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Utilising the Antimicrobial Resistance Index to Identify Multidrug Resistance Profiles of Priority Pathogens: A Case Study from Central Tanzania

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Abstract

Background: Antimicrobial stewardship (AMS) programs have implemented various surveillance interventions, such as profiling bacterial resistance patterns and developing economic cases for effective management. However, there has been comparatively less focus on evaluating the Drug Resistance Index (DRI). The DRI serves as a crucial instrument for evaluating the efficacy of antimicrobial therapies and examining the patterns of bacterial resistance. Evaluating the efficacy of antibiotics and effectively communicating the issue of antimicrobial resistance are crucial components in developing AMS programs within hospital environments.

Objective: This study utilised the DRI to analyse the distribution of multidrug-resistant organisms (MDROs) associated with widely prescribed antimicrobials at Benjamin Mkapa Hospital (BMH), focusing on their application in treating both Gram-positive and Gram-negative infections.

Methods: A retrospective descriptive study was conducted using combined data on total bacterial isolates, resistance isolates, and antibiotic usage to calculate the DRI over the years 2020, 2021, and 2022.

Results: The three-year DRI for the priority pathogens *Escherichia coli* and *Klebsiella pneumoniae* isolated from urine samples is 46%. The average three-year DRIs for pathogens isolated from blood samples were as follows: *Acinetobacter baumannii* (37%), *Escherichia coli* (65%), *Klebsiella pneumoniae* (62%), *Streptococcus pneumoniae* (60%), and *Staphylococcus aureus* (63%). Additionally, the DRIs for bacteria isolated from pus and wound swabs were: *Acinetobacter baumannii* (60%), *Escherichia coli* (57%), *Klebsiella pneumoniae* (66%), *Pseudomonas aeruginosa* (34%) and *Staphylococcus aureus* (75%).

Conclusion: All evaluated priority pathogens displayed multidrug resistance, with DRI values surpassing 25%, a clear indicator of escalating antimicrobial resistance (AMR). These findings underscore the necessity for robust antibiotic stewardship programs within healthcare institutions, alongside the regular dissemination of antibiotic consumption data to the BMH. Additionally, the formulation of comprehensive policies and treatment guidelines is essential to regulate antibiotic prescriptions effectively, thereby preserving their long-term efficacy. These initiatives are pivotal in the fight against AMR, facilitating the restoration of antimicrobial susceptibility and mitigating the DRI.

Keywords: *Antimicrobial Resistance Index, Multidrug Resistance, Priority Pathogens, Central Tanzania, Antimicrobial use.*

Highlights

- A retrospective AMR surveillance study was conducted at BMH to calculate and utilise the DRI in addressing antibiotic resistance trends in bacterial infections.
- Our findings highlight the significant impact of AMR at this zonal referral hospital in Tanzania, a key healthcare institution in the region.
- It is essential to note that our study was limited to a single hospital, which may not accurately represent the broader AMR burden nationwide.
- Therefore, the DRI may not be the most appropriate tool for addressing the AMR burden from a single source within a larger population.

Introduction

The prevalence of antimicrobial resistance among Gram-negative pathogens is escalating more rapidly than that observed in Gram-positive bacteria, with a concerning lack of novel antibiotics in the immediate development pipeline targeting these resistant strains. This alarming increase in resistant bacterial variants significantly limits treatment options, including those for blood, urinary, and surgical site infections(1,2).

The drug resistance index (DRI) is among the metrics used to measure the effectiveness and compare the resistance pattern of bacteria to a list of tested antimicrobials (3). The DRI can be calculated at the ward, facility, and sometimes at the country level as among the cardinal measures of performance of antimicrobial stewardship (AMS) interventions (4). DRIs improve the ability to quantify and communicate the cumulative impact of antimicrobial resistance (AMR) on the likelihood that an organism will be susceptible to initial antimicrobial treatment (5). Also, for policymakers and other non-expert groups, DRIs are an essential communication tool for translating knowledge about antimicrobial resistance into practice and could guide antibiotics' future procurement budgets (4). The drug resistance index has been used on many occasions to measure the effectiveness of AMS interventions in tackling AMR. It was developed as a simple tool to assist policymakers and health personnel in understanding the estimate of ward, hospital, and country's availability of effective antibiotics to treat illnesses caused by bacteria (3,6,7). It could be more readily understood as an indicator of hospital quality (7). Limited research exists on using the DRI to evaluate the burden of Antimicrobial Resistance (AMR). According to Klein and colleagues, DRI rates varied across countries, with lower rates observed in high-income countries such as Sweden (8.1), Canada (9.7), and Norway (16.5) and higher rates in countries like India (71.6), Thailand (60.6), and Ecuador (60.3) (3). King Abdulaziz Medical City, a tertiary care facility in Jeddah, Saudi Arabia, reported a similar study This study took place from 2015 to 2017 and calculated the DRI for four of the most common Gram-negative pathogens and eight commonly used antibiotic classes (8). Overall, the DRI for the adult intensive care unit (ICU) was higher at 59.45% compared to the hospital-wide DRI of 47.96%. The leading antibiotics with higher DRI were carbapenems and penicillins/beta-lactamase

inhibitors. *Acinetobacter baumannii* had the highest DRI, followed by *Klebsiella spp* (8).

