) | 1 (0.2) | 61 (10.3) | 591 (100.0) |

n = number of resistant AST outcomes; % = percentage of resistant isolates. FOX = cefoxitin; E = erythromycin; CRO = ceftriaxone; CXT = cefotaxime; CN = gentamicin; CIP = ciprofloxacin; DA = clindamycin; SXT = co-trimoxazole; VA = vancomycin; CAZ = ceftazidime; MEM = meropenem; AMP = ampicillin

## 4.3. Gram-Negative Isolates

## 4.3.1. Specimen Distribution and Resistance Burden

The distribution of Gram-negative antimicrobial resistance events varied by sample type, with urine isolates contributing the highest number of resistance events (263/358; 73.5%), followed by blood isolates (82/358; 22.9%) and sputum isolates (13/358; 3.6%), reflecting a dominant burden of resistance in urinary tract infections.

Across antibiotic classes, resistance to aminoglycosides (gentamicin) was most frequent overall (82/358; 22.9%), with comparable distribution across urine (60; 22.8%) and blood (18; 22.0%) isolates, while sputum isolates showed a relatively higher proportion (4; 30.8%). Resistance to fluoroquinolones (ciprofloxacin) was similarly high (80/358; 22.3%), being most pronounced in urine isolates (67; 25.5%), followed by sputum (3; 23.1%) and blood (10; 12.2%). Resistance to third-generation cephalosporins was also substantial, with ceftriaxone and ceftazidime each accounting for 61/358 (17.0%) resistance events. Ceftriaxone resistance was highest in urine isolates (43; 16.3%) and blood isolates (16; 19.5%), while ceftazidime resistance was relatively higher in blood isolates (22; 26.8%) compared to urine (37; 14.1%) and sputum (2; 15.4%).

Resistance to penicillins (ampicillin) accounted for 61/358 (17.0%) events, with urine isolates contributing the largest proportion (44; 16.7%), followed by blood (15; 18.3%) and sputum (2; 15.4%). Resistance to cefotaxime remained comparatively low (12/358; 3.4%) across all sample types. Importantly, resistance to the carbapenem meropenem was rare (1/358; 0.3%) and detected only in urine isolates. (Table 3).

Table 3
Distribution of Gram-Negative Antimicrobial Resistance Events by Sample Type and Antibiotic Class, 2018–2023.

| Type of Sample | Number of Bacterial Isolate | CRO n (%) | CXT n (%) | CAZ n (%) | MEM n (%) | CN n (%) | CIP n (%) | AMP n (%) | Total Events |
|---|---|---|---|---|---|---|---|---|---|
| **Blood** | 47 | 16 (19.5) | 1 (1.2) | 22 (26.8) | 0 (0.0) | 18 (22.0) | 10 (12.2) | 15 (18.3) | 82 |
| **Urine** | 158 | 43 (16.3) | 11 (4.2) | 37 (14.1) | 1 (0.4) | 60 (22.8) | 67 (25.5) | 44 (16.7) | 263 |
| **Sputum** | 7 | 2 (15.4) | 0 (0.0) | 2 (15.4) | 0 (0.0) | 4 (30.8) | 3 (23.1) | 2 (15.4) | 13 |
| **Total** | 212 | 61 (17.0) | 12 (3.4) | 61 (17.0) | 1 (0.3) | 82 (22.9) | 80 (22.3) | 61 (17.0) | 358 |

Abbreviations: CRO = Ceftriaxone; CXT = Cefotaxime; CAZ = Ceftazidime; MEM = Meropenem; CN = Gentamycin; CIP = Ciprofloxacin; AMP = Ampicillin; n = number of events; % = percentage.

## 4.3.2. Resistance Associations by Specimen Type

The distribution of Gram-negative antimicrobial resistance varied across specimen types, although most antibiotics showed no statistically significant association with sample source. Resistance to third-generation cephalosporins, including ceftriaxone (Fisher's Exact Test = 0.964, p = 0.66) and cefotaxime (Fisher's Exact Test = 1.271, p = 0.54), did not differ significantly across blood, sputum, and urine samples. Similarly, resistance to the penicillin class (ampicillin) showed no significant association with specimen type (Fisher's Exact Test = 0.429, p = 0.87).

Resistance to the aminoglycoside gentamicin also demonstrated no statistically significant variation by sample type (Fisher's Exact Test = 1.115, p = 0.66), despite resistant isolates being more common in urine samples (60; Adj. Res = -0.4) compared to blood (18; Adj. Res = -0.1) and sputum samples (4; Adj. Res = 1.0). However, statistically significant associations were observed for resistance to third-generation ceftazidime (Fisher's Exact Test = 9.278, p = 0.01) and the fluoroquinolone ciprofloxacin (Fisher's Exact Test = 7.252, p = 0.02). For ceftazidime, resistant isolates were disproportionately higher in blood samples (22; Adj. Res = 3.1) and lower in urine samples (37; Adj. Res = -2.9). In contrast, ciprofloxacin resistance was significantly concentrated in urine samples (67; Adj. Res = 2.4), while blood samples showed fewer resistant isolates than expected (10; Adj. Res = -2.6). Resistance to the carbapenem meropenem remained extremely low and showed no significant association with sample type (Fisher's Exact Test = 2.133, p = 1.00), with only one resistant isolate identified from urine samples (Table 4).

