Study of microbial infection and associated antimicrobial resistance among patients admitted in intensive care unit of a tertiary care level hospital of Nepal

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ABSTRACT

Background & objectives: In recent years, the rise in antibiotic resistance has posed challenges to the choice of empirical treatment for difficult cases. The objective of this study was to evaluate the prevalence of microbiological infections and the corresponding antibiotic resistance among patients admitted to the intensive care unit of a tertiary care hospital. **Methods:** The Microbiology laboratory received bacterial isolates from diverse clinical specimens originating from multiple Intensive Care Units (ICUs) for the purpose of culture and sensitivity testing. The identification of all species was conducted using both morphological and biochemical techniques, following established laboratory protocols. Additionally, the antibiotic susceptibility pattern was assessed by the utilization of disc diffusion methods. **Results:** The organisms were successfully isolated from 66.57% of the total 2920 samples collected. In 71.19% of the samples, a single organism was isolated, whereas in 28.8% of the samples, two or more organisms were found. Pseudomonas aeruginosa was the most often isolated bacterium, accounting for 38.17% of the total isolates. In the case of Pseudomonas aeruginosa, tobramycin has the most notable susceptibility rate at 94.2%, followed by meropenem at 93.93%, carbenicillin at 79.11%, and levofloxacin at 73.45%. The majority of commonly isolated pathogens have a high level of resistance to ampicillin, cephalexin, cefepime, and ciprofloxacin. **Conclusions:** The appropriate utilization of antibiotics in ICU plays a significant role in mitigating the development and spread of multi-drug resistance. Improved management of infections caused by resistant organisms in ICU necessitates the implementation of antibiotic policies and the establishment of robust surveillance systems.

Key words: antibiotic susceptibility, organisms, culture

INTRODUCTION

Infection and drug resistance are significant public health concerns. There is little doubt that the ramifications of heightened drug resistance are extensive.

The global emergence of antibiotic-resistant forms of bacteria, particularly within hospital settings and the broader population, presents a significant challenge that necessitates substantial resources and financial investment in

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order to effectively manage. The user's text is already academic in nature. The rationality of mitigating resistance through antibiotic usage control is acknowledged, although the practical implementation of successful policies has proven challenging in the majority of cases. Nevertheless, it is imperative to adopt a comprehensive strategy that encompasses the limitation of antibiotic usage, robust surveillance measures, and stringent infection control techniques in order to effectively address the issue of antibiotic resistance. The user's text is too short to be rewritten academically.

The Intensive Care Unit (ICU) has been identified as a possible origin of nosocomial infections, even in nations where comprehensive infection control measures are consistently practiced. The intensive care unit (ICU) presents a conducive setting for the proliferation and dissemination of nosocomial infections due to the presence of several immunocompromised patients and the performance of nursing care and invasive procedures. The numerical values 3 and 4 are provided. On a global scale, patients admitted to intensive care units (ICUs) have been confronted with a growing prevalence and dissemination of infections that display resistance to antibiotics. While intensive care units (ICUs) typically constitute only 5% of the total hospital bed capacity, they are responsible for a significant proportion, ranging from 20% to 25%, of all nosocomial infections. The harshness of patient contact with healthcare personnel and the duration of their stay in the intensive care unit (ICU) are factors that are correlated with an elevated susceptibility to infections. The user's text is too short to be rewritten in an academic manner.

In recent years, the rise in antibiotic resistance has posed challenges to the choice of empirical treatment for complex medical conditions. The establishment of effective patient management and the development of an appropriate antibiotic policy are contingent upon a comprehensive understanding of the prevailing strains and their patterns of antimicrobial resistance. Hence, the current study was designed with the aim of assessing the bacteriological profile and determining the prevalence of antibiotic resistance among various infections in patients admitted to the intensive care unit (ICU) of this hospital. This study is a humble endeavor to consolidate the strategic patterns of organisms and their resistance patterns, which have been isolated from patients hospitalized to various intensive care units (ICUs) within a tertiary care hospital.

