

Antibiotic resistance pattern of bacterial clinical isolates in tertiary care hospital of Nepal: An observational study

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ABSTRACT

Introduction: Assessment of antibiotic resistance patterns in hospitals is functional for antibiotic stewardship. This study aims to describe the prevalence of antibiotic resistance patterns of bacterial clinical isolates in a tertiary care hospital.

Methods: A cross-sectional study was conducted in the Microbiology Department of Lumbini Medical College and Teaching Hospital, Tansen, Palpa, Nepal, from 13 February 2024 to 6 September 2024 for a seven-month duration after approval from the Institutional Review Committee (Protocol No: IRC-LMC-022/N-23). Data of bacterial clinical isolates from different specimens, such as urine, pus/swab, sputum, and vaginal swab, were collected. Further, data were entered in a pre-designed case proforma, which included information on the types of bacteria causing infections and their antibiotic susceptibility and resistance. Data were expressed in frequency and percentage.

Results: A total of 202 bacterial clinical isolates from patients were reviewed. Of the total clinical isolates, 86 (42.6%) were urine specimens. *Escherichia coli* growth was commonly observed in 76 (37.6%) of various clinical isolates. A total of 1730 number of antibiotics were tested for culture & sensitivity. Of them, intermediate and resistance were seen in 53 and 804 antibiotics, respectively. The average number of antibiotic resistances was 4.24 ± 3.04 . In 171 (84.7%) clinical isolates, resistance was seen in more than one antibiotic. Ampicillin (14.7%) was the most common resistant antibiotic, followed by ciprofloxacin (7.0%).

Conclusion: Antibiotic resistance was observed in more than one antibiotic. Thus, this study may help in antibiotic stewardship.

Keywords: Anti-bacterial Agent, Bacterial Infections, Drug Resistance, Tertiary Health Care Centers

INTRODUCTION

Antibiotic resistance has been emerging as a serious global health problem according to the World Health Organization (WHO) [1]. Approximately 4.95 million deaths were attributed to antibiotic resistance worldwide in the year 2019, including the mortalities in low-and middle-income countries [1,2]. This problem is also rapidly emerging in Nepal because of inadequate governmental measures on infection control [3].

Several factors are responsible for antibiotic resistance, such as unnecessary use of antibiotics and overuse of antibiotics [4,5]. The major consequences of antibiotic resistance are treatment failure and the use of higher classes of expensive antibiotics. These all can lead to an increase in morbidity, mortality, health-care-related costs, and burden of treatment [6,7]. Thus, assessing the antibiotic resistance pattern in hospitals is helpful for antibiotic stewardship, increasing the knowledge of the rational use of antibiotic therapy, and ensuring the appropriate use of antibiotics. Many studies have been done previously on antibiotic resistance patterns worldwide, including Nepal [3,4,5,6,7,8].

Thus, the study aimed to describe the prevalence of antibiotic resistance patterns of bacterial clinical isolates in a tertiary care hospital.

METHODS

An observational descriptive cross-sectional study was conducted in Lumbini Medical College & Teaching Hospital (LMC-TH), Nepal, from 13 February 2024 to 6 September 2024 for seven months. The study was approved by the Institutional Review Committee (Protocol No: IRC-LMC-022/N-23). Formal approval was also taken from the person in charge of the microbiology department of LMC-TH. The availability of an electronic health record system made it possible to access all clinical and laboratory records.

Data on bacterial clinical isolates from patients, including complete microbiological culture and sensitivity testing results, were collected

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from the microbiology department. The bacterial clinical isolates included different specimens such as blood, urine, pus/swab, stool, sputum, vaginal swab, and peritoneal fluid. The duplicates from the same patients were avoided. Likewise, data of those patients that could not be revealed because of maintaining confidentiality were excluded from the study. According to the healthcare professionals of the microbiology department of LMC-TH, the sample processing, identification of organisms to genus / species level, and antibiotic sensitivity were conducted as per Clinical and Laboratory Standards Institute Guidelines [9].

A standardized abstraction form was designed, which included demographic profiles of patients, clinical characteristics of patients, and information related to antibiotic susceptibility. This form was also circulated to two pharmacologists and two microbiologists within the LMC-TH. They independently rated each item of the case proforma satisfactory. Then, the primary data were consecutively and conveniently collected and entered into the case proforma. The confidentiality was ensured by de-identifying the data in the records. The data were also secured by password-protected software.

Data were exported to Statistical Package for Social Sciences (SPSS), version 18. Categorical variables were expressed as frequency and percentage, while continuous variables were reported as the mean \pm standard deviation (SD). For inferential statistics, an independent t-test was used. A p-value less than 0.05 was considered statistically significant.

