



Characterization of Multi-Drug-Resistant Gram-Negative Bacteria Isolated from Outpatient at Kabwe Central Hospital

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How to cite this paper: Mumbole, H. and Nakazwe, M. (2025) Characterization of Multi-Drug-Resistant Gram-Negative Bacteria Isolated from Outpatient at Kabwe Central Hospital. *Open Access Library Journal*, 12: e13308.

<https://doi.org/10.4236/oalib.1113308>

Received: March 20, 2025

Accepted: April 19, 2025

Published: April 22, 2025

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Abstract

The prevalence of multi-drug resistant (MDR) Gram-negative bacteria has emerged as a significant public health concern, particularly among outpatients. In low-income countries like Zambia, infectious diseases stand as prominent contributors to mortality rates. The absence of robust indigenous data on pathogenic agents and antimicrobial resistance hampers the effectiveness of empirical treatment. The escalating concern of multi-drug resistance (MDR) across various diseases poses a significant public health challenge, leading to prolonged treatment durations, increased disabilities, and diminished life expectancy. This study aimed to characterize MDR Gram-negative isolates collected from outpatient settings at Kabwe central hospital (KCH) to identify prevalence and resistance patterns. Clinical specimens, including urine, stool, blood, wound swabs, etc. were collected. Antibiotic susceptibility testing was conducted to identify multi-drug-resistant gram-negative bacteria. Descriptive analysis was used to characterize multi-drug-resistant gram-negative Bacteria isolated from outpatient. A total of 441 Gram-negative isolates clinical samples were analyzed, of which 342 (77.6%) were classified as MDR with percentages ranging from 57.7% for *Proteus* species to 100.0% for *Salmonella*, *Shigella*, and *Proteus species*. Urinary tract infection (32.5%) was the most common cause of infections among children and young people, and which was predominantly caused by *E. coli*, *Proteus spp.* and *Citrobacter spp.* during the period of our study. These findings highlight the urgent need for surveillance and antimicrobial stewardship programs for the empirical treatment of infections in Kabwe General Hospital in Zambia as appropriate.

Subject Areas

Microbiology

Keywords

Multidrug-Resistance, Antimicrobial, Gram-Negative, Outpatient

1. Introduction

1.1. Background

Multi-drug-resistant Gram-negative bacteria have become a significant global health concern, with their prevalence increasing in healthcare settings. These bacteria, such as *Escherichia coli*, *Klebsiella pneumoniae*, *proteus species*, *Citrobacter species*, *Salmonella* and *Shigella* have developed resistance to multiple antibiotics, limiting treatment options and leading to high rates of treatment failure and mortality [1]. *Escherichia coli* (*E. coli*), *Klebsiella pneumoniae*, *proteus species*, *Citrobacter species*, *Salmonella* and *Shigella* are gram-negative rod belonging to the *Enterobacteriales* order [2]. They are among the microorganisms that have developed considerable levels of resistance to most antimicrobials used in humans [3].

According to recent statistics from the World Health Organization (WHO), approximately 700,000 deaths worldwide are attributed to antimicrobial-resistant infections every year, with Gram-negative bacteria accounting for a significant portion of these cases [4]. In outpatient settings, the prevalence of multi-drug-resistant Gram-negative bacteria is a growing concern, with studies reporting up to 30% of outpatient infections being resistant to commonly prescribed antibiotics [5]. Understanding the prevalence and characteristics of multi-drug-resistant Gram-negative bacteria among Outpatient Department (OPD) patients is essential for implementing infection control measures and optimizing treatment strategies to combat these resistant pathogens. Despite the escalating crisis of antimicrobial resistance, there is a notable gap in comprehensive data regarding the epidemiology of multi-drug-resistant bacteria specifically in OPD settings in Zambia [6]. Therefore, a comprehensive assessment of multi-drug resistant Gram-negative bacterial prevalence and characterization in outpatient department patients is crucial for understanding the scope of the problem and implementing effective intervention strategies. The findings of this study are expected to contribute valuable information to the existing body of knowledge on antimicrobial resistance and inform future interventions in outpatient care settings.