MATERIALS AND METHODS

The current investigation was conducted in response to the presence of bacterial isolates obtained from diverse clinical specimens originating from various intensive care units (ICUs) within the Gandaki Medical College & Research Centre, situated in the Pokhara district of Nepal. These isolates were submitted to the Microbiology laboratory for culture and sensitivity testing between October 2020 and September 2021. The study included all patients who were hospitalized to different intensive care units (ICUs) within the designated study period and whose laboratory reports were obtained.

The study employed laboratory reports and data obtained from the medical records department as instrumental tools for analysis and investigation. A total of 2920 specimens were received within the specified time frame. Multiple sources of clinical specimens including blood, urine, pus, cerebrospinal fluid (CSF), catheter tips, endotracheal tips, drainage fluids (such as trauma, pleural, and ascitic fluids), bronchial aspirates, and central venous catheters (CVC), among others.

The identification of all species was conducted using normal laboratory procedures, encompassing both morphological and biochemical analyses. The received specimens were inoculated onto blood agar and MacConkey agar plates, and thereafter incubated under aerobic conditions at a temperature of 37 degrees Celsius for a period of one night. The identification of single and mixed growth (including two or more isolates) within the specimens obtained from all samples was accomplished by the observation of colony features on blood agar and Mac-Conkey agar plates, as well as the analysis of biochemical responses using established microbiological protocols.

The disc diffusion method was employed to conduct antibiotic susceptibility testing.6,7 The following antibiotics were tested using Hi-media discs: ampicillin (10µg), cephalexin (30µg), cefotaxime (30µg), amoxycillin/clavulanic acid (20/10µg), piperacillin (100µg), ceftazidime (30µg), ceftriaxone (30µg), meropenem (10µg), gentamicin (10µg), amikacin (30µg), ciprofloxcian (5µg), nitrofurantoin (100µg), cotrimoxazole (25µg), levofloxacin (5µg), and cefepime (30µg). The measurement and interpretation of the diameter zone were conducted in accordance with the guidelines provided by the Clinical and Laboratory Standard Institute.8-12 The ATCC control strains of Staphylococcus ATCC 43300, Escherichia coli ATCC 25922, and Pseudomonas aeruginosa ATCC 27873 were employed for the purpose of quality control in disc diffusion experiments.

The acquired data was inputted into Microsoft Excel 7, and afterwards analyzed utilizing the SPSS (Statistical Package for Social Sciences) 22.0 software package. Categorical variables have been represented using numerical counts and corresponding percentages. The statistical tests employed in this study were the Independent T test and the Chi Square test. A p-value of less than 0.05 was deemed to indicate statistical significance.

RESULTS

A cumulative count of 2920 samples was obtained over the course of the investigation, spanning from October 2020 to September 2021. Organisms were successfully isolated from 1944 samples, accounting for 66.57% of the total samples received. In a total of 1944 samples, a single organism was isolated in 1384 instances, accounting for 71.19% of the samples. Conversely, in 560 samples, two or more organisms were found, representing 28.8% of the total. The bacteria that were most commonly isolated in this study were Pseudomonas aeruginosa (P. aeruginosa) with a frequency of 742 (38.17%) and Klebsiella pneumoniae (K. pneumonia) with a frequency of 462 (23.76%). Following these, Acinetobacter anitratus (A. anitratus) was isolated with a frequency of 291 (14.96%). The Citrobacter species exhibited the lowest number of isolates, accounting for only 0.46% of the total. (Table 1)

Table 1: Patten of microorganisms isolated from study subjects.

Microorganisms	Frequency of isolates	Percentage
P. aeruginosa	742	38.17
K. pneumoniae	462	23.76
A. anitratus	291	14.96

Enterobacter Species	119	6.12
E. Coli	107	5.50
P. mirabilis	91	4.69
Staphylococcus aureus	39	2.01
CONS	41	2.11
Candida albicans	12	0.62
Klebsiella oxytoca	19	0.98
Enterococcus Species	12	0.62
Citrobacter Species	09	0.46
Total	1944	100

The antibiotic susceptibility profile of Pseudomonas aeruginosa indicates that a vast majority of the isolates exhibit resistance to Cephalexin, with a prevalence of 97.29%. Within the Pseudomonas aeruginosa bacterial species, tobramycin exhibits the most notable susceptibility rate, reaching 94.2%. This is closely followed by meropenem at 93.93%, carbenecillin at 79.11%, and levofloxacin at 73.45%. (Table 2)

Table 2: Antibiotic pattern of P. aeruginosa among the study subjects.