RESULTS

A total of 202 bacterial clinical isolates from patients were observed. Of which 131 (64.9%) belonged to females. The mean age of the patients was 44.35 ± 25.24 years. The mean age of females and males was 41.72 ± 22.75 years and 49.21 ± 28.83 years, respectively ($t = -1.89$, $df = 117.98$, $p = 0.061$) as shown in Table 1.

Table 2: Pattern of bacterial growth from various specimens (N = 202)

Bacterial Group	Frequency (%)	Bacterial Growth	Frequency (%)
Gram positive	60 (29.7)	Staphylococcus aureus	43 (21.3)
		Enterococcus spp	16 (7.9)
		Streptococcus pneumoniae	1 (0.5)
Gram negative	142 (70.3)	Escherichia coli	76 (37.6)
		Klebsiella pneumoniae	25 (12.4)
		Pseudomonas aeruginosa	17 (8.4)
		Enterobacter	7 (3.5)
		Acinetobacter	6 (3.0)
		Proteus mirabilis	5 (2.4)
		Proteus vulgaris	2 (1.0)
		Citrobacter koseri	2 (1.0)
		Klebsiella oxytoca	2 (1.0)

Of the total bacterial clinical isolates, 86 (42.6%) were urine specimens, followed by pus or swab. Gram-negative bacterial growth was seen in 142 (70.3%) clinical isolates, while Gram-negative bacterial growth was seen in 60 (29.7%) clinical isolates. Of the total bacterial clinical isolates, Escherichia coli growth was observed in 76 (37.6%), followed by Staphylococcus aureus and Klebsiella pneumonia in 43 (21.3%) and 25 (12.4%), respectively (Table 2).

A total of 1730 number of antibiotics were tested for culture and sensitivity. Of them, antibiotic sensitivity, intermediate, and resistance were seen in 873 (50.5%), 53 (3.1%), and 804 (46.4%) antibiotics, respectively. Similarly, the average number of antibiotic sensitivities was 4.32 ± 1.48 , and the average number of antibiotic resistances was 4.24 ± 3.04 . In 171 (84.7%) bacterial clinical isolates of patients, antibiotic resistance was seen in more than one antibiotic. Furthermore, ampicillin (14.7%) was the most common resistant antibiotic, followed by ciprofloxacin (7.0%) and ceftriaxone (6.5%), as shown in Table 3.

Table 1: Socio-Demographic Profile (N = 202)

Variables	Frequency (%)
Age (In years)	
0-10	18 (8.9)
11-20	15 (7.4)
21-30	40 (19.8)
31-40	24 (11.8)
41-50	17 (8.4)
>50	88 (43.7)
Gender	
Female	131 (64.9)
Male	71 (35.1)

DISCUSSION

The study aimed to describe the antibiotic resistance pattern of bacterial clinical isolates of patients in a tertiary care hospital. Many risk factors have been found out for the rapid emergence of antibiotic resistance such as unnecessary use of antibiotics when they are not needed like in viral fever, use of many antibiotic for a single infection, not completing the course of antibiotic, overcrowding, poor hygiene practices, self-medication practices and marketing by pharmaceutical companies to sell their branded antibiotics [10,11]. Meanwhile, many mechanisms are responsible for antibiotic resistance, including horizontal transfer of resistant genes between bacteria, such as conjugation, transformation, transduction, and intrinsic factors like point mutation, gene amplification [7]. Thus, the coordinated approach to antibiotic stewardship is significant for increasing the maximum benefits of antibiotic use and minimizing the antibiotic resistance as

well as the adverse effects of antibiotics.

Our study observed that the majority of the patients from whom clinical isolates were obtained were aged more than 50 years. This finding was comparable with some other studies [5,10,11]. The reasons behind this could be the presence of pathological conditions at old age, like impaired immune defense mechanism, increased incidence of diabetes mellitus, and use of invasive devices such as urinary catheter, implants. These conditions may result in recurrent attacks of bacterial infections, which may lead to frequent irrational use of antibiotics and then to antibiotic resistance [12]. Similarly, this study also showed that approximately two-thirds of total clinical isolates belonged to females, which was also supported by a few other studies [6,8]. However, in some other studies, the clinical isolates belonged to males and females in a similar manner or more in males [5,10,13]. Females are more susceptible to bacterial infections like urinary tract infections and sexually transmitted diseases. Consequently, all these infections

Table 3: Pattern of intermediate and antibiotic resistance (N = 857)