The use of DRI to communicate the burden of AMR and emphasise AMS was not implemented, despite its comprehensibility for healthcare professionals and supportive staff. The absence of this parameter in a specialised hospital like Benjamin Mkapa Hospital (BMH) significantly affects the ability to address the burden of multi-drug-resistant organisms (MDROs) and to plan measures aimed at protecting certain antimicrobials for routine use. Although BMH conducts an annual antibiogram, performs antimicrobial susceptibility testing, carries out infection and prevention surveillance twice a year, and audits antimicrobial use (9–11), the lack of DRI is noteworthy as it is a crucial metric that can be easily understood by policymakers and other key hospital stakeholders. This study utilised DRI to analyse the distribution of MDROs associated with commonly prescribed antimicrobials at BMH, with a focus on their application in treating both Gram-positive and Gram-negative infections. DRI serves as an essential tool for evaluating the efficacy of antimicrobial therapies and examining patterns of bacterial resistance. Evaluating the efficacy of antibiotics and effectively communicating the issue of antimicrobial resistance are essential elements in the development of AMS programs within hospital settings.

Methodology

Study Site

The research was conducted at BMH in Dodoma, Tanzania, a facility affiliated with the University of Dodoma, with a capacity of up to 400 beds. The BMH Laboratory holds accreditation from the Southern African Development Community Accreditation Services (SADCAS) in accordance with ISO 15189:2012(12). This laboratory rigorously follows standard operating procedures for analysing clinical specimens, utilising conventional methodologies to identify bacterial pathogens. Antibiotic susceptibility testing results are interpreted in accordance with the standards established by the Clinical and Laboratory Standards Institute (CLSI) (13). Moreover, the laboratory plays a crucial role in monitoring antimicrobial resistance trends in Tanzania and serves as a training centre for medical students from the University of Dodoma.

Study designs and Sampling process

A single-centre retrospective cross-sectional study was conducted at The Benjamin Mkapa Zonal Referral Hospital in Dodoma, Tanzania, from January 2020 to December 2022. The study involved a review of electronic medical records and laboratory results of patients to analyse antimicrobial susceptibility trends in urine, wounds/pus swabs, and blood for eligible patients meeting the inclusion criteria.

The sample size utilised in this study was derived from a convenient sampling method, where all isolates meeting the inclusion criteria were sourced from the hospital microbiology repositories. The bacterial isolates included in the analysis were specifically selected based on their relevance as priority organisms essential for surveillance purposes.

Priority isolates for urine samples were *Escherichia coli* and *Klebsiella pneumoniae*, which were tested for several antibiotics as

stated in the guidelines. Surveillance of AMR in wound/pus swabs were *Escherichia coli, Acinetobacter baumannii, Pseudomonas, Klebsiella pneumoniae, Staphylococcus aureus* and *Streptococcus pneumoniae. Escherichia coli, Acinetobacter baumannii, Klebsiella pneumoniae, Staphylococcus aureus* and *Streptococcus pneumoniae* were isolated from the blood sample (14).

We used AMR to calculate DRI, incorporating three years of cumulative data from 2020, 2021, and 2022, including the combined total isolates, resistance isolates, and antibiotic use data for inpatients. All patient records from the Integrated Health Management Information System (IHMIS) were included in the study. Data on blood, pus, and urine sample growth patterns and samples with positive culture pathogens were assessed. Subsequently, the data were exported to Microsoft Excel for cleaning and analysis.

Laboratory Procedures

Blood, pus and urine sample collection and culture procedures

Venous blood was aseptically collected from each patient. For pediatric patients, 2-5 ml of blood was drawn into BD BACTEC Plus™/F culture vials (Becton Dickinson and Company), while for adults, 8-10 ml was collected in BD BACTEC Plus Aerobic/F culture vials (Becton Dickinson and Company). The blood samples were promptly transported to the BMH laboratory at room temperature, where they were incubated in the BACTEC machine for further analysis. The blood samples were incubated in the BD BACTEC machine for a maximum of 5-7 days. Positive blood cultures were subsequently inoculated onto Blood agar, Chocolate agar, and MacConkey agar, which were then incubated for 18-24 hours at 37°C. Standard microbiological techniques were utilised to identify the bacteria, incorporating evaluations of colony morphology, Gram staining, and various biochemical tests (Oxoid, UK). Gram-positive cocci were identified based on their Gram reaction and the results of catalase and coagulase tests. Gram-negative rods were identified through biochemical tests, including Kligler Iron Agar (KIA), Simon's citrate agar, Indole, urea, and motility assessments (15,16).

A pus sample was collected from the discharge area of the wound. The swab was carefully taken from the center of the wound, ensuring that the surrounding skin margin was avoided to prevent contamination. The swab was gently rotated to allow for thorough absorption of the pus and was then immediately placed into a sterile container for testing. Subsequently, a primary Gram stain of the pus sample was performed, based on the average observations from ten fields. This process was undertaken to characterize and quantify polymorphonuclear cells (PMNCs) and microorganisms. A moderate presence (2–10 PMNCs and microorganisms) or a high presence (>10 PMNCs and microorganisms) per oil immersion field at 100× magnification was deemed positive, resulting in those samples being subjected to culture. Each sample that met these criteria was cultured under aerobic conditions on blood agar (Oxoid, UK) and MacConkey agar (Oxoid, UK). Following growth, biochemical identification tests were systematically performed for Gram-positive

bacteria, utilizing hemolysis on blood agar, as well as tests for catalase, coagulase/Staphlex/DNase, bile esculin, optochin, and bacitracin. For Gram-negative bacteria, identification tests included lactose fermentation on MacConkey agar, alongside oxidase testing, triple sugar iron agar (TSI), sulfur-indole-motility (SIM), urease, and citrate tests (Oxoid, UK)(1,16).