Table 4
Association between clinical specimen type and antimicrobial susceptibility patterns among Gram-negative bacterial isolates using Fisher's exact test and adjusted residual analysis

| Gram Negative Antibiotic | Types of Sample Tested | | | | | | |
|---|---|---|---|---|---|---|---|
| | Drug Sensitivity Test | Blood (n, Adj. Res) | Sputum (n, Adj. Res) | Urine (n, Adj. Res) | Total Resistant n (%) | Fisher's Exact Test | p-value |
| **Ceftriaxone** | | | | | | 0.964 | 0.66 |
| | Sensitive | 31 (-0.9) | 5 (0.0) | 115 (0.9) | 151 (71.2) | | |
| | Resistant | 16 (0.9) | 2 (0.0) | 43 (-0.9) | 61 (28.8) | | |
| **Cefotaxime** | | | | | | 1.271 | 0.54 |
| | Sensitive | 46 (1.2) | 7 (0.7) | 147 (-1.4) | 200 (94.3) | | |
| | Resistant | 1 (-1.2) | 0 (-0.7) | 11 (1.4) | 12 (5.7) | | |
| **Ceftazidime** | | | | | | 9.278 | 0.01* |
| | Sensitive | 25 (-3.1) | 5 (0.0) | 121 (2.9) | 151 (71.2) | | |
| | Resistant | 22 (3.1) | 2 (0.0) | 37 (-2.9) | 61 (28.8) | | |
| **Ampicillin** | | | | | | 0.429 | 0.87 |
| | Sensitive | 32 (-0.5) | 5 (0.0) | 114 (0.5) | 151 (71.2) | | |
| | Resistant | 15 (0.5) | 2 (0.0) | 44 (-0.5) | 61 (28.8) | | |
| **Gentamycin** | | | | | | 1.115 | 0.66 |
| | Sensitive | 29 (0.1) | 3 (-1.0) | 98 (0.4) | 130 (61.3) | | |
| | Resistant | 18 (-0.1) | 4 (1.0) | 60 (-0.4) | 82 (38.7) | | |
| **Ciprofloxacin** | | | | | | 7.252 | 0.02* |
| | Sensitive | 37 (2.6) | 4 (-0.3) | 91 (-2.4) | 132 (62.3) | | |
| | Resistant | 10 (-2.6) | 3 (0.3) | 67 (2.4) | 80 (37.7) | | |
| **Meropenem** | | | | | | 2.133 | 1.00 |
| | Sensitive | 47 (0.5) | 7 (0.2) | 157 (-0.6) | 211 (99.5) | | |
| | Resistant | 0 (-0.5) | 0 (-0.2) | 1 (0.6) | 1 (0.5%) | | |

Adj.Res = adjusted residual; n = number; % = percentage; * indicates significant values.

## 4.3.3. Resistance Associations by Bacterial Species

The distribution of antimicrobial resistance among Gram-negative bacterial isolates varied across antibiotic classes, although most antibiotics demonstrated no statistically significant association with bacterial species. Resistance to the third-generation cephalosporin ceftriaxone showed a statistically significant association with bacterial isolate type (Fisher's Exact Test = 11.38, p = 0.02). Resistant ceftriaxone isolates were disproportionately higher among Enterobacter spp. (21; Adj. Res = 3.3), while Escherichia coli demonstrated fewer resistant isolates than expected (27; Adj. Res = -2.2), indicating species-specific variation in resistance distribution. Resistance to other third-generation cephalosporins, including cefotaxime (Fisher's Exact Test = 1.61, p = 0.73) and ceftazidime (Fisher's Exact Test = 2.06, p = 0.75), showed no statistically significant association with bacterial species despite variable resistance frequencies across isolates.

Similarly, resistance to the penicillin class (ampicillin) did not significantly differ among bacterial isolates (Fisher's Exact Test = 4.61, p = 0.32), although resistant isolates were relatively more common in Klebsiella oxytoca (14; Adj. Res = 1.6) and less common in Escherichia coli (29; Adj. Res = -1.6). Resistance to the aminoglycoside gentamicin (Fisher's Exact Test = 3.43, p = 0.50) and the fluoroquinolone ciprofloxacin (Fisher's Exact Test = 5.89, p = 0.20) also showed no significant association with bacterial isolate type, although Escherichia coli accounted for the greatest proportion of resistant isolates for both gentamicin (52; Adj. Res = 1.7) and ciprofloxacin (52; Adj. Res =

2.0). Resistance to the carbapenem meropenem remained extremely low and showed no significant association with bacterial isolates (Fisher's Exact Test = 7.05, p = 0.24), with only one resistant isolate identified in Klebsiella oxytoca (Adj. Res = 2.3).. (Table 5).