Antibiotics	Intermediate	Resistant	Total n(%)
Ampicillin	4	122	126 (14.7)
Ciprofloxacin	3	57	60 (7.0)
Ceftriaxone	4	52	56 (6.5)
Cotrimoxazole	1	47	48 (5.6)
Cefotaxime	2	38	40 (4.6)
Pipracillin	2	38	40 (4.6)
Penicillin	1	38	39 (4.5)
Cefalexin	0	38	38 (4.4)
Cefazolin	3	35	38 (4.4)
Cefixime	4	31	35 (4.0)
Carbencillin	1	32	33 (3.8)
Ceftazidime	1	29	30 (3.5)
Erythromycin	0	25	25 (2.9)
Ofloxacin	0	23	23 (2.7)
Norfloxacin	0	22	22 (2.5)
Cefepime	1	18	19 (2.2)
Amoxicillin + Clavulanic Acid	4	14	18 (2.1)
Nitrofurantoin	3	14	17 (1.9)
Amikacin	2	13	15 (1.8)
Imipenem	4	11	15 (1.8)
Cefoxitin	0	13	13 (1.6)
Tetracycline	2	11	13 (1.6)
Gentamicin	3	10	13 (1.6)
Vancomycin	1	10	11 (1.2)
Netillin	2	7	9 (1.1)
Aztreonam	4	5	9 (1.1)
Meropenem	0	8	8 (1.0)
Cloxacillin	0	8	8 (1.0)
Cefuroxime	1	7	8 (1.0)
Clindamycin	0	5	5 (0.6)
*Others	0	23	23 (2.7)
Total	53	804	857 (100)

*Azithromycin, Doxycycline, Polymyxin B, Levofloxacin, Bacitracin, Linezolid, Tobramycin, Cefpodoxime

in females may lead to frequent use of antibiotics and the chances of developing antibiotic resistance. Besides, differences in geographical area and type of organisms causing infections are also other factors that are responsible for resulting variation in antibiotic resistance patterns [13].

Furthermore, the present study also reported that the majority of the specimens tested for culture and sensitivity were urine samples. Approximately two-thirds of the clinical isolates were gram-negative bacteria from various specimens such as urine, pus, swabs, or sputum. Of the various growths, *Escherichia coli* was prevalent in about one-third of total specimens. Again, this finding was comparable with other studies conducted at the national and international levels [7, 8, 13-16]. In contrast to this study, few studies have demonstrated that other gram-negative bacteria, such as *Enterobacteriaceae*, *Acinetobacter*, and *Klebsiella*, are common isolates from different specimens. [4, 5, 10, 11]. *Escherichia coli* is a gram-negative bacillus that is commonly grown in urine specimens in diseases such as urinary tract infections [8]. Besides, urinary tract infections are common in females because of the smaller size of the urethra compared to males. These may be some reasons for

the prevalence of *Escherichia coli* in our study [8].

Moreover, this study also observed a similar distribution of antibiotic sensitivity and resistance. In the majority of the clinical isolates of patients, resistance was seen in more than one antibiotic. Among resistant antibiotics, ampicillin was the most common, followed by ciprofloxacin, ceftriaxone, and cotrimoxazole. Like our study, two other studies also found that antibiotic resistance was commonly seen in more than one antibiotic [4,10]. Similarly, the findings of another study also approximate the result of our study, which showed ampicillin as the common resistant antibiotic [6]. Nonetheless, few other studies demonstrated cotrimoxazole and ceftriaxone as the common resistant antibiotics [7,11]. Ampicillin is an aminopenicillin and a beta-lactam antibiotic. The basis of the mechanism of resistance to ampicillin is the inactivation of the beta-lactam ring by the beta-lactamase enzyme produced by many gram-positive or gram-negative bacteria [17].

This study relied on existing medical records, which may lack detailed information on antibiotic usage and resistance patterns. Likewise, the single-centered nature of the study was another limitation, which decreases the ability of generalization. However, this study may provide a basis for conducting similar types of studies in multiple centers in the future.

CONCLUSION

This study summarizes that Gram-negative bacteria, particularly *Escherichia coli*, were commonly isolated from the various bacterial clinical isolates. Antibiotic resistance was seen in more than one antibiotic. Similarly, antibiotic resistance was observed in commonly used antibiotics such as ampicillin, ciprofloxacin, and ceftriaxone. Thus, the findings of this study may be helpful at a tertiary care hospital for antibiotic stewardship and the development of a protocol for the rational use of antibiotics.

DECLARATION

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Author Contributions

All authors conceptualized and designed the research. Except for PP & KK, all authors contributed to data collection. NK & KB performed statistical analysis and prepared the results. All authors drafted the manuscript, and all authors reviewed and approved the final version. All authors agreed to be accountable for all aspects of the research work, and all authors reviewed and approved the final version of the manuscript. All authors agreed to be responsible for all aspects of the research work.

Ethical Approval

This research was approved by the IRC of Lumbini Medical College with Protocol number: IRC-LMC-022/N-23 on 13 February 2024.

Consent/Assent

Not applicable

Data Availability Statement

The data that support the findings of this study are available from the corresponding author upon reasonable request.

Conflicts of Interest

The authors declare no conflict of interest.

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