Urine samples were collected using the midstream urine method, while the clean catch method was employed for children. Participants were instructed to collect urine samples in two separate sterile containers. These samples were then immediately stored in a refrigerator at 4°C, and cultures were performed within 24 hours of collection. To isolate microorganisms, urine samples were plated on cysteine lactose electrolyte-deficient (CLED) agar medium. A calibrated loop that delivers approximately 0.001 mL was used to inoculate the CLED agar plates, which were then incubated aerobically at 37°C for 24 hours. The growth of a single type of organism at a concentration greater than 10^5 colony-forming units was considered indicative of bacteriuria. Clinical isolates were identified and confirmed biochemically following standard laboratory procedures. The confirmed bacterial isolates were suspended in nutrient broth supplemented with 16% glycerol and stored at -80°C. These isolated bacterial samples were subsequently used for antimicrobial susceptibility testing (16,17).

Antimicrobial susceptibility testing

Antimicrobial susceptibility test (AST) was performed on Muller Hinton agar (Oxoid, UK) using the conventional disc diffusion method as previously described by the Clinical Laboratory Standard Institute (CLSI) for the respective antibiotic disks for Gram-positive and Gram-negative bacteria. Respective disks for Gram-positive bacteria included were penicillin G (10µg), erythromycin (15µg), clindamycin (2µg), ciprofloxacin (5µg), gentamicin (10µg), gentamicin (120µg–high level for *Enterococcus* spp), trimethoprim-sulfamethoxazole (1.25µg/ 23.7µg), and chloramphenicol (30µg). Antibiotic discs for Gram-negative bacteria included were ampicillin (10µg), ciprofloxacin (5µg), gentamicin (10µg), amikacin (30µg), ceftriaxone (30µg), ceftazidime (10µg), and cefepime (10µg), trimethoprim/sulfamethoxazole (1.25µg/23.7µg), piperacillin/tazobactam (100/10µg), and meropenem (10µg). After incubating the plates at 37°C for 18–24 hours, the diameter (nearest whole mm) of the inhibition zones for each antibiotic was measured (1,15,17). The interpretation breakpoints were based on whether the bacterium was susceptible (S), intermediate (I), or resistant (R) to the tested drugs according to the CLSI recommendations (16). The choice of antibiotic agents varied depending on the range of antibiotics available to the laboratory.

Calculation of Drug Resistance Index (DRI)

Data used in the calculation of DRI included cumulative three years (2020, 2021, and 2022), total isolates, resistance isolates, and antibiotics use data. The given data were used to calculate: -

1. Calculating Drug Resistance Rates

Final and verified results of AST were obtained from the hospital's antibiogram, alongside the antimicrobial resistance (AMR) trend data for the years 2020, 2021, and 2022. Frequently

utilized antibiotics were examined and classified according to their pharmacological categories. The findings pertaining to AMR were articulated as percentages of susceptibility. The interpretation of the AST results adhered to the guidelines established by the Clinical Laboratory Standards Institute (CLSI) (16). Relevant data were systematically compiled and entered into a Microsoft Excel spreadsheet to facilitate comprehensive cleaning and analysis of the AMR data.

Samples of urine, wound/pus swabs, and blood collected from 2020, 2021 and 2022 were analysed to differentiate between cases with growth isolates, cases with no growth, and those with mixed or contaminated growth. Samples exhibiting growth isolates were subjected to further testing for antimicrobial susceptibilities to ascertain whether they exhibited susceptibility, resistance, or intermediate results. In calculating the Drug Resistance Index (DRI), the total number of resistant isolates within specific antimicrobial classes was employed (18). For the development of antimicrobial susceptibility trends, the total number of isolates served as the denominator, while the number of resistant isolates constituted the numerator (18).

The priority isolates for urine samples included *Escherichia coli* and *Klebsiella pneumoniae*, which were evaluated against a range of antibiotics as specified by the guidelines. The surveillance of AMR in wound/pus swabs focused on *Escherichia coli, Acinetobacter baumannii, Pseudomonas, Klebsiella pneumoniae, Staphylococcus aureus,* and *Streptococcus pneumoniae*. *Escherichia coli, Acinetobacter baumannii, Klebsiella pneumoniae, Staphylococcus aureus,* and *Streptococcus pneumoniae* were also isolated from blood samples. Records containing incomplete or missing data were excluded from this study (14,19). By national AMR surveillance guidelines, isolates from stool, urethral, cervical swabs, and cerebrospinal fluid specimens were not included in our surveillance. Following the Tanzania AMR surveillance framework, we excluded non-priority pathogens from the Gram-negative and Gram-positive categories (14). The antimicrobial classes utilised in the DRI included Penicillins, 3rd generation Cephalosporins, 2nd generation Cephalosporins, Fluoroquinolones, Aminoglycosides, Tetracyclines, Carbapenems, Sulfonamides, Macrolides, Lincosamides, and Glycopeptides.