1.2. Statement of the Problem

The emergence of multidrug-resistant Gram-negative bacteria is a major concern in hospital settings in many parts of the world. Infections caused by these pathogens have become significantly challenging over the past two decades, particularly in developing countries, and are associated with high morbidity and mortality rates as well as protracted hospital stays [7]. *Enterobacteriaceae*, including *Esche-*

richia coli (E. coli), Klebsiella pneumoniae, proteus species, Citrobacter species, Salmonella and Shigella have been identified as major cause of multi-drug-resistant bacterial infections [2].

Numerous studies have established that the overuse and misuse of antibiotics in human medical sectors promote the development and spread of multidrug-resistant (MDR) pathogens and allow for the emergence of novel resistance mechanisms [8].

The significance of MDR infections has been estimated by the global burden of disease (GBD) study, where it was shown that ~1.27 million (95% UI: 0.91 - 1.71 million) deaths were directly attributable to bacterial MDR globally in the year 2019 alone [9]. Among these MDR bacteria, *Escherichia coli (E. coli), Klebsiella pneumoniae, proteus species, Citrobacter species, Salmonella and Shigella* were the most significant and associated with ~0.93 million (95% UI: 0.66 - 1.27 million) directly attributable deaths [9].

In recent years, the rise of MDR *Enterobacteriaceae* mentioned have been documented in almost all countries worldwide [3].

The presence of these antimicrobial-resistant in humans calls for a holistic, multi-disciplinary collaborative action guided by the World Health Organization Global Action Plan (GAP) on AMR [10]. The One Health approach aims to address AMR across all humans as there is a higher transmission potential at the human interface [10]. Therefore, a one health approach (*i.e.*, the systems thinking within ecological systems) promotes, and is an integral part of, antimicrobial stewardship (AMS) programmes for the prudent of antimicrobials in humans [11].

Most AMR data come from high-income countries (HICs), while the AMR burden of sub-Saharan Africa (SSA) including Zambia is inadequately documented.

In Zambia, the National Action Plan (NAP) on AMR was developed in 2017 in line with the GAP on AMR to tackle this problem using a One Health approach [12]. Alongside this, some studies have been published to promote AMS in humans in this geographical region [13]. However, there is still very little information on the isolation, resistance patterns and antibiotic susceptibility of *Escherichia coli (E. coli), Klebsiella pneumoniae, proteus species, Citrobacter species, Salmonella and Shigella* originating in outpatient at KCH in Zambia.

1.3. Rationale and Justification

Kabwe Central Hospital serves as a critical healthcare facility in central province and surrounding region, catering to a diverse patient population. Understanding the prevalence and characteristics of multi-drug-resistant Gram-negative bacteria among OPD patients at this hospital is essential for devising targeted interventions to address local challenges. We can also contribute to ongoing surveillance efforts and support evidence-based antimicrobial prescribing practices. Finally, addressing the threat of multi-drug-resistant Gram-negative bacteria is paramount to ensuring patient safety and maintaining the quality of care provided at Kabwe Central Hospital.

1.4. Objectives

1.4.1. General Objective

To investigate the characteristics of multi-drug-resistant Gram-negative bacteria isolated from outpatient at Kabwe central hospital.

1.4.2. Specific Objectives

1) To determine the prevalence of multi-drug-resistant Gram-negative bacteria such as *Escherichia coli*, *Klebsiella pneumoniae*, *proteus species*, *Citrobacter species*, *Salmonella* and *Shigella* among different age groups of OPD patients at Kabwe Central Hospital.

2) To phenotypically characterize multi-drug-resistant Gram-negative bacteria such as *Escherichia coli*, *Klebsiella pneumoniae*, *proteus species*, *Citrobacter species*, *Salmonella* and *Shigella* isolated from outpatients at KCH.

3) To determine the susceptibility profiles of multi-drug-resistant Gram-negative bacteria such as *Escherichia coli*, *Klebsiella pneumoniae*, *proteus species*, *Citrobacter species*, *Salmonella* and *Shigella* isolated from outpatient at KCH.

2. Literature Review

2.1. Epidemiology of Multi-Drug-Resistant Gram-Negative Bacteria

2.1.1. Global Burden

In the United States, the 2013 CDC report revealed that approximately 6.6% of the 140,000 most severe healthcare-associated *Enterobacterales* infections annually are resistant to *carbapenems*. Additionally, 63% of the 12,000 *Acinetobacter* infections and 13% of the estimated 51,000 *Pseudomonas* infections demonstrate multidrug resistance. Although the 2019 report indicates a relative decline in the incidence of several of these infections, the prevalence of *carbapenem*-resistant cases remains stable, emphasizing the persistent global threat posed by MDR organisms. In Europe, *Pseudomonas aeruginosa* stands out with the highest reported levels of MDR infections, particularly in some Southern and Southeastern European countries, where carbapenem resistance reached alarming rates of up to 63% in 2017.