Table 5
Antimicrobial Resistance Patterns of Gram-Negative Bacterial Isolates by Species

| Antibiotic | | Bacterial Isolate | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | Drug Sensitivity Test | Acinetobacter spp. (n, Adj.Res) | Escherichia coli (n, Adj.Res) | Enterobacter spp (n, Adj.Res) | Klebsiella oxytoca (n, Adj.Res) | Klebsiella pneumoniae (n, Adj.Res) | n (%) | Fisher's Exact Test | p-value |
| **Ceftriaxone** | | | | | | | | 11.38 | 0.02* |
| | Sensitive | 4 (0.4) | 92 (2.2) | 22 (-3.3) | 27 (0.8) | 6 (-0.8) | 151 (71.2) | | |
| | Resistant | 1 (-0.4) | 27 (-2.2) | 21 (3.3) | 8 (-0.8) | 4 (0.8) | 61 (28.8) | | |
| **Cefotaxime** | | | | | | | | 1.61 | 0.73 |
| | Sensitive | 5 (0.6) | 112 (-0.2) | 39 (-1.2) | 34 (0.8) | 10 (0.8) | 200 (94.3) | | |
| | Resistant | 0 (-0.6) | 7 (0.2) | 4 (1.2) | 1 (-0.8) | 0 (-0.8) | 12 (5.7) | | |
| **Ceftazidime** | | | | | | | | 2.06 | 0.75 |
| | Sensitive | 3 (-0.6) | 86 (0.4) | 28 (-1.0) | 27 (0.8) | 7 (-0.1) | 151 (71.2) | | |
| | Resistant | 2 (0.6) | 33 (-0.4) | 15 (1.0) | 8 (-0.8) | 3 (0.1) | 61 (28.8) | | |
| **Ampicillin** | | | | | | | | 4.61 | 0.32 |
| | Sensitive | 3 (-0.6) | 90 (1.6) | 31 (0.1) | 21 (-1.6) | 6 (-0.8) | 151 (71.2) | | |
| | Resistant | 2 (0.6) | 29 (-1.6) | 12 (-0.1) | 14 (1.6) | 4 (0.8) | 61 (28.8) | | |
| **Gentamycin** | | | | | | | | 3.43 | 0.50 |
| | Sensitive | 4 (0.9) | 67 (-1.7) | 30 (1.3) | 23 (0.6) | 6 (-0.1) | 130 (61.3) | | |
| | Resistant | 1 (-0.9) | 52 (1.7) | 13 (-1.3) | 12 (-0.6) | 4 (0.1) | 82 (38.7) | | |
| **Ciprofloxacin** | | | | | | | | 5.89 | 0.20 |
| | Sensitive | 5 (1.8) | 67 (-2.0) | 30 (1.1) | 23 (0.5) | 7 (0.5) | 132 (62.3) | | |
| | Resistant | 0 (-1.8) | 52 (2.0) | 13 (-1.1) | 12 (-0.5) | 3 (-0.5) | 80 (37.7) | | |
| **Meropenem** | | | | | | | | 7.05 | 0.24 |
| | Sensitive | 5 (0.2) | 119 (1.1) | 43 (0.5) | 34 (-2.3) | 10 (0.2) | 211 (99.5) | | |
| | Resistant | 0 (-0.2) | 0 (-1.1) | 0 (-0.5) | 1 (2.3) | 0 (-0.2) | 1 (0.5) | | |

Adj.Res = adjusted residual; n = number; % = percentage; * indicates significant values.

## 4.4. Gram-Positive Isolates

## 4.4.1. Specimen Distribution and Resistance Burden

The distribution of Gram-positive antimicrobial resistance events varied across specimen types, with blood samples contributing the highest proportion of resistance events (134/233; 57.5%), followed by urine samples (73/233; 31.3%) and sputum samples (26/233; 11.2%), indicating a predominant burden of resistance among bloodstream infections.

Across antibiotic classes, resistance to aminoglycosides (gentamicin) was the most frequently observed overall (71/233; 30.5%), particularly in blood isolates (48; 35.8%) and urine isolates (20; 27.4%), while sputum isolates contributed fewer cases (3; 11.5%). Resistance to fluoroquinolones (ciprofloxacin) was also high (61/233; 26.2%), with relatively consistent distribution across blood (37; 27.6%), urine (18; 24.7%), and sputum (6; 23.1%) samples. Resistance to glycopeptides (vancomycin) accounted for 28/233 (12.0%) of events and was more pronounced in sputum (6; 23.1%) and urine (9; 12.3%) isolates compared to blood (13; 9.7%), suggesting concern for resistant Gram-positive organisms in respiratory and urinary infections.