Drug resistance rate data was calculated by dividing the number of resistant isolates by the total number of isolates found in AMR surveillance, as shown in the equation below(18).

$$Drug\ Resistance\ Rates = \frac{Resistant\ Isolates}{Total\ number\ of\ Isolates}$$

2. Calculating Drug Use Weight

$$Drug\ Use\ Weight = \frac{Antibiotics\ Use\ Data}{Total\ Period\ Antibiotics\ Use\ Data}$$

3. Calculating the Drug Resistance Index

The final step is to calculate the DRI, which is done by finding a product of resistance rates and drug use weight for each bacterium to obtain the drug-weighted resistance. The summation of Drug-weighted resistance of all therapeutic classes of antibiotics for each

bacterium will be the DRI of individual bacteria, as expressed in the equation below,

$$Drug\ Weighted\ Resistance = Drug\ Resistance\ Rate \times Drug\ Use\ Weight$$

Then,

$$the\ DRI = \sum Drug\ Weighted\ Resistance \times 100$$

DRI will either be presented in % or a fraction (decimal)

Drug Resistance Index Findings Interpretation

The DRI provides a reference to assess just how much of a threat AMR pose. A DRI below 25% is indicative that AMR is under control (20). Results are represented as a score of out of 100% between 0 and 100, with 0 indicating 100% susceptibility and 100 indicating 100% resistance (18).

Data Management and Analysis

Conventional methods were employed to identify bacterial infections, and the CLSI guidelines were used to interpret the results of antibiotic sensitivity tests (13). According to the Tanzania National Action Plan for Antimicrobial Resistance (NAP-AMR), 2023-2028, AST data was generated for antibiotic-resistant microorganisms in both priority samples (blood, pus, and urine). According to the NAP-AMR, 2023, data was evaluated to create antibiograms for each bacterium against various tested antibiotics(19). All relevant data were collected and entered into a Microsoft Excel spreadsheet for cleaning and analysis. Antimicrobial resistance surveillance in human health was done by collecting AST data from the hospital microbiology lab database for three years (2020, 2021, and 2022).

Patient and public involvement statement

Patients or the public were not involved in research designing, conducting, reporting, or disseminating plans

Results

Drug resistance indexes were obtained from *Escherichia coli* and *Klebsiella pneumoniae*, priority bacteria isolated from urine samples, and tested along antimicrobial groups, including Penicillins, 2nd and 3rd-generation Cephalosporins, Fluoroquinolones, Aminoglycosides, Tetracycline, Carbapenems, and Sulfonamide, as shown in Figure 1 below.

The DRI for bacteria isolated from blood samples included *Acinetobacter baumannii Escherichia coli Klebsiella pneumoniae, Streptococcus pneumoniae* and *Staphylococcus aureus*. These pathogens were tested on Penicillins, 3rd Generation Cephalosporins, Fluoroquinolones, Lincosamides, Tetracycline, Carbapenems, Sulfonamide, Glycopeptide and 2nd Generation Cephalosporins antimicrobial classes as shown in Figure 2 below.

The DRI for bacteria isolated from wounds/pus swabs included *Acinetobacter baumannii, Escherichia coli, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Staphylococcus aureus*. These pathogens were tested on Penicillins, 3rd Generation Cephalosporins, Fluoroquinolones, Aminoglycosides, Tetracycline, Carbapenems, Sulfonamide and 2nd Generation Cephalosporins antimicrobial classes, as shown in Figure 3 below.

