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Types and Transmission Routes of Nosocomial Antibacterial Resistance

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Abstract

Purpose: To evaluate elements involved in nosocomial bacterial infections in Lubumbashi hospitals and determine the specific antimicrobial resistance types circulating in the region.

Methodology: A cross-sectional study was performed in four different hospitals in Lubumbashi from March 2017 to October 2019. Hospital surfaces, medical equipment, and hospitalized patients' stools were screened. Escherichia coli, Staphylococcus aureus, and Pseudomonas aeruginosa isolates were identified and subjected to antibiotic sensitivity tests and screened for extended-spectrum beta-lactamase activity.

Results: Most hospital surfaces and medical devices were contaminated (90.4 %), with a predominance of Staphylococcus aureus and Pseudomonas aeruginosa species. These bacteria exhibited various resistance rates, with high rates (≥ 50 %) registered towards penicillin, gentamicin, fosfomycin, fusidic acid, and ciprofloxacin. About 37.5 % of Pseudomonas aeruginosa isolates and 53 % of Staphylococcus aureus isolates showed extended-spectrum beta-lactamase activity. Escherichia coli isolates exhibited resistance to several antibiotics with the highest rate of resistance (91.5 %) against Trimethoprim/sulfamethoxazole and β-lactamase activity registered in 44.3 %.

Conclusions: While asserting intestinal Escherichia coli as a reliable marker for the study of bacterial resistance. This study also found that surfaces and medical devices in Lubumbashi

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hospitals play a crucial role in the dynamics of drug-resistance. The findings emphasize the burden of antibiotic resistance, suggesting an urgent need for effective management strategies to limit the propagation of this phenomenon.

Keywords: Antibacterial resistance, nosocomial infections, Escherichia coli, Pseudomonas aeruginosa, Staphylococcus aureus, extended-spectrum beta-lactamase.

1. Introduction

One of the most threatening public health problems in the world resides in nosocomial infections that should be given particular attention in programs to improve healthcare provision especially in low-income countries [1, 2]. Apart from leading to antibacterial resistance spread among the population and complicating strategies to treat common bacterial infections, it constitutes an economic and financial burden that also provides an insight in the practical expertise of healthcare providers and the effectiveness of the healthcare settings management. Along the African continent, the situation is alarming especially regarding Gram-negative bacilli such as *Enterobacteriaceae*, *Pseudomonas*, and *Acinetobacter* that have been reported to present high rates of resistance to almost all antibiotics used for humans, including multi-drug resistance [3, 4].

Antimicrobial resistance arises mostly from a selection pressure in presence of excessive and sometimes inappropriate use of antibiotics in humans and livestock such in Sub-Saharan Africa where the use of uncontrolled drugs sold in markets increases the risk of resistance occurrence [5]. Bacteria bearing resistance genes can then be transmitted between animals, humans, or from animals to humans and vice versa [6, 7]. Moreover, resistance genes can be transferred between bacteria in the same ecosystem. Regardless of their origin, resistant bacteria can emerge in a hospital and proliferate when appropriate conditions are granted, causing nosocomial infections in patients consulting for other reasons. While posing serious challenges to healthcare providers, these infections are costly, both in time and money [1]. Hence, to prevent and manage antibacterial resistance genes transmission in hospital settings, the implication of the various stakeholders involved in healthcare is required, including healthcare providers, patients attending hospitals, patients' visitors, and the personnel responsible for surface cleaning and equipment maintenance [7]. Additionally, as one of the most important aspects of the prevention of this threat, surveillance and epidemiologic data collection are indispensable. However, these are ineffective in most African countries, notably due to the lack of expertise and equipment [8, 9]. In the Democratic Republic of Congo, there is no available data regarding the nosocomial transmission of antibacterial resistance. This observation triggered the present study which aimed at identifying the most prevalent resistance genes in the province of Lubumbashi and the routes of nosocomial transmission of resistant bacteria in hospitals in the same province.