Resistance to macrolides (erythromycin) accounted for 26/233 (11.2%) of events and was highest in urine isolates (10; 13.7%) followed by blood (14; 10.4%) and sputum (2; 7.7%). Similarly, resistance to lincosamides (clindamycin) (26/233; 11.2%) was most prominent in sputum isolates (7; 26.9%), indicating a localized burden of resistance in respiratory infections. Resistance to folate pathway inhibitors (co-trimoxazole) was relatively low (15/233; 6.4%), with most events occurring in blood isolates (13; 9.7%) and none detected in sputum samples. Resistance to cefoxitin, a marker of methicillin resistance, was low overall (6/233; 2.6%) but proportionally higher in sputum isolates (2; 7.7%) compared to blood (1; 0.7%) (Table 6).

Table 6
Distribution of Gram-Positive Antimicrobial Resistance Events by Sample Type and Antibiotic Class, 2018–2023

| Type of Sample | Number of Bacterial Isolate | FOX n (%) | E n (%) | CN n (%) | CIP n (%) | DA n (%) | SXT n (%) | VA n (%) | Total Events |
|---|---|---|---|---|---|---|---|---|---|
| Blood | 86 | 1 (0.7) | 14 (10.4) | 48 (35.8) | 37 (27.6) | 8 (6.0) | 13 (9.7) | 13 (9.7) | 134 |
| Urine | 50 | 3 (4.1) | 10 (13.7) | 20 (27.4) | 18 (24.7) | 11 (15.1) | 2 (2.7) | 9 (12.3) | 73 |
| Sputum | 15 | 2 (7.7) | 2 (7.7) | 3 (11.5) | 6 (23.1) | 7 (26.9) | 0 (0.0) | 6 (23.1) | 26 |
| Total | 151 | 6 (2.6) | 26 (11.2) | 71 (30.5) | 61 (26.2) | 26 (11.2) | 15 (6.4) | 28 (12.0) | 233 |

FOX = Cefoxitin; E = Erythromycin; CN = Gentamicin; CIP = Ciprofloxacin; DA = Clindamycin; SXT = Trimethoprim-sulfamethoxazole; VA = Vancomycin, n= number of events

## 4.4.2. Resistance Associations by Specimen Type

The distribution of antimicrobial resistance among Gram-positive isolates varied across specimen types, with several antibiotics demonstrating statistically significant associations with sample source. Resistance to the cephamycin cefoxitin, a marker of methicillin resistance, showed a significant association with specimen type ($\chi^2 = 5.66$, $p = 0.03$), with resistant isolates disproportionately higher in sputum samples (2; Adj. Res = 2.0) and lower in blood samples (1; Adj. Res = -2.0), suggesting greater methicillin resistance among respiratory isolates.

Resistance to the aminoglycoside gentamicin also differed significantly across sample types ($\chi^2 = 8.06$, $p = 0.02$), with resistant isolates more frequently observed in blood samples (48; Adj. Res = 2.5), while sputum samples showed fewer resistant isolates than expected (3; Adj. Res = -2.2). Similarly, resistance to the lincosamide clindamycin demonstrated a strong significant association with specimen type ($\chi^2 = 13.71$, $p < 0.01$), with sputum isolates contributing disproportionately to resistance (7; Adj. Res = 3.2), whereas blood isolates showed fewer resistant isolates than expected (8; Adj. Res = -3.0).

Resistance to the macrolide erythromycin did not significantly vary across specimen types ($\chi^2 = 0.48$, $p = 0.79$), although blood isolates accounted for the largest proportion of resistant cases (14; 17.2%). Similarly, resistance to the fluoroquinolone ciprofloxacin showed no significant association with sample type ($\chi^2 = 0.65$, $p = 0.72$), despite resistant isolates being more common in blood samples (37; 40.4%).

Resistance to the folate pathway inhibitor co-trimoxazole approached statistical significance ($\chi^2 = 5.36$, $p = 0.05$), with resistant isolates concentrated mainly in blood samples (13; Adj. Res = 2.4), while sputum isolates demonstrated no resistant cases. Resistance to the glycopeptide vancomycin did not significantly differ across sample types ($\chi^2 = 5.25$, $p = 0.07$), although sputum isolates showed relatively higher resistant counts (6; Adj. Res = 2.3), indicating potential concern for resistant respiratory Gram-positive pathogens ((Table 7).

Table 7
Association Between Gram-Positive Antimicrobial Resistance Patterns and Sample Type