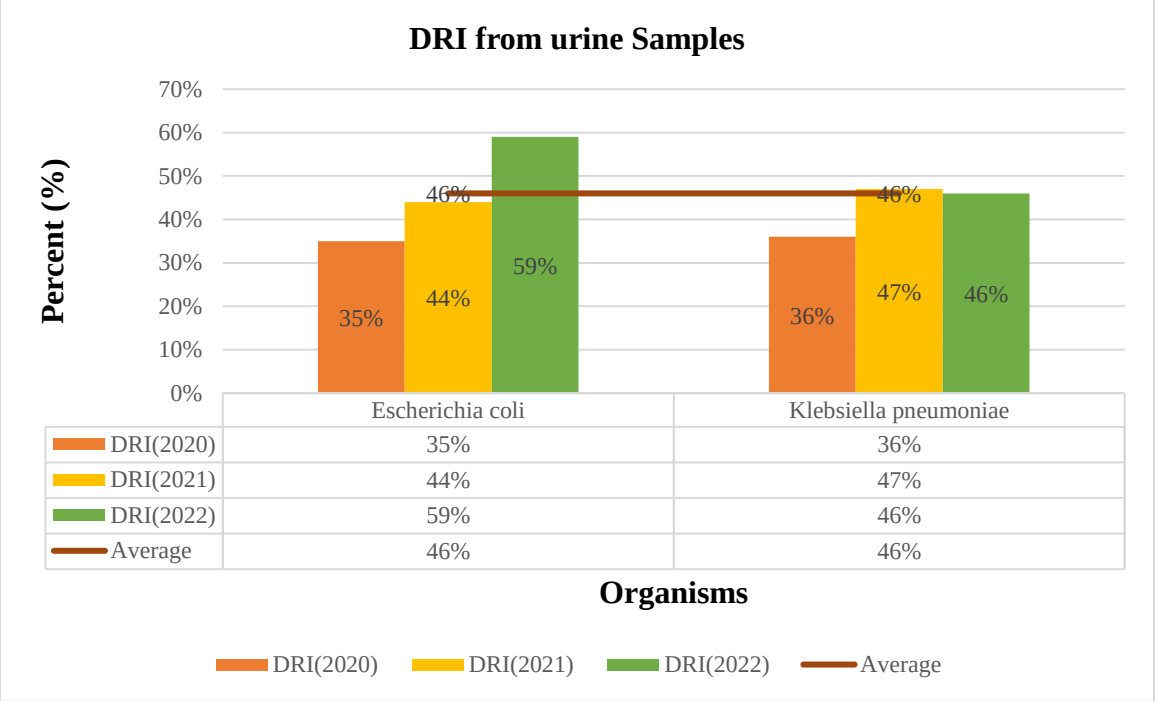

Figure 1. The DRI for bacteria isolated from urine sample

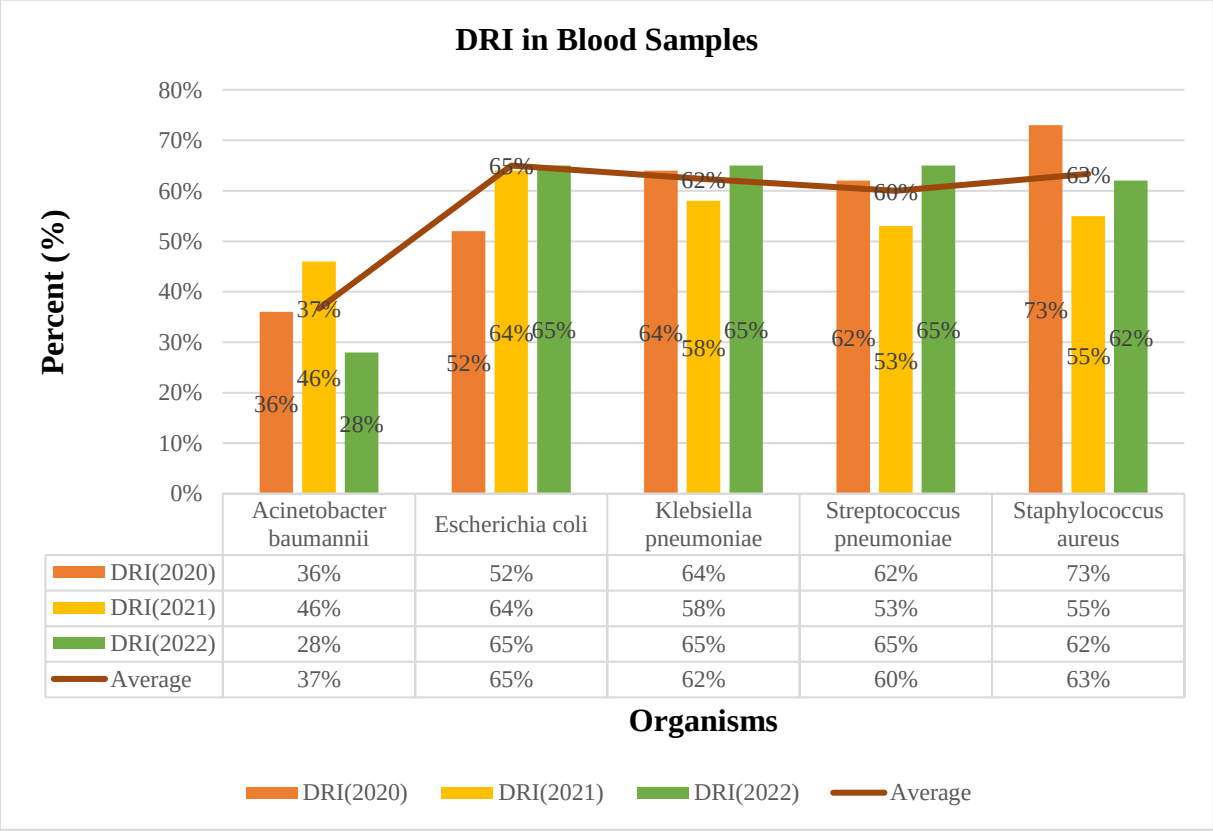

Figure 2. The DRI for bacteria isolated from blood samples

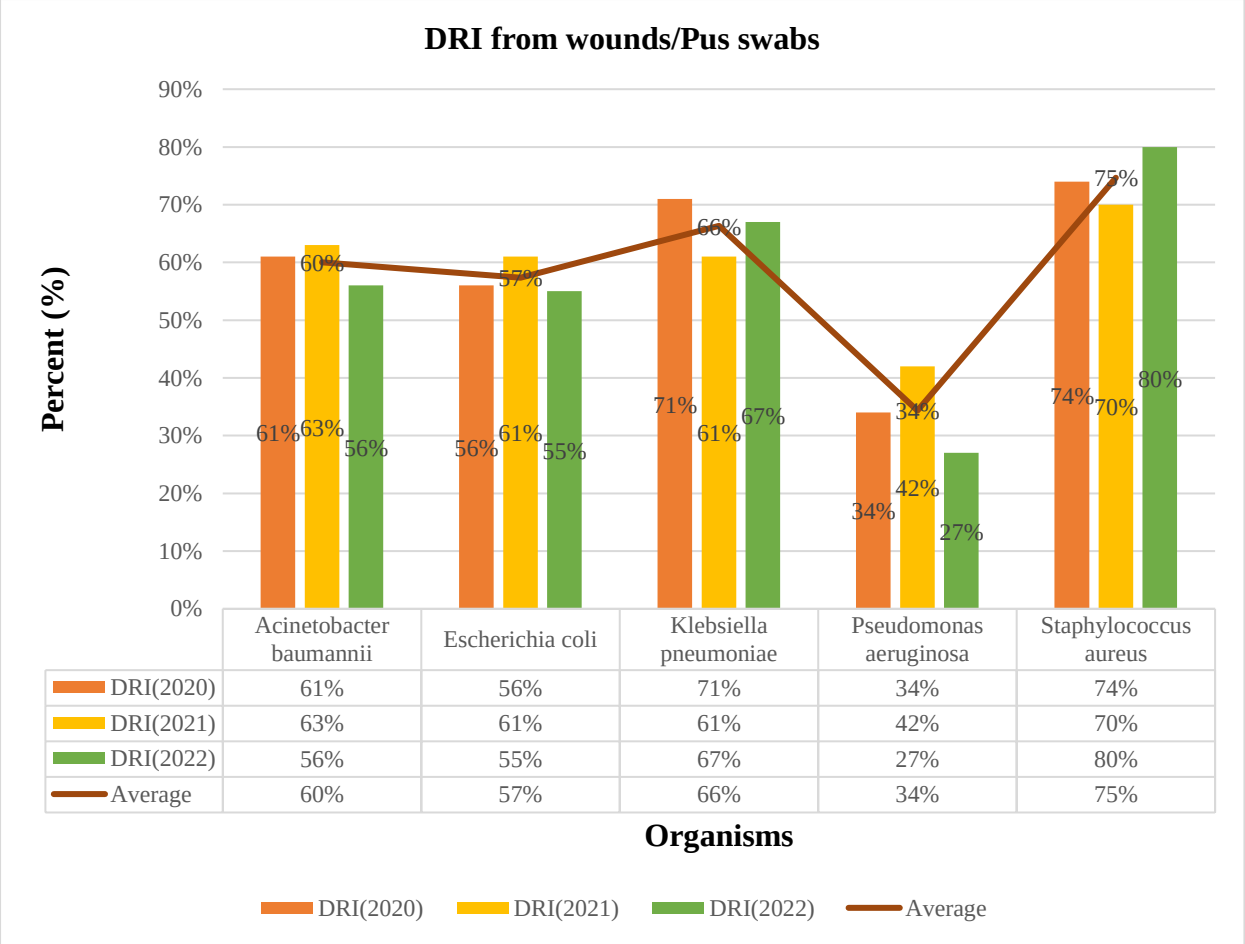

Figure 3. The DRI for bacteria isolated from wound/pus samples (swabs)

Discussion

In our study evaluating the DRI of bacterial isolates from blood, urine, and pus/wound swabs, we utilized aggregated data from various antimicrobial pharmacological classes. This data was instrumental in determining the extent of multidrug resistance (MDR) development among the bacteria within specific pharmacological categories.

Drug resistance indices were obtained from *Escherichia coli* and *Klebsiella pneumoniae*, priority bacteria isolated from urine samples, and tested in conjunction with antimicrobial groups, including Penicillins, 2nd and 3rd generation Cephalosporins, Fluoroquinolones, Aminoglycosides, Tetracyclines, Carbapenems, and Sulfonamides. The DRI for *Escherichia coli* and *Klebsiella pneumoniae* ranges from 35% to 39% and 36% to 47%, respectively. The assessment of the DRI for bacteria isolated from blood samples included *Acinetobacter baumannii* (26% to 46%), *Escherichia