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2. Methods

2.1 Identification of resistance types

In order to identify the types of resistance genes that are present in the studied population, a prospective study was performed on patients hospitalized in hospitals in Lubumbashi using commensal intestinal *Escherichia coli* as an indicator.

2.2 Studied population

Patients hospitalized in four different hospitals in Lubumbashi participated in this study from March 2017 to October 2019. The inclusion criteria were: (i) absence of gastroenteritis, and (ii) being under antibiotic treatment. Recruited patients that fulfilled the inclusion criteria were invited to the Laboratory of the Higher Institute of Medical Techniques of Lubumbashi. After providing informed consent, patients were subjected to stool sampling using sterile containers. Patients' socio-demographic data, as well as treatment histories, were collected through oral interviews and medical file screening.

2.3 Identification of bacteria from stools

Stool specimens were used for bacterial isolation by plating on SS agar. Plates were incubated at 37°C for 24 hours. *Escherichia coli* colonies (red, lactose positive, and acid-producing colonies) were selected and subjected to macroscopic, microscopic, and biochemical characterization with API 20 E Gallery, BioMerieux.

2.4 Hospital surfaces screening

In order to identify spots in healthcare settings with a high proliferation of antibacterial resistant bacteria and routes of nosocomial bacterial acquisition, four intensive care units (ICUs) were screened. These ICUs were selected in Surgery, Internal medicine, Paediatrics, and Gynaecology - Obstetrics departments of 4 hospitals.

Sterile swabs moistened with Trypticase Soy Broth (TSB) were used to collect samples on the surfaces of doorknob/door handle, operating table, fixed table, bed frames, bed rails, sinks, stethoscopes, masks, thermometers, catheters (venous and bladder catheters maintained more than 48 hours), and mobile phones. Samples were collected by spinning swabs around their axis on surfaces before putting them in tubes containing TSB for incubation at 37°C for 24 hours.

2.5 Identification of bacteria from surfaces

After the enrichment incubation in TSB for 24 hours, the culture is sampled and seeded on plates of specific media (Mac Conkey, Chapman, chocolate blood agar). Colonies were identified according to their aspects and their morphologies and standard microbiological techniques (Gram stain, catalase, Spore staining methods (Moeller and Schaeffer) staphylocoagulase test, oxidase test) and by the API Staph system (BioMérieux) for *Staphylococcus aureus*, API 20NE for *Pseudomonas aeruginosa* and API 20E for enterobacteria. Antibacterial resistance and extended-spectrum beta-lactamases (ESBL) activity of isolated bacteria were evaluated with the same procedure as for bacteria isolated from stools.

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2.6 Antimicrobial susceptibility and β-lactamase activity tests

In accordance with the clinical laboratory standards guidelines (CLSI, 2013), antimicrobial susceptibility tests were done on Mueller-Hinton agar using the Kirby Bauer disk diffusion method [10]. On *Escherichia coli* isolates, 12 antibiotics were tested, while 16 were used for *Staphylococcus aureus* and *Pseudomonas aeruginosa*. Reference strains of *Escherichia coli* (ATCC 2592), *Staphylococcus aureus (ATCC 25923), and Pseudomonas aeruginosa* (*ATCC* 27853) were used as controls. The most prescribed antibiotic formulations in Lubumbashi were tested: Ampicillin (10 µg), Ciprofloxacin (5 µg), Amoxycillin (25 µg), Gentamicin (15 µg), Norfloxacin (5 µg), Cefotaxime (30 µg), Ceftriaxone (30 µg), Amoxycillin/clavulanic acid (30 µg), trimethoprim/sulfamethoxazole (25 µg), Tetracycline (10 µg), Nalidixic acid (30 µg), Amikacin (30 µg). The antibiotic disc content in microgram (µg) was provided by the pharmaceutical company according to CLSI for antibiotic susceptibility testing. For each bacteria, a clinical categorization (Resistant, Intermediate, Sensitive) was given according to the diameter observed and the critical diameters of the antibiotic tested. These clinical categorization criteria according to critical diameters are periodically updated by the CLSI [10]. An isolate was qualified multidrug-resistant (MDR) when it exhibited resistance to at minimum three diverse classes of antibiotics [11].