| Gram Positive Antibiotics | Type of Samples Tested | | | | | | |
|---|---|---|---|---|---|---|---|
| | Drug Sensitivity Tes | Blood (n, Adj.Res) | Sputum (n, Adj.Res) | Urine (n, Adj.Res) | n (%) | $\chi^2$ / Fisher's Exact Test | p-value |
| Cefoxitin (FOX) | | | | | | 5.66 | 0.03* |
| | Sensitive | 85 (2.0) | 13 (-2.0) | 47 (-0.9) | 145 (96.0) | | |
| | Resistant | 1 (-2.0) | 2 (2.0) | 3 (0.9) | 6 (4.0) | | |
| Erythromycin (E) | | | | | | 0.48 | 0.79 |
| | Sensitive | 72 (0.4) | 13 (0.4) | 40 (-0.6) | 125 (82.8) | | |
| | Resistant | 14 (-0.4) | 2 (-0.4) | 10 (0.6) | 26 (17.2) | | |
| Gentamycin (CN) | | | | | | 8.06 | 0.02* |
| | Sensitive | 38 (-2.5) | 12 (2.2) | 30 (1.2) | 80 (53.0) | | |
| | Resistant | 48 (2.5) | 3 (-2.2) | 20 (-1.2) | 71 (47.0) | | |
| Ciprofloxacin (CIP) | | | | | | 0.65 | 0.72 |
| | Sensitive | 49 (-0.8) | 9 (0.0) | 32 (0.8) | 90 (59.6%) | | |
| | Resistant | 37 (0.8) | 6 (0.0) | 18 (-0.8) | 61 (40.4) | | |
| Clindamycin (DA) | | | | | | 13.71 | < 0.01* |
| | Sensitive | 78 (3.0) | 8 (-3.2) | 39 (-1.1) | 125 (82.8) | | |
| | Resistant | 8 (-3.0) | 7 (3.2) | 11 (1.1) | 26 (17.2) | | |
| Co-trimoxazole (SXT) | | | | | | 5.36 | 0.05 |
| | Sensitive | 73 (-2.4) | 15 (1.4) | 48 (1.7) | 136 (90.1) | | |
| | Resistant | 13 (2.4) | 0 (-1.4) | 2 (-1.7) | 15 (9.9) | | |
| Vancomycin (VA) | | | | | | 5.25 | 0.07 |
| | Sensitive | 73 (1.2) | 9 (-2.3) | 41 (0.1) | 123 (81.5) | | |
| | Resistant | 13 (-1.2) | 6 (2.3) | 9 (-0.1) | 28 (18.5) | | |

Adj.Res = adjusted residual; n = number; % = percentage; $\chi^2$ = Chi-square Test * indicates significant values.

## Discussion

This study characterized antimicrobial resistance patterns among 363 bacterial isolates generating 591 resistance events at Dodoma Regional Referral Hospital (DRRH), Tanzania, over a six-year period (2018–2023). *Staphylococcus aureus* and *Escherichia coli* were the predominant pathogens, collectively accounting for 73.2% of all resistance events. Significant specimen- and organism-dependent resistance associations were identified, with ciprofloxacin and gentamicin resistance posing the greatest clinical burden, while meropenem retained near-complete activity.

The dominance of *S. aureus* (41.6%) and *E. coli* (32.8%) is consistent with continental surveillance data, where these two pathogens were the most frequently isolated across 14 African countries, with high resistance rates reported in both(15). A Uganda tertiary hospital study similarly reported *S. aureus* and gram-negative organisms as the leading bloodstream isolates, with substantial resistance to first-line

agents(16). Conversely, a West African bacteraemia study found a different hierarchy, with *Streptococcus pneumoniae* dominating at 45.2%, and *S. aureus* and *E. coli* contributing 18.3% and 9.7%, (17).

Moreover, Ciprofloxacin resistance was persistently elevated throughout the study period (peak 29.5% in 2020) and was significantly concentrated in urine specimens ($p = 0.02$). This aligns with a systematic review of African uropathogens reporting an overall ciprofloxacin resistance rate of 34% with East Africa contributing 79.5% of included studies(18). A 2019–2023 hospital systemic review similarly found ciprofloxacin resistance in *E. coli* consistently exceeding 30% from 2020 onward(19). In contrast, a sub-Saharan Africa paediatric meta-analysis reported a lower pooled resistance of 25.3% (20), suggesting resistance rates are generally lower in paediatric or community settings than in mixed hospital populations. The specimen-specific concentration of ciprofloxacin resistance in urine likely reflects intense fluoroquinolone selection pressure from empirical urinary tract infection treatment.

*E. coli* contributed 52 gentamicin-resistant isolates, the highest absolute burden among individual organism-antibiotic pairs. A sub-Saharan Africa meta-analysis reported a comparable pooled *E. coli* gentamicin resistance of 42.7% across 17 studies(20), while a Zambian hospital study documented that 90% of inpatients carried Enterobacteriaceae resistant to gentamicin, ciprofloxacin, and/or ceftriaxone(21). Conversely, a Tanzanian neonatal unit study, also noting high gentamicin resistance — found only 1% of extended-spectrum beta-lactamase (ESBL) producing isolates resistant to meropenem(22), consistent with our near-intact carbapenem susceptibility, suggesting that gentamicin and meropenem resistance trajectories remain dissociated in the region.