coli* (52% to 65%), *Klebsiella pneumoniae* (58% to 65%), *Streptococcus pneumoniae* (53% to 65%) and *Staphylococcus aureus* (55% to 73%). These pathogens were tested on Penicillins, 3rd Generation Cephalosporins, Fluoroquinolones, Lincosamides, Tetracycline, Carbapenems, Sulfonamide, Glycopeptide and 2nd Generation

Cephalosporins antimicrobial classes. The DRI for bacteria isolated from wounds/pus swabs included *Acinetobacter baumannii* (56% to 63%), *Escherichia coli* (55% to 61%), *Klebsiella pneumoniae* (61% to 71%), *Pseudomonas aeruginosa* (27% to 42%) and *Staphylococcus aureus* (70% to 80%). These pathogens were tested against Penicillins, 3rd Generation Cephalosporins, Fluoroquinolones, Aminoglycosides, Tetracyclines, Carbapenems, Sulfonamides, and 2nd Generation Cephalosporins, representing various antimicrobial classes. A DRI score below 25% signifies a reduced risk of MDR. The DRI serves as a valuable metric for evaluating the extent of the AMR and MDR threat. Specifically, a DRI score below 25% suggests that AMR and MDR is effectively managed(20). The results are quantified as a percentage score out of 100%, where 0% reflects complete susceptibility and 100% denotes total resistance (18).