Extended-spectrum beta-lactamase (ESBL) activity was determined by the double-disk synergy method at 20 mm (DDS20): Ceftazidime (CAZ, 30 µg) and cefpodoxime (CPD, 10 µg) disks were placed by a disk distributer on Mueller-Hinton (MH) agar at a distance of 20 mm each from an AMC disk (containing 20 µg of amoxicillin and 10 µg of clavulanic acid) for *Escherichia coli,* or a TIM disk (containing 20 µg of ticarcillin and 10 µg of clavulanic acid) for both *Staphylococcus aureus* and *Pseudomonas aeruginosa*. Following 24 h incubation, the existence of ESBL was deduced when the inhibition zone surrounding any of the two antibiotic disks (CAZ and CPD) was enhanced towards the clavulanic acid-containing disk with a typically formed zone referred to as ellipsis [12].

The combination disk method was also used to evaluate ESBL activity. Disks holding 30 µg of cefotaxime (CTX) and 30 µg of CAZ respectively, and disks holding a mixture of the two drugs additionally to 10 µg of clavulanic acid (CCTX and CCAZ, respectively) were placed on MH agar. Bacteria were detected ESBL positive when the measured inhibition zone around one of the mixture disks after daily incubation was at a minimum of 5 mm larger than that of the conforming cephalosporin disk [12].

2.7 Data analysis

All recorded data and obtained results were computed and analyzed using Microsoft Excel software. Statistical analyses were performed with IBM SPSS software version 20. All results are expressed in mean ± standard deviations. When tests or comparisons are performed, the significance of cut-off is fixed at p-value < 0.05.

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3. Results

3.1 Bacterial isolates in hospital surfaces

In the investigation of the hospital and material surfaces, a total of 315 samples were collected and used for bacterial culture and isolation. From these samples, 285 (90.4 %) showed bacterial contamination. Most contaminated samples were those from internal medicine (142 samples) followed by the departments of Emergency (60 samples), Paediatrics (30 samples), Surgery (28 samples), Gynaecology and Obstetrics (25 samples). From each contaminated sample, representative isolates were selected to proceed with identification. The predominant bacteria were *Staphylococcus aureus* (83 isolates) followed by *Pseudomonas aeruginosa* (72 isolates), coagulase-negative *Staphylococci* (48 isolates), *Bacillus sp* (35 isolates), *Klebsiella pneumonia* (24 isolates), *Enterobacter cloacae* (12 isolates), *Proteus vulgaris* (7 isolates), and *Escherichia coli* (4 isolates). The distribution of these isolates by the sampled department is presented in Table 1.

When considering the specific area of sampling, most contaminating bacteria were isolated from bed frames as 60 isolates were obtained from these surfaces. To a second extended, mobile phones also presented a high rate of bacterial contamination with 47 samples presenting contaminants. The third most contaminated surfaces in the study were sinks that allowed the isolation of 39 isolates followed by thermometers (30 isolates). As shown in Table 2 which presents the distribution of isolates according to screened surfaces, the less contaminated surfaces in the study were bladder catheters (4 isolates).

3.2 Antibacterial resistance of isolated *Staphylococcus aureus* and *Pseudomonas aeruginosa*

Due to their abundance among the isolated bacteria, *Staphylococcus aureus* and *Pseudomonas aeruginosa* isolates were selected to assess their resistance towards the most prescribed antibiotics in the region. Both bacteria were found to present high rates of multidrug resistance. *Staphylococcus aureus* isolates presented the highest rate of resistance which was towards fosfomycin (91.5 %), followed by oxacillin (78.3 %), ciprofloxacin (74.3 %), ampicillin (73.4 %), fusidic acid (62.6 %), lincomycin (62.6 %), gentamicin (62.6 %), and penicillin (54.2 %). ESBL activity was recorded in 53 % of isolated *Staphylococcus aureus*. None of the isolates was susceptible to oxacillin but vancomycin appeared to be the most effective antibiotic as 91.5 % of the isolated *Staphylococcus aureus* were susceptible to it. *Pseudomonas aeruginosa* isolates showed high resistance rates towards ciprofloxacin (90.2 %), kanamycin (87.5 %), fosfomycin (83.3 %), penicillin (59.7 %), fusidic acid (56.9 %), gentamicin (55.5 %), and amikacin (54.1 %) with 37.5 % demonstrating ESBL activity. *Pseudomonas aeruginosa* isolates were mostly sensitive to imipenem (75 %) and ticarcillin/clavulanic acid composition (72.2 %). The complete antibacterial resistance profile of *Staphylococcus aureus* and *Pseudomonas aeruginosa* are presented in Tables 3 and 4 respectively.