2.1.2. Regional Perspective

In the context of epidemiology, the burden of multi-drug resistant (MDR) Gram-negative bacteria in Africa is a topic of critical concern. The World Health Organization (WHO) and other global health bodies recognize the escalating threat posed by these pathogens. Among the WHO's priority-resistant bacteria, three *carbapenem*-resistant *Enterobacterales*, *carbapenem*-resistant *Acinetobacter baumannii*, and *carbapenem*-resistant *Pseudomonas aeruginosa* are classified as "critical," signifying the highest level of concern [14]. These formidable adversaries, all belonging to the Gram-negative family, exhibit intricate resistance mechanisms, including AmpC enzymes, extended-spectrum β -lactamases (*ESBLs*), and *carbapenemases*. Notably, Africa faces specific challenges, including socio-economic conflicts, over/misuse of antibiotics, and inadequate infection control measures. Ongoing research and surveillance efforts are essential to monitor prev-

alence, track resistance genes, and understand geographical distribution. By addressing these challenges, the global health community can safeguard patient outcomes and combat this critical threat [15].

In the vast landscape of medical bacteria, certain Gram-negative species stand out. From a comprehensive review of 167 articles by WHO, ten key players were selected for closer examination. These bacteria include *Acinetobacter baumannii*, *Escherichia coli* (*E. coli*), *Haemophilus spp.*, *Klebsiella spp.*, *Neisseria spp.*, *Proteus mirabilis*, *Pseudomonas spp.*, *Salmonella Typhi*, non-typhoidal *Salmonella serovars*, and *Shigella spp* [14].

To assess their resistance patterns, these Gram-negative bacteria were tested against an array of 28 antibiotics. The list includes familiar names like amoxicillin, ciprofloxacin, and tetracycline. Among these contenders, *Klebsiella spp.* emerged as the most frequently tested and, unfortunately, the most resistant. *E. coli*, on the other hand, displayed notable resistance percentages for several antibiotics, including amoxicillin, ampicillin, and trimethoprim/sulfamethoxazole. Interestingly, when it comes to *imipenem* resistance, *E. coli* takes the lead, while *meropenem* resistance is evenly shared between *E. coli* and *Haemophilus spp.* These findings underscore the urgent need for effective antibiotic stewardship and infection control measures to combat the rising tide of resistance.

2.1.3. Local Perspective

The burden of antimicrobial resistance (AMR) in Zambia

The epidemiology of multi-drug resistant Gram-negative (MDR-GN) bacteria in Zambia. This critical issue has garnered attention from global health organizations, including the World Health Organization (WHO). Among the WHO's priority resistant bacteria, three-*carbapenem*-resistant *Enterobacterales*, *carbapenem*-resistant, *Acinetobacter baumannii*, and *carbapenem*-resistant *Pseudomonas aeruginosa* are classified as "critical," signifying the highest level of concern [14]. These formidable adversaries, all belonging to the Gram-negative family, exhibit intricate resistance mechanisms, including *AmpC* enzymes, extended-spectrum β -lactamases (*ESBLs*), and *carbapenemases*.

In 2019, Zambia witnessed 3700 deaths directly attributable to antimicrobial resistance (AMR) and an additional 15,600 deaths associated with AMR. Notably, Zambia ranks 14th globally in age-standardized mortality rates associated with AMR. Within the Eastern Sub-Saharan Africa region, Zambia stands as the 5th highest in age-standardized mortality across 15 countries. The impact of AMR surpasses deaths from respiratory infections, tuberculosis, and other significant causes. Key pathogens of concern in Zambia include *Klebsiella pneumoniae*, *Staphylococcus aureus*, *Streptococcus pneumoniae*, *Escherichia coli*, and *Salmonella Typhi*. These bacteria commonly cause lower respiratory infections, bloodstream infections, and other serious conditions [15]. Efforts are underway, including the development of a National AMR action plan, to combat this critical threat. By enhancing surveillance, understanding local epidemiology, and ensuring adequate resources, Zambia aims to safeguard patient outcomes and address the ever-

increasing challenge of antibiotic resistance [15]. Unfortunately, there is a huge deficit on literature about MDR-GN in Zambia.