*Enterobacter* spp. showed significantly higher ceftriaxone resistance than expected ($p = 0.02$). A Kenyan hospital study corroborates this, reporting that all *Enterobacter* spp. isolates were non-susceptible to ceftriaxone and cefepime(23, 24). Meropenem retained exceptional activity (99.5%), with only one resistant isolate detected. This is consistent with a Tanzanian neonatal study where only 1% of ESBL-producing isolates were meropenem-resistant(22) and with broader sub-Saharan Africa data confirming that carbapenem resistance remains low despite high cephalosporin resistance(25). However, a Kenyan hospital environment study reported that 95.6% of *A. baumannii* isolates were non-susceptible to meropenem(23), a stark contrast underscoring that, while carbapenems remain effective at DRRH, the regional precedent for rapid resistance emergence demands continuous vigilance to preserve this last-resort agent.

Clindamycin resistance demonstrated the strongest specimen-type association among Gram-positive isolates ($\chi^2 = 13.71$; $p < 0.01$), disproportionately elevated in sputum. A five-year South African study (2019–2023) reported that MRSA isolates exhibited over 50% resistance to clindamycin, gentamicin, and erythromycin(26), substantially higher than observed at DRRH, likely reflecting a higher institutional MRSA prevalence. A Gabon study similarly found erythromycin resistance significantly higher in MRSA (73%) than in methicillin-susceptible isolates (10%), with clindamycin resistance detected exclusively in MRSA(27), suggesting that the sputum-concentrated clindamycin resistance at DRRH may represent a subpopulation of MRSA. Conversely, a Kenyatta National Hospital study reported good gentamicin susceptibility and excellent vancomycin susceptibility across *S. aureus* isolates (28), more favourable than the 30.6% gentamicin resistance in blood and borderline vancomycin associations observed here, highlighting marked intra-regional variability in Gram-positive resistance profiles.

Resistance events peaked in 2020 and 2022, with gentamicin resistance fluctuating from 53.6% in 2018 to a nadir of 13.1% in 2021 before rebounding to 22.7% in 2023. The 2020 peak may, in part, reflect pandemic-related disruptions to prescribing oversight, as reported elsewhere, though this cannot be confirmed from the available data(19). The downward trends in clindamycin and erythromycin resistance, despite transient 2021 spikes, may reflect partial stewardship responsiveness, though the subsequent rebound in gentamicin and ciprofloxacin resistance by 2023 underscores that without sustained, structured stewardship programs, resistance gains are easily reversed.

Given near-complete gentamicin and ciprofloxacin resistance in E. coli urinary isolates, empirical UTI treatment at DRRH should shift toward agents retaining higher susceptibility. Meropenem's preserved activity supports its continued role as a last-resort agent, with restriction policies warranted. These temporal dynamics reinforce the need for continuous, real-time antibiogram monitoring at DRRH and comparable regional referral hospitals in Tanzania.

## Limitations

This study has several limitations. First, the retrospective design limited the availability of clinical information and prevented assessment of patient outcomes. Second, the study was conducted in a single hospital, which may limit generalizability to other healthcare settings. Third, variations in antibiotic testing panels over time may have influenced resistance estimates. Fourth, patient-level clinical data including age, sex, ward of admission, prior antibiotic exposure, total number of isolates per year and comorbidities were unavailable, precluding risk factor analysis for resistant infections. Fifth, resistance rates were calculated as proportions of total resistance events rather than

individual isolate-antibiotic pairs, which may affect direct comparability with studies using standard denominator-based resistance calculations. Sixth, Phenotypic resistance was not confirmed by molecular methods; therefore, ESBL production, MRSA status, and carbapenemase genes were not characterized, limiting mechanistic interpretation.

## Conclusions

Ciprofloxacin and gentamicin resistance were the dominant resistance burdens at DRRH, disproportionately affecting urinary and bloodstream isolates of E. coli and S. aureus respectively. Meropenem retained near-complete activity, underscoring the need for carbapenem stewardship. Facility-specific antibiograms, updated annually, should be formally integrated into DRRH empirical prescribing guidelines and Tanzania's national AMR surveillance framework.

## Abbreviations

AMR
Antimicrobial Resistance
CLSI
Clinical and Laboratory Standards Institute
DRRH
Dodoma Regional Referral Hospital
LMICs
Low–and Middle–Income Countries

## Declarations

**9.1. Ethics clearance**

Ethical approval was obtained from St. John University of Tanzania (SJUT) approval number (SJUT/DRI/UREC/2023-01/PRO-RSR/05-0001), on January 4, 2023. Permission to access laboratory records was granted by DRRH administration. The study adhered to the ethical principles outlined in the Declaration of Helsinki for medical research involving human data. Given the retrospective nature of the study and the use of routinely collected secondary data, the requirement for informed consent was waived by the institutional ethics review committee.

**9.2. Consent for publication**

Not applicable.

**9.3. Availability of data**

The datasets used and analyzed during the current study are available from the corresponding author upon reasonable request.

**9.4. Competing interests**

The authors declare no competing interests.

**9.5. Funding**

No external funding was received for this study.