3.3 Antibacterial resistance of isolates from hospitalized patients

A total of 416 hospitalized patients aged between 16 and 65 were recruited. Among them, 232 were female with a mean age of 34.5±16.4, and 184 were male with an average age of 35.7±17.4. The three most prescribed and most administered antibiotics in the selected population were

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Ampicillin (20.6%), Ciprofloxacin (18.4%), and Amoxicillin (16.8 %), with the utilization of other antibiotics recorded at variable rates as presented in Table 5.

Escherichia coli isolates were identified based on their biochemical characteristics. For each patient, lactose positive and acid-producing colonies were selected and screened for drug resistance and ESBL activity. The highest rate of antibiotic resistance was registered for Trimethoprim and Sulfamethoxazole which did not show any inhibition zone for 91.5% of the screened isolates. Resistance to other antibiotics was recorded at variable rates as presented in Table 6, while the *Escherichia coli* isolates were most susceptible to amoxicillin/clavulanic acid, with 2.8 % resistance rate. Among the isolates, 44.3 % expressed an ESBL activity.

4. Discussion

One of the first steps in the management of public health regarding bacterial drug resistance is to determine its nature and causes along with the epidemiologic evaluation of its rate and ways of transmission. The present preliminary study of antibacterial resistance was focused on one of the most populated cities in the Democratic Republic of Congo, Lubumbashi. The main goal was to identify the most common drug-resistant bacteria in hospital environments, and the factors involved in nosocomial bacterial transmission. Hospital surfaces and tools were thus screened in departments of Emergency, Gynaecology and Obstetrics, Internal medicine, Paediatrics, and Surgery. Moreover, stool samples from hospitalized patients in the four hospitals in the city of Lubumbashi were analyzed.

The first finding in this study was the fact that all screened hospital surfaces and medical equipment presented bacterial contamination. This shows that the studied medical environment is not well managed especially regarding bacterial dissemination and nosocomial infections. In fact, very sensitive departments such as Surgery, Paediatrics, and Gynaecology and Obstetrics presented high rates of contaminations, exposing patients and healthcare providers in these departments to infections. Bacterial infection from such a source is a contributing factor to worsened maternal and perinatal health, increasing the rate of under-five mortality as bacterial infections are more and more shown to be an associated factor [13, 14]. The presence of bacterial contaminations in Emergency services and Internal medicine departments that are frequently consulted by outpatients should be considered as an indicator of the high rate of nosocomial infections in the hospital, with a high potential of outbreaks [15]. The identified contaminants were *Staphylococcus aureus, Pseudomonas aeruginosa*, coagulase-negative *Staphylococci*, *Bacillus sp*, *Klebsiella pneumonia*, *Enterobacter cloacae*, *Proteus vulgaris*, and *Escherichia coli* which are commonly found in nosocomial infections across the world [16, 17]. Beyond the possibility of contaminations of human origins, the vectorial carriage of these bacteria should be considered given the specific context of low-income countries and the proliferation of several infects such as cockroaches that are good carriers [18].