2.2. Mechanisms of Resistance

Antimicrobial resistance is a global health concern, particularly in Gram-negative bacteria. Key mechanisms include *AmpC* enzymes, Extended-spectrum β -lactamases (*ESBLs*), and *Carbapenemases*, which confer resistance to a wide range of antibiotics. Current treatments involve a combination of older drugs (such as meropenem, colistin, and tigecycline) and newer agents (including ceftazidime/avibactam, ceftolozane/tazobactam, and eravacycline) [5]. Researchers are exploring novel targets like efflux pumps and strategies to improve outer membrane permeability. Continued research is crucial to combat this global health challenge. For further reading, refer to Bassetti and Garau's article on the treatment of multidrug-resistant Gram-negative infections.

Antimicrobial resistance is a global public health crisis, with multidrug-resistant Gram-negative bacteria posing a significant threat to patient care and healthcare systems. In outpatient departments, the presence of MDR-GN pathogens has far-reaching clinical implications, including prolonged hospital stays, increased healthcare costs, and higher mortality rates. Effective infection control measures, antimicrobial stewardship programs, and surveillance strategies are essential to mitigate the impact of resistant pathogens on patient outcomes [1]. Antimicrobial resistance is a multifaceted and dynamic phenomenon, influenced by intricate interactions among various factors. These factors include direct elements like the inappropriate use of antimicrobials in both humans and agricultural animals, as well as indirect factors such as environmental pollution and inadequate sanitation [5]. Additionally, as Matteo B & javier cited [16], the inherent characteristics of bacteria play a significant role. Researchers have identified previous antibiotic exposure, underlying health conditions, and invasive medical procedures as key risk factors associated with resistance. However, it's important to note that the specific risk factors for the spread of resistance can vary based on geographical context. For instance, in developing countries, poor sanitation and limited access to clean drinking water contribute significantly to the dissemination of antimicrobial resistance [1].

Despite the growing recognition of the multi-drug-resistant Gram-negative bacteria as posing threat to human health, there are still gaps in existing literature. Limited research has been conducted in specific geographic regions, such as Kabwe Central Hospital, Kabwe district, Zambia. Furthermore, more comprehensive studies are needed to analyze the prevalence and characterization of multi-drug-resistant Gram-negative bacteria among Outpatient Department (OPD) patients in resource-constrained settings. The literature review serves as the foundation for the study by identifying gaps in the literature, providing a comprehensive overview of the existing knowledge related to the prevalence and impact of multi-drug-resistant Gram-negative bacteria among Outpatient.

2.3. Conceptual Framework

This framework guides the research on understanding the prevalence and characterization of multi-drug-resistant Gram-negative bacteria among OPD patients at Kabwe Central Hospital, contributing to improved treatment approaches and antimicrobial stewardship. (See **Figure 1**)

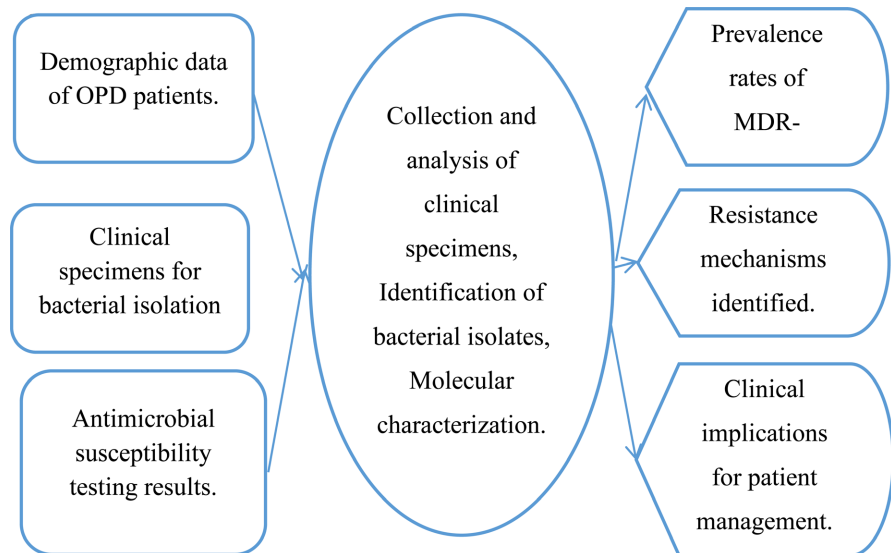


Figure 1. Conceptual framework.