**10. Authors' contributions**

CA conceived, designed the study, conducted preliminary data analysis, and drafted the manuscript. EM contributed substantially to the study design, led the data analysis and interpretation of results, and critically revised the manuscript. RS and BK collected and cleaned data, reviewed and edited the manuscript. RP provided technical inputs, reviewed and edited the manuscript. All authors read and approved the final manuscript.

**11. Availability of data and materials**

The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

## References


1. WHO WHO. Antimicrobial resistance [Internet]. 2024 [cited 2026 Apr 12]. Available from: https://www.who.int/europe/news-room/fact-sheets/item/antimicrobial-resistance
2. Murray CJL, Ikuta KS, Sharara F, Swetschinski L, Aguilar GR, Gray A, et al. Global burden of bacterial antimicrobial resistance in 2019: a systematic analysis. The Lancet. 2022 Feb 12;399(10325):629–55. doi:10.1016/S0140-6736(21)02724-0 PubMed PMID: 35065702.
3. Laurence T, Lamberti O, Smith R, Drake T, McDonnell A. The Global Direct Inpatient Cost of Antimicrobial Resistance: A Modelling Study. 2025 Jan.
4. Sartorius B, Gray AP, Weaver ND, Aguilar GR, Swetschinski LR, Ikuta KS, et al. The burden of bacterial antimicrobial resistance in the WHO African region in 2019: a cross-country systematic analysis. The Lancet Global Health. 2024 Feb 1;12(2):e201–16. doi:10.1016/S2214-109X(23)00539-9 PubMed PMID: 38134946.
5. Kariuki S, Kering K, Wairimu C, Onsare R, Mbae C. Antimicrobial Resistance Rates and Surveillance in Sub-Saharan Africa: Where Are We Now? Infect Drug Resist. 2022 Jul 7;15:3589–609. doi:10.2147/IDR.S342753 PubMed PMID: 35837538; PubMed Central PMCID: PMC9273632.
6. WBG WBG. Drug-Resistant Infections: A Threat to Our Economic Future [Internet]. 2017 [cited 2026 Apr 12]. Available from: https://documents1.worldbank.org/curated/en/323311493396993758/pdf/final-report.pdf
7. WHO WHO. Antimicrobial resistance [Internet]. 2023 [cited 2026 Apr 12]. Available from: https://www.who.int/news-room/fact-sheets/detail/antimicrobial-resistance
8. WHO WHO. Global Antimicrobial Resistance and Use Surveillance System (GLASS) Report 2022. 1st ed. Geneva: World Health Organization; 2022. 1 p.
9. Olpengs D, Munjuri AK, Benson AE, Othman ZK, Adebisi YA. The supply chain lens of the burden of antimicrobial resistance in Sub-Saharan Africa. Discov Public Health. 2025 Dec 14;22(1):828. doi:10.1186/s12982-025-01242-w
10. Sangeda RZ, Kibona J, Munishi C, Arabi F, Manyanga VP, Mwambete KD, et al. Assessment of Implementation of Antimicrobial Resistance Surveillance and Antimicrobial Stewardship Programs in Tanzanian Health Facilities a Year After Launch of the National Action Plan. Front Public Health. 2020;8:454. doi:10.3389/fpubh.2020.00454 PubMed PMID: 32974264; PubMed Central PMCID: PMC7481440.
11. Seni J, Mapunjo SG, Wittenauer R, Valimba R, Stergachis A, Werth BJ, et al. Antimicrobial use across six referral hospitals in Tanzania: a point prevalence survey. BMJ Open. 2020 Dec 15;10(12):e042819. doi:10.1136/bmjopen-2020-042819 PubMed PMID: 33323448; PubMed Central PMCID: PMC7745526.
12. WHO WHO, FAO F and AO of the UN, OIE WO for AH. Antimicrobial Resistance and the United Nations Sustainable Development Cooperation Framework [Internet]. 2021 [cited 2026 Apr 12]. Available from: https://iris.who.int/server/api/core/bitstreams/dc23338c-ae68-4eaf-868a-a0a777ca40c2/content
13. Aslam B, Asghar R, Muzammil S, Shafique M, Siddique AB, Khurshid M, et al. AMR and Sustainable Development Goals: at a crossroads. Global Health. 2024 Oct 17;20(1):73. doi:10.1186/s12992-024-01046-8
14. Camara N, Moremi N, Mghamba J, Eliakimu E, Shumba E, Ondoa P, et al. Surveillance of antimicrobial resistance in human health in Tanzania: 2016–2021. Afr J Lab Med. 2023 May 22;12(1):2053. doi:10.4102/ajlm.v12i1.2053 PubMed PMID: 37293314; PubMed Central PMCID: PMC10244825.
15. Osena G, Kapoor G, Kalanxhi E, Ouassa T, Shumba E, Brar S, et al. Antimicrobial resistance in Africa: A retrospective analysis of data from 14 countries, 2016–2019. PLOS Medicine. 2025 juin;22(6):e1004638. doi:10.1371/journal.pmed.1004638
16. Kajumbula H, Fujita AW, Mbabazi O, Najjuka C, Izale C, Akampurira A, et al. Antimicrobial Drug Resistance in Blood Culture Isolates at a Tertiary Hospital, Uganda - Volume 24, Number 1—January 2018 - Emerging Infectious Diseases journal - CDC [Internet]. doi:10.3201/eid2401.171112
17. Hill PC, Onyeama CO, Ikumapayi UNA, Secka O, Ameyaw S, Simmonds N, et al. Bacteraemia in patients admitted to an urban hospital in West Africa. BMC Infect Dis. 2007 Jan 26;7:2. doi:10.1186/1471-2334-7-2 PubMed PMID: 17257423; PubMed Central PMCID: PMC1794245.
18. Kibwana UO, Manyahi J, Sabas DM, Chande R, Bwire G, Moyo SJ, et al. Ciprofloxacin resistance in community and hospital-acquired urinary tract infections: a systematic review and meta-analysis from African population. BMC Infect Dis. 2025 Dec 28;26(1):212. doi:10.1186/s12879-025-11546-6 PubMed PMID: 41455903; PubMed Central PMCID: PMC12859862.
19. Goleanu (Vasiloiu) CD, Vrancianu CO, Goleanu DA, Tantu MM, Csutak O. Trends in Antibiotic Resistance of Escherichia coli Strains Isolated from Clinical Samples (2019–2023): A Hospital-Based Retrospective Analysis. Pathogens. 2025 Sep 13;14(9):927.