The results show that patients' beds are the most highly contaminated surfaces; thus, hospitalizing patients increases their risk of getting a nosocomial bacterial infection. Interestingly, mobile phones present the second-highest rate of contamination, demonstrating

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that they play an important role in nosocomial infections transmission and dissemination even before sinks and shared medical tools such as thermometers and stethoscopes. Specific measures should be taken to control this source of nosocomial infections, as mobile phones are among bacteria-carrying equipment that is transported even in operating rooms without specific decontamination [19, 20]. Regarding catheters, the presence of bacterial contaminants on their surface shows that there is a need for more control and better management procedures at their receipt and along with their storage.

Like in many other studies, *Staphylococcus aureus* and *Pseudomonas aeruginosa* were the most common contaminants of the hospital environment. They were therefore chosen as markers to identify the specific resistance types that circulate on the surfaces and equipment in the screened hospital. This evaluation presented, as a result, high resistance of isolated bacteria towards fosfomycin, oxacillin, ciprofloxacin, and ampicillin for *Staphylococcus aureus*, and ciprofloxacin, kanamycin, and fosfomycin for *Pseudomonas aeruginosa*. The presence of fosfomycin among the top antibiotics with high rates of resistance is a worrying fact because this antibiotic is one of the recommended antibiotics to overcome infecting multidrug-resistant bacteria [21, 22]. Resistance to the two members of the Beta-lactam family (oxacillin and ampicillin) is also distressful because of their importance in bacterial infection treatment especially in the eradication of penicillin-resistant and methicillin-resistant bacteria. Unfortunately, this resistance is getting more frequent as reported in other regions [23–24]. Noteworthy, because these two antibiotics are quite accessible in the region, their inefficiency increases the threat of antibacterial resistance in DR Congo, owing to the latter counting among low-income countries with high rates of poverty and thus an inability of patients to procure new classes of antibiotics.

In order to evaluate the level at which the medical use of antibiotics contributed to generating antimicrobial resistance, hospitalized patients were screened to isolate and establish the antibiotic susceptibility profile of their gastrointestinal commensal *Escherichia coli*. The highest rate of antimicrobial resistance in isolated commensal *Escherichia coli* was towards the composition trimethoprim/sulfamethoxazole which appeared to be the least prescribed antibiotic drug in the region. However, ampicillin which is the most prescribed antibiotic showed high rates of resistance (63 %), underlining the necessity to proceed to its replacement by alternative molecules for more effectiveness. Interestingly, more than 44 % of these bacteria expressed ESBL activity, proving that these bacteria are resistant to several antibiotics of the family of Beta-Lactams as presented in other studies [21]. However, the composition of amoxicillin/clavulanic acid seems more effective as it showed the lowest resistance in the tested isolates. Other tested antibiotics presented variable resistance rates in the population of isolated *Escherichia coli*, indicating the importance of healthcare-associated antibiotic resistance [25].

Overall, the present study sheds light on the silent public health threat of antimicrobial resistance and its spread through healthcare settings. Screened hospitals' surfaces are exposed to several contaminants and constitute niches where bacteria not only proliferate but also share resistant genes. In this motion, *Staphylococcus aureus* and *Pseudomonas aeruginosa* play an important

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role as they are the most populating bacteria surviving in the specific conditions of Hospitals in Lubumbashi. Even though the studied population is not representative of the countrywide population and hospital environment, it appears that all types of antibiotics have given rise to resistance and horizontal gene transfers allowing the emergence of multidrug resistance. Even if the medical use of antibiotics is determinant in the generation of this resistance, bacterial infections treatment regimens of antibiotics are still effective because they show moderate rates of resistance. However, there is a serious need for the design of new management and control procedures to reduce the transmission of nosocomial infections by resistant bacteria.

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Compliance with Ethical Standards

The present study with all the procedures was approved by the Research Ethics Committee of the Higher Institute of Medical Techniques of Lubumbashi. All patients were informed about the study and gave their consent to be part of the study.