A study conducted on community isolates of *Escherichia coli* from urinary samples in British Columbia between 2007 and 2010 revealed an overall DRI of 18% (5). This figure is notably lower than the 30% DRI reported by Laxminarayan and Klugman in 2006 (7), highlighting a potential shift in resistance patterns over the years. Our findings indicate a significantly elevated DRI for *Escherichia coli* across various clinical specimens, with percentages noted at 46% in urine, 65% in blood, and 57% in wound swabs. This contrasts sharply with the results presented in prior studies, underscoring the potential threat to infection management, particularly in cases of urinary tract infections (UTIs), resulting from the troubling rise in MDR. The DRI observed in our investigation has doubled compared to baseline metrics. Notably, our study is more contemporary than earlier research and is poised to substantially affect the cumulative antimicrobial resistance index at BMH. Moreover, a recent surveillance of AMR conducted within a tertiary hospital in Iasi, Romania, reported a markedly lower DRI of 12% in *Streptococcus pneumoniae* and 39% in *Klebsiella pneumoniae*. In stark contrast to these earlier findings, our results reveal even higher DRI values in these pathogens, with *Streptococcus pneumoniae* recorded at 68% and *Klebsiella pneumoniae* at 62%. In comparison with evidence, a pooled dataset from 41 countries in 2018, as reported by Klein and colleagues, showed variability in DRI from one country to another, with geographical differences being a suggested reason for the identified variability (7). This study indicated higher DRI (60 to 80%) in Thailand and India while South Africa had a DRI of <60%, as only sub-Saharan Africa (SSA) country was assessed. At the same time, developed countries like Sweden, Canada, and Norway had lower DRI than the United States and Germany, with DRI of 20-40% and 0-20%, respectively (7). The Mapping AMR and antimicrobial use (AMU) Partnership (MAAP project) was conducted in 14 African countries to measure and monitor AMR and AMU status and identify, collect, and analyse existing historical AMR data from 2016-2019. This MAAP project report calculated DRI scores from 12 of 14 African countries, showing that AMR is a significant hazard. All countries assessed scored at least twice the benchmark

of 25%. Scores of individual countries were Senegal, 79.80%; Malawi, 74.10%; Uganda, 69.0%; Cameroon, 68.60%; Zimbabwe, 66.60%; Nigeria, 65.90%; Gabon, 65.20%; Eswatini, 64.80%; Zambia, 60.80%; Burkina Faso, 64.0%; and Kenya, 56.20%. Fortunately, Tanzania had 56.10% of DRI and the lowest index compared with other countries participating in the surveillance(20).

Our findings underscore the significant impact of AMR at BMH, a key tertiary healthcare facility in the region. The elevated DRI observed at BMH can be primarily linked to its role as a tertiary-level hospital, where complex medical and surgical procedures are routinely performed. This environment necessitates a high volume of antibiotic usage for both prophylaxis and therapeutic purposes in response to infectious diseases. Furthermore, the hospital's extensive referral network and the prevalence of patients with treatment-resistant infections who have exhausted first-line and second-line antibiotic options contribute to a marked increase in severe infections and resistant pathogens. This scenario exacerbates the DRI, indicating that a substantial proportion of antibiotics prescribed at BMH may become ineffective over time due to resistance development. The emergence of MDR strains poses a significant threat to clinical practice, potentially restricting effective treatment options for bacterial infections such as sepsis, pneumonia, and UTI. This dilemma complicates the selection of empiric antibiotic regimens and surgical prophylaxis, thereby challenging standard care practices and requiring urgent attention to AMR mitigation strategies.

Study limitation

The results from this study cannot be generalised since it was a single-centre study. Only population samples were involved in the analysis. Another, key limitation of the DRI value is its reliance on an arithmetic model that aggregates data across all antimicrobials within the same pharmacological class, as well as total antimicrobial usage data. This aggregation can obscure the susceptibility profiles of individual antimicrobials, particularly those with retained susceptibilities or low rates of AMR, by masking them with those exhibiting high levels of AMR. The DRI is an essential instrument for assessing the effectiveness of antimicrobial therapies and scrutinising trends in bacterial resistance. A comprehensive evaluation of antibiotic efficacy, coupled with effective communication regarding the consequences of antimicrobial resistance, forms the foundation for designing AMS programs in healthcare environments. This framework not only aids institutions in conducting similar evaluations but also supports the formulation of more effective strategies to address this pressing global issue of antimicrobial resistance.

Conclusion and recommendation

All tested priority pathogens demonstrate a high likelihood of developing MDR, with a DRI exceeding 25%. This underscores the critical situation regarding AMR at the BMH. It is essential to enhance AMR surveillance, strengthen AMS initiatives, promote the rational use of antimicrobials, and strictly follow established treatment protocols. These actions are vital for restoring antibiotic sensitivity and mitigating the DRI. Further research could be conducted to compare the DRI across multiple

centres and to analyse trends over time. Such studies would be instrumental in evaluating DRI values across different facilities and could provide insights when correlated with patterns of high antimicrobial consumption and AMR trends.

Abbreviations

AMR: Antimicrobial Resistance
AMS: Antimicrobial Stewardship
AMU: Antimicrobial Use
AST: Antimicrobial Susceptibility Testing
BMH: Benjamin Mkapa Hospital
CLSI : Clinical Laboratory Standard Institute
DRI: Drug Resistance Index
ICU: Intensive Care Units
IDDS: Infectious Disease Detection and Surveillance
IHMIS: Integrated Health Management Information System
ISO: International Standard Organisation
MAAP: Mapping Antimicrobial Resistance and Antimicrobial Use Partnership
MDR: Multi-Drug Desistance
MDROs: Multi-Drug Resistance Organisms
MTaPS: Medicines, Technologies, and Pharmaceutical Services
NatHREC: The National Institute for Medical Research and the National Health Research Ethics Committee
SADCAS: Southern African Development Community Accreditation Services
SSA: Sub-Saharan Africa
UTIs: Urinary Tract Infections

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Ethics approval

The National Institute for Medical Research and the National Health Research Ethics Committee (NatHREC) granted the study an ethical clearance certificate with reference number NIMR/HQ/R. 8a/Vol. IX/4260 and BMH authority permitted the study to be conducted in the hospital.