doi:10.3390/pathogens14090927 PubMed PMID: 41011827.

20. Kowalski M, Obama BM, Catho G, Dewez JE, Merglen A, Ruef M, et al. Antimicrobial resistance in Enterobacterales infections among children in sub-Saharan Africa: a systematic review and meta-analysis. eClinicalMedicine. 2024 Apr 1;70. doi:10.1016/j.eclinm.2024.102512 PubMed PMID: 38495519.
21. Nagelkerke MMB, Sikwewa K, Makowa D, Vries I de, Chisi S, Dorigo-Zetsma JW. Prevalence of antimicrobial drug resistant bacteria carried by in- and outpatients attending a secondary care hospital in Zambia. BMC Research Notes. 2017 Aug 10;10:378. doi:10.1186/s13104-017-2710-x PubMed PMID: 28797299.
22. Mshana HJ, Kovacs D, Muro F, Zadoks R, Oravcova K, Matthews L, et al. The burden, risk factors, and antimicrobial susceptibility pattern associated with extended-spectrum beta-lactamase-producing E. coli and K. pneumoniae carriage among neonates and their surroundings at a referral hospital in the Moshi municipality. Front Antibiot. 2025 May 21;4. doi:10.3389/frabi.2025.1556842
23. Odoyo E, Matano D, Tiria F, Georges M, Kyanya C, Wahome S, et al. Environmental contamination across multiple hospital departments with multidrug-resistant bacteria pose an elevated risk of healthcare-associated infections in Kenyan hospitals. Antimicrob Resist Infect Control. 2023 Mar 29;12(1):22. doi:10.1186/s13756-023-01227-x PubMed PMID: 36978195; PubMed Central PMCID: PMC10053033.
24. Hardy ME, Kenney RM, Tibbetts RJ, Shallal AB, Veve MP. Leveraging stewardship to promote ceftriaxone use in severe infections with low- and no-risk AmpC Enterobacterales. Shields RK, editor. Antimicrob Agents Chemother. 2023 Nov 15;67(11):e00826-23. doi:10.1128/aac.00826-23
25. Tompkins K, Juliano JJ, Duin D van. Antimicrobial Resistance in Enterobacterales and Its Contribution to Sepsis in Sub-saharan Africa. Frontiers in Medicine. 2021 Jan 26;8:615649. doi:10.3389/fmed.2021.615649 PubMed PMID: 33575265.
26. Rexe N, Kajee A, Singh R, Swe Swe-Han K. The Distribution of Methicillin-Resistant *Staphylococcus aureus* and Carbapenem-Resistant *Pseudomonas aeruginosa* in the Academic Complex Central Hospital in KwaZulu-Natal, South Africa: A 5-Year Retrospective Study From 2019 to 2023. Flora SJS, editor. International Journal of Microbiology. 2025 Jan;2025(1):6364811. doi:10.1155/ijm/6364811
27. Gouleu CS, Daouda MA, Oye Bingono SO, McCall MBB, Alabi AS, Adegnika AA, et al. Temporal trends of skin and soft tissue infections caused by methicillin-resistant Staphylococcus aureus in Gabon. Antimicrob Resist Infect Control. 2024 Jun 25;13(1):68. doi:10.1186/s13756-024-01426-0
28. Wangai FK, Masika MM, Maritim MC, Seaton RA. Methicillin-resistant Staphylococcus aureus (MRSA) in East Africa: red alert or red herring? BMC Infect Dis. 2019 Jul 9;19(1):596. doi:10.1186/s12879-019-4245-3