3. Methodology

3.1. Study Site

Kabwe Central Hospital is a prominent healthcare facility serving a large population in the Central Province of Zambia. It is a tertiary care hospital offering a wide range of medical services, including outpatient department consultations, inpatient care, and specialized treatment.

By conducting the study at Kabwe Central Hospital, the research aims to leverage the diverse patient population, clinical expertise, and infrastructure of the facility to investigate the prevalence and characterization of multi-drug-resistant Gram-negative bacteria among OPD patients in the Zambian healthcare setting.

KCH, located in Zambia, serves as a vital healthcare facility catering to a diverse patient population. With the rise of antimicrobial resistance worldwide, monitoring the prevalence of multi-drug-resistant Gram-negative bacteria in outpatient settings at this hospital is essential for guiding clinical decision-making and infection control measures. Previous studies have highlighted the growing concern of antimicrobial resistance in healthcare settings, emphasizing the need for continuous surveillance and research in this area [6].

3.2. Study Design

A cross-sectional study was conducted from May to October 2024 at Kabwe Central Hospital outpatient department. A total of 441 clinical samples (urine, wound

swabs, and sputum) were collected from outpatients presenting with infections.

3.3. Bacterial Isolation and Identification

Isolates were identified using standard microbiological techniques, including Gram staining, biochemical assays, and matrix-assisted laser desorption ionization-time of flight (MALDI-TOF) mass spectrometry.

3.4. Antimicrobial Susceptibility Testing

Antibiotic susceptibility was determined by the Kirby-Bauer disk diffusion method. Minimum inhibitory concentrations (MICs) for critical antibiotics were measured using broth micro-dilution. Resistance was interpreted according to Clinical and Laboratory Standards Institute (CLSI) guidelines.

3.5. Data Analysis

The raw data of the isolates was summarized, cleaned, and coded in Microsoft Excel 2016 (Microsoft Corp., Redmond, WA, USA). Descriptive analysis was conducted using the data using means, medians, ranges, and percentages to calculate the following:

- The proportion of patients with multi-drug-resistant Gram-negative bacteria.
- Compare resistance patterns across different demographic and clinical sub-groups.
- Identify types of bacteria that are multi-drug resistant.

The analyses will be performed using the Statistical Package for Social Sciences (SPSS), version 26.0 (IBM Corp, Armonk, NY, USA). The normality of the data will be assessed through the Kolmogorov-Smirnov test.

All statistical tests will be performed at a 95% confidence level with a $p < 0.05$ indicating statistical significance.

4. Results

The samples were collected from patients with the clinical conditions listed in supplementary information.

Of the 441 resistant Gram-negative bacterial isolates obtained, *E. coli* was most frequent pathogen 269 (61%), followed by *Proteus spp* 54 (12%), *Citrobacter spp* 52 (12%), *Klebsiella spp* 16 (4%), *Salmonella spp* 2 (0.5%), *Shigella spp* 2 (0.5%) and Other 46 (10%). The other 46 (10%) (**Table 1**) consisted of *Bacillus spp.*, *Enterobacter spp.*, *Vibrio.cholerae*, *Yersinia enterocolitica* and *psuedomonas spp.* The distribution of the specimen types showed the highest proportion of isolates, were from pus specimens 128 (29%), followed by stool specimens 119 (27%), urine specimen 104 (24%) and high vaginal swab 42 (9%). The remaining (others) 48 (11%) included Cerebral spinal fluid, Ascitic fluid, Aspirate, blood, rectal swab, semen, sputum, throat swab and urethral swab. The highest cause of infection during the period of our study was urinary tract infection 144 (32.5%) followed by suspected cholera 40 (9.1%) and the remaining individual cause of infection was

Table 1. Demographic & clinical characteristics of patients with bacterial infections.