Authors' contributions

KBZ and YJY were responsible for developing the conceptual framework of the study. The manuscript design was collaboratively undertaken by KBZ and CAC. All authors contributed to data collection and the sourcing

of relevant references. YJY, CAC, and MMS drafted the initial version of the manuscript, which was subsequently enhanced and refined by KBZ. Both KBZ and MMS approved the final version. KBZ served as the guarantor, ensuring the integrity and accountability of the overall content.

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Patient consent for publication

Not required

Data availability statement

The data that support the findings of this study are available on request from the corresponding author. The data are not publicly available due to privacy or ethical restrictions.

Supplementary material

STROBE Checklist: STROBE Statement-Checklist of items that should be included in reports of cross-sectional studies.

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Supplementary material

STROBE Statement—Checklist of items that should be included in reports of cross-sectional studies.

	Item No	Recommendation	Reported in section
Title and abstract	1	(*a*) Indicate the study's design with a commonly used term in the title or the abstract	YES, tittle page and page 1
		(*b*) Provide in the abstract an informative and balanced summary of what was done and what was found	YES page 1, 2
Introduction			
Background/rationale	2	Explain the scientific background and rationale for the investigation being reported	YES, page 3 and 4
Objectives	3	State specific objectives, including any prespecified hypotheses	YES page 1, 3 and 4
Methods			
Study design	4	Present key elements of study design early in the paper	YES page 4
Setting	5	Describe the setting, locations, and relevant dates, including periods of recruitment, exposure, follow-up, and data collection	YES page 4
Participants	6	(*a*) Give the eligibility criteria, and the sources and methods of selection of participants	N/A We included three years cumulative from (2020-2022) of combined total isolates, resistance isolates, and antibiotics use data.
Variables	7	Clearly define all outcomes, exposures, predictors, potential confounders, and effect modifiers. Give diagnostic criteria, if applicable	N/A We included three years cumulative from (2020-2022) of combined total isolates, resistance isolates, and

			antibiotics use data.
Data sources/ measurement	8*	For each variable of interest, give sources of data and details of methods of assessment (measurement). Describe comparability of assessment methods if there is more than one group	YES page 5 and 6
Bias	9	Describe any efforts to address potential sources of bias	YES page 7
Study size	10	Explain how the study size was arrived at	YES, PAGE 6
Quantitative variables	11	Explain how quantitative variables were handled in the analyses. If applicable, describe which groupings were chosen and why	YES, 6-7
Statistical methods	12	(*a*) Describe all statistical methods, including those used to control for confounding	YES, page 5-7
		(*b*) Describe any methods used to examine subgroups and interactions	N/A
		(*c*) Explain how missing data were addressed	YES, 7
		(*d*) If applicable, describe analytical methods taking account of sampling strategy	YES, page 7
		(*e*) Describe any sensitivity analyses	N/A
Results			
Participants	13*	(a) Report numbers of individuals at each stage of study—eg numbers potentially eligible, examined for eligibility, confirmed eligible, included in the study, completing follow-up, and analysed	N/A
		(b) Give reasons for non-participation at each stage	N/A
		(c) Consider use of a flow diagram	N/A
Descriptive data	14*	(a) Give characteristics of study participants (eg demographic, clinical, social) and information on exposures and potential confounders	N/A
		(b) Indicate number of participants with missing data for each variable of interest	N/A

Outcome data	15*	Report numbers of outcome events or summary measures	N/A
Main results	16	(*a*) Give unadjusted estimates and, if applicable, confounder-adjusted estimates and their precision (eg, 95% confidence interval). Make clear which confounders were adjusted for and why they were included	YES, 8 and figures
		(*b*) Report category boundaries when continuous variables were categorized	N/A
		(*c*) If relevant, consider translating estimates of relative risk into absolute risk for a meaningful time period	N/A
Other analyses	17	Report other analyses done—eg analyses of subgroups and interactions, and sensitivity analyses	YES, 8
Discussion			
Key results	18	Summarise key results with reference to study objectives	YES, page 8 to 10
Limitations	19	Discuss limitations of the study, taking into account sources of potential bias or imprecision. Discuss both direction and magnitude of any potential bias	YES, page 10
Interpretation	20	Give a cautious overall interpretation of results considering objectives, limitations, multiplicity of analyses, results from similar studies, and other relevant evidence	YES, page 10
Generalisability	21	Discuss the generalisability (external validity) of the study results	YES, 11
Other information			
Funding	22	Give the source of funding and the role of the funders for the present study and, if applicable, for the original study on which the present article is based	YES, 12

*Give information separately for exposed and unexposed groups.

Note: An Explanation and Elaboration article discusses each checklist item and gives methodological background and published examples of transparent reporting. The STROBE checklist is best used in conjunction with this article (freely available on the Web sites of PLoS Medicine at http://www.plosmedicine.org/, Annals of Internal Medicine at http://www.annals.org/, and Epidemiology at http://www.epidem.com/). Information on the STROBE Initiative is available at www.strobe-statement.org.