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Competing interests: None declared

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Table 1. Distribution of bacterial isolates by departments

	Internal medicine	Surgery	Emergency	Pediatrics	Gynaecology and Obstetrics
Staphylococcus aureus (n=83)	37 (44.5 %)	8 (9.6 %)	16 (19.2 %)	12 (14.4 %)	10 (12 %)
Pseudomonas aeruginosa (n=72)	31 (43 %)	6 (8.3 %)	15 (20.8 %)	11 (15.2 %)	9 (12.5 %)
Coagualse negative Staphylococci (n= 48)	25 (52 %)	6 (12.5 %)	12 (25 %)	2 (4.1 %)	3 (6.2 %)
Bacillus sp (n=35)	20 (57.1 %)	6 (17.1 %)	8 (22.8 %)	-	1 (2.8 %)
Klebsiella pneumoniae (n=24)	14 (58.3 %)	1 (4.1 %)	5 (20.8 %)	4 (16.6 %)	-
Enterobacter cloacae (n=12)	9 (75 %)	-	2 (16.6 %)	-	1 (8.3 %)
Proteus vulgaris (n=7)	4 (57.1 %)	-	2 (28.5 %)	1 (14.2 %)	-
Escherichia coli (n=4)	2 (50 %)	1 (25 %)	-	-	1 (25 %)

Table 2. Distribution of isolates by screened surfaces

	Staphylococcus aureus (n=83)	*Pseudomonas aeruginosa* (n=72)	*Coagulase negative staphylococci* (n= 48)	*Bacillus sp* (n=35)	*Klebsiella pneumonia* (n=24)	*Enterobacter cloacae* (n=12)	*Proteus vulgaris* (n=7)	*Escherichia coli* (n=4)	*All*
Bedframes/ Bedrails	11 (13.2 %)	25 (34.7 %)	2 (4.1 %)	14 (40 %)	6 (25 %)	1 (8.3 %)	1 (14.2 %)	0	60
Mobile phones	10 (12 %)	8 (11.1%)	9 (18.75 %)	7 (20 %)	6 (25 %)	3 (25 %)	2 (28.5 %)	2 (50 %)	47
Sinks	7 (8.4 %)	17 (23.6 %)	3 (6.25 %)	8 (22.8%)	2 (8.3 %)	2 (16.6 %)	0	0	39
Thermometers	8 (9.6 %)	7 (9.7 %)	7 (14.5 %)	0	1 (4.1 %)	3 (25%)	4 (57.1 %)	0	30
Door knobs/handles	16 (19.2 %)	6 (8.3 %)	0	2 (5.7 %)	2 (8.3 %)	1 (8.3 %)	0	1 (25 %)	28
Operating tables	12 (14.4 %)	3 (4.1 %)	2 (4.1 %)	2(5.7 %)	4 (16.6 %)	0	0	0	23
Venous Catheters	9 (10.8 %)	2 (2.7 %)	8 (16.6 %)	0	2 (8.3 %)	1 (8.3 %)	0	0	22
Masks	4 (4.8 %)	0	12 (25 %)	0	0	0	0	0	16
Stethoscopes	5 (7.2 %)	4 (5.5 %)	4 (8.3 %)	2 (5.7 %)	1 (4.1 %)	0	0	0	16
Bladder catheters	1 (1.2%)	0	1 (2 %)	0	0	1 (8.3 %)	0	1 (25 %)	4

Table 3. Antibacterial resistance profile of Staphylococcus aureus isolates

Antibiotics	Resistant	Intermediate resistance	Susceptible
Penicillin	45 (54.2 %)	17 (20.4 %)	21 (25.3 %)
Oxacillin	65 (78.3 %)	18 (21.6 %)	0
Gentamicin	52 (62.6 %)	12 (14.4 %)	19 (22.8 %)
Erythromycin	39 (46.9 %)	20 (24 %)	24 (28.9 %)
Amikacin	34 (40.9 %)	29 (34.9 %)	20 (24 %)
Lincomycin	52 (62.6 %)	17 (20.4 %)	14 (16.8 %)
Vancomycin	3 (3.6 %)	4 (4.8 %)	76 (91.5 %)
Fosfomycin	76 (91.5 %)	2 (2.4 %)	5 (6 %)
Fusidic Acid	52 (62.6 %)	14 (16.8 %)	17 (20.4 %)
Kanamycin	17 (20.4 %)	37 (44.5 %)	29 (34.9 %)
Ticarcillin	32 (38.5 %)	20 (24 %)	31 (37.3 %)
Ticarcillin/Clavulanic acid	14 (16.8 %)	12 (14.4 %)	57 (68.6 %)
Ceftazidime	28 (33.7 %)	14 (16.8 %)	41 (49.3 %)
Ciprofloxacin	62 (74.3 %)	10 (12 %)	11 (13.2 %)
Imipenem	7 (8.4 %)	15 (18 %)	61 (73.4 %)
Ampicillin	61 (73.4 %)	14 (16.8 %)	8 (9.6 %)