	Total (N = 441)	<i>E. coli</i> 269 (61%)	Citrobacter spp 52 (12%)	Klebsiella spp 16 (4%)	Proteus spp 54 (12%)	Salmonella spp 2 (0.5%)	Shigella spp 2 (0.5%)	Other 46 (10%)
Age group (years)								
1 - 22	157 (36%)	89 (33%)	22 (42%)	9 (56%)	22 (41%)	0 (0%)	0 (0%)	15 (33%)
23 - 45	156 (35%)	93 (35%)	10 (19%)	6 (38%)	26 (48%)	0 (0%)	2 (100%)	19 (41%)
46 - 68	72 (16%)	55 (20%)	12 (23%)	1 (6%)	0 (0%)	0 (0%)	0 (0%)	4 (9%)
69 - 88	56 (13%)	32 (12%)	8 (16%)	0 (0%)	6 (11%)	2 (100%)	0 (0%)	8 (17%)
Sex								
Female	242 (55%)	151 (56%)	28 (54%)	6 (38%)	29 (54%)	2 (100%)	0 (0%)	26 (57%)
Male	199 (45%)	118 (44%)	24 (46%)	10 (62%)	25 (46%)	0 (0%)	2 (100%)	20 (43%)
Sample type								
Pus	128 (29%)	58 (21%)	12 (23%)	4 (25%)	38 (71%)	0 (0%)	0 (0%)	16 (35%)
Urine	104 (24%)	78 (29%)	16 (31%)	2 (13%)	4 (7%)	0 (0%)	0 (0%)	4 (9%)
Stool	119 (27%)	79 (30%)	11 (21%)	7 (44%)	4 (7%)	2 (100%)	2 (100%)	14 (30%)
HVS*	42 (9%)	34 (13%)	6 (12%)	0 (0%)	2 (4%)	0 (0%)	0 (0%)	0 (0%)
Other**	48 (11%)	20 (7%)	7 (13%)	3 (18%)	6 (11%)	0 (0%)	0 (0%)	12 (26%)
Clinical conditions								
UTI	144(32.5%)	75 (28%)	30 (58%)	6 (38%)	32 (59%)	2 (100%)	0 (0%)	20 (43%)
Suspected cholera	40 (9.1%)	19 (7%)	11 (21%)	5 (31%)	12 (22%)	0 (0%)	0 (0%)	19 (41%)
***	257 (58.4%)	175 (65%)	11 (21%)	5 (31%)	10 (19%)	0 (0%)	2 (100%)	7 (16%)

*High vaginal swab **Includes Cerebral spinal fluid, Ascitic fluid, Aspirate, blood, rectal swab, semen, sputum, throat swab and urethral swab ***Denotes the rest of clinical conditions listed in the supplementary information.

negligible but cumulatively the rest cause infection listed in the opening paragraph of this chapter accounted for the remaining 58.4%.

4.1. Demographic Characteristics of Patients with Bacterial Infections

The patients' ages ranged between 1 to 88 years and mean age was 35.16 ± 22.56 years with the gender distribution of 199 (45%) males and 242 (55%) females. The prevalence of infections were highest among the patients of age-group 1 - 22 years 157 (36%) followed by 23 - 45 years 156 (36%), 46 - 68 years 72 (16%) and 69 - 88 years 56 (13%) (Table 1). *E. coli* was highest among the age-group 23 - 45 years 93 (35%) followed by 1 - 22 years 89 (33%) and least 69 - 88 years 32 (12%). Among gender, *E. coli* was highest among females 151 (56%).

4.2. Susceptibility Profile

The antibiotic susceptibility profile showed that the isolates were most resistant

to Ciprofloxacin 206 (59%), Chloramphenicol 122 (49%), Gentamycin 105 (50%), Doxycycline 85 (93%), Tetracycline 82 (87%), Cefotaxime 81 (58%) and were least resistant to Tazobactam 13 (52%) (**Table 2**).

Table 2. Antibiotic susceptibility profile of isolates.