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Table 4. Antibacterial resistance profile of Pseudomonas aeruginosa isolates

Antibiotics	Resistant	Intermediate resistance	Susceptible
Penicillin	43 (59.7 %)	14 (19.4 %)	15 (20.8 %)
Oxacillin	32 (44.4 %)	33 (45.8 %)	7 (9.7 %)
Gentamicin	40 (55.5 %)	17 (23.6 %)	15 (20.8 %)
Erythromycin	28 (37.3 %)	21 (29.1 %)	23 (31.9 %)
Amikacin	39 (54.1 %)	17 (23.6 %)	16 (22.2 %)
Lincomycin	32 (44.4 %)	28 (38.8 %)	12 (16.6 %)
Vancomycin	13 (18 %)	14 (19.4 %)	45 (62.5 %)
Fosfomycin	60 (83.3%)	6 (8.3 %)	6 (8.3 %)
Fusidic Acid	41(56.9 %)	19 (26.3 %)	12 (16.6 %)
Kanamycin	63 (87.5 %)	9 (12.5 %)	0
Ticarcillin	23 (31.9 %)	24 (33.3 %)	25 (34.7 %)
Ticarcillin/Clavulanic acid	12 (16.6 %)	8 (11.1 %)	52 (72.2 %)
Ceftazidime	14 (19.4 %)	19 (26.3 %)	39 (54.1 %)
Ciprofloxacin	65 (90.2 %)	4 (5.5 %)	3 (4.1 %)
Piperacillin	26 (36.1 %)	17 (23.6 %)	29 (40.2 %)
Imipenem	8 (11.1%)	10 (13.8 %)	54 (75 %)

Table 5. Frequency of antibiotics prescribed in the study population

Antibiotics	Consumption rate (%)
Ampicillin	20.6
Ciprofloxacin	18.4
Amoxicillin	16.8
Gentamicin	10.4
Norfloxacin	8.6
Cefotaxime	8.4
Ceftriaxone	5.9
Amoxicillin/clavulanicacid	5.5
Trimethoprim/Sulfamethoxazole	3

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Table 6. Antimicrobial resistance in *Escherichia coli* isolates from hospitalized patients

Antibiotics	Resistant	Intermediate resistance	Susceptible
Amoxicillin	191 (45.9 %)	46(11%)	179 (43.7 %)
Amikacin	130 (31.2 %)	58 (13.9 %)	228 (54.8 %)
Amoxycillin/Clavulanic acid	12 (2.8 %)	2 (0.4 %)	402 (96.6 %)
Ampicillin	264 (63.4 %)	144 (34.6 %)	8 (1.98 %)
Cefotaxime	88 (21.1 %)	97 (23.3 %)	231 (55.5 %)
Ceftriaxone	86 (20.7 %)	98 (23.5 %)	232 (55.7 %)
Ciprofloxacin	176 (42.3 %)	96 (23 %)	144 (34.7 %)
Gentamicin	212 (50.9 %)	151 (36.3 %)	53 (12.7 %)
Nalidixicacid	189 (45.4 %)	134 (32.2 %)	93 (22.35 %)
Norfloxacin	123 (29.5 %)	170 (40.8 %)	123 (29.5 %)
Tetracycline	324 (77.8 %)	42 (10 %)	50 (12 %)
Trimethoprim/Sulfamethoxazole	381(91.5 %)	23 (5.5 %)	12 (2.8 %)