	Total (N = 441)	Resistant N (%)	Susceptible N (%)	Sensitive N (%)	Intermediate N (%)
Penicillin	26 (6%)	26 (100%)	-	-	-
Azithromycin	89 (20%)	39 (44%)	36 (40%)	-	14 (16%)
Doxycycline	91 (21%)	85 (93%)	6 (7%)	-	-
Ciprofloxacin	352 (80%)	206 (59%)	103 (29%)	-	43 (12%)
Ceftriaxone	69 (16%)	39 (57%)	23 (33%)	-	7 (10%)
Co-trimoxazole	34 (8%)	34 (100%)	-	-	-
Imipenem	2 (1%)	-	2 (100%)	-	-
Nitrofurantoin	95 (22%)	59 (62%)	22 (23%)	-	14 (15%)
Erythromycin	54 (13%)	44 (81%)	1 (2%)	-	9 (17%)
Tetracycline	94 (21%)	82 (87%)	12 (13%)	-	-
Gentamycin	212 (48%)	105 (50%)	101 (48%)	-	6 (2%)
Chloramphenicol	251 (57%)	122 (49%)	117 (47%)	2 (1%)	10 (3%)
Tazobactam	25 (5%)	13 (52%)	3 (12%)	-	9 (36%)
Cephalexin	50 (11%)	45 (90%)	5 (10%)	-	-
Amoxicillin	37 (8%)	31 (84%)	4 (11%)	-	2 (5%)
Nalidixic acid	79 (18%)	59 (74%)	14 (18%)	-	6 (8%)
Peperocillin	1 (0.5%)	-	-	-	1 (100%)
Cefotaxime	141 (32%)	81 (58%)	31 (22%)	3 (2%)	26 (18%)
Ampicillin	71 (16%)	55 (78%)	8 (11%)	-	8 (11%)
Meropen	5 (3%)	-	-	5 (100)	-

4.3. Multi-Drug Resistance

Multidrug resistance was observed in 77.6% of the bacterial isolates, ranging from 57.7% in *Proteus spp* to 100.0% in *Proteus spp.*, *Salmonella spp.* and *Shigella spp.* (**Table 3**).

Table 3. MDR among isolates.

Bacterial isolates	Number of isolates N	MDR N (%)
<i>E. coli</i>	269	200 (74.3%)
Citrobacter spp	52	50 (96.2)
Klebsiella spp	16	16 (100%)
Proteus spp	54	30 (57.7%)

Continued

Salmonella spp	2	2 (100%)
Shigella spp	2	2 (100%)
Other	46	42 (91.3%)
Total	441	342 (77.6)

5. Discussion

Our study observed the higher prevalence of infections among the patients of age-group 1 - 22 years 157 (36%) followed by 23 - 45 years 156 (36%). The frequency of bacterial pathogens isolated from male (45%) and female (55%) patients, showed appreciable difference. Urinary tract infection (32.5%) was most prevalent within the period of our study and is comparable to 31.5% reported from a study on prevalence and antibiotic susceptibility pattern of pathogens conducted in secondary hospital in Zambia for outpatients [17].

The susceptibility profile of the isolates displayed high-level drug resistance of Ciprofloxacin (59%), Chloramphenicol (49%), Gentamycin (50%), Doxycycline (93%), Tetracycline (87%), Cefotaxime (58%) and were least resistant to Tazobactam (52%) observed, was consistent with other studies conducted in Zambia [13].

The study also observed a high prevalence of MDR Gram-negative bacteria. The high prevalence of MDR Gram-negative bacteria among outpatients underscores the growing threat of antibiotic resistance in community settings. The predominance of *E. coli* and *Proteus spp* aligns with previous studies, suggesting the need for targeted interventions. Ciprofloxacin resistance, though less frequent, highlights the importance of monitoring emerging resistance mechanisms [18]-[20].

5.1. Limitation

The study didn't explore phenotypic characterization to determine the genetic basis of antibiotic resistance. The study didn't also explore risk factors of MDR due to insufficient information on the outpatient's data collection sheet. There is limited literature on which these findings can be comparable to.

5.2. Conclusion

The study demonstrated high multidrug resistant Gram-negative bacteria implicated in the infections, with UTI as most frequently diagnosed among outpatients. Infections were common among young adults and infants, and predominantly caused by *E. coli*, *Proteus spp* and *Citrobacter spp*. during the period of our study. This study emphasizes the critical need for routine surveillance of MDR bacteria in outpatient settings. The findings call for strengthened antimicrobial stewardship and public health policies to mitigate the spread of resistance.

Conflicts of Interest

The authors declare no conflicts of interest.

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Abbreviations and Acronyms

AMR	Anti-microbial Resistance
KCH	Kabwe Central Hospital
MDR	Multi-Drug Resistant
MDR-GM	Multi-Drug-Resistant Gram Negative
OPD	Outpatient Department
PCR	Polymerase Chain Reaction
SPP	Species
WHO	World Health Organization