Antibiotics	**Sensitive**		**Resistant**	
	N	**%**	**N**	**%**
Cephalexin	22	2.96	720	97.29
Tobramycin	699	94.2	43	5.8
Piperacillin	339	45.68	403	54.32
Carbenecillin	587	79.11	155	20.89
Cefotaxime	514	69.27	228	30.73
Amikacin	496	66.84	246	33.16
Ceftriaxone	381	51.34	361	48.66
Ceftazidime	419	56.46	323	43.54
Gentamicin	294	39.62	448	60.38
Ciprofloxacin	113	15.22	629	84.78
Levofloxacin	545	73.45	197	26.55
Meropenem	697	93.93	45	6.07

The majority of commonly isolated organisms, such as K. pneumoniae, Acinetobacter anitratus, and Enterobacter, have a high level of resistance to antibiotics such as ampicillin, cephalexin, cefepime, and ciprofloxacin. (Table 3)

Table 3: Pattern of Antibiotic resistance among predominant microorganisms isolated from the study subjects (in %).

Antibiotics	**K. pneumoniae** N= 462	**A. anitratus** N= 291	**Enterobacter spp.** N=119	**E. coli** N=107	**P. mirabilis** N=91	**S. aureus** N=39	**CONS** N=41
Ampicillin	97.23	98.1	81.7	83	92.1	90.30	89.5
Amoxycillin/Cl	87.6	74.4	66.7	76.2	72.4	72.6	88.6

avulinic acid							
Ciprofloxacin	70.9	37.2	25.7	66.4	37.2	30.21	54.2
Amikacin	29.4	76.1	54.8	47.8	59.4	57.3	48.9
Gentamicin	89.2	72.34	32	41.9	72.2	69.23	57.4
Cotrimoxozole	39.5	45.17	59	26.27	58.5	59.5	61.29
Cefepime	54.5	86.3	98.7	51.09	67.2	68.71	35.54
Ceftrixone	67.2	50,18	96.4	52.78	70.21	67.4	98.7
Cephalixin	93.5	95.6	29.7	76.36	20.2	14.5	37.21
Meropenem	24.2	37.2	35.56	11.97	50.10	50.2	39.41
Levofloxacin	37.47	39.4	44.67	21.92	65.76	38.98	24.87
Vancomycin	-	-	-	-	-	0	0
Penicillin	-	-	-	-	-	100	98.7
Cefotaxime	67.3	71.8	55.14	32.9	67.84	68-14	58.6

DISCUSSION

Infection among patients in the intensive care unit (ICU) can arise from either community acquisition or iatrogenic causes. Modern intensive care is a collaborative endeavor including a diverse team led by the intensivist and clinical microbiologist, with additional help from relevant medical and surgical specialties as needed. The establishment of a long-term collaboration between the intensivist and the clinical microbiologist is crucial, since it not only enhances clinical outcomes but also maximizes the efficient use of resources.8

Of the 2920 samples that were obtained, organisms were successfully isolated from 66.57% of them. In 71.19% of the samples, a single organism was isolated, whereas in 28.8% of the samples, two or more organisms were found. The current investigation demonstrates that Pseudomonas aeruginosa was the most commonly isolated bacteria, accounting for 38.17% of the total isolates. These findings are consistent with previous studies.9,10 This finding stands in opposition to the research conducted by Kumari HB and Erb A.11,12 In her investigation, Kumari HB observed that non-fermenting gram-negative bacilli, excluding Pseudomonas aeruginosa, were identified as the predominant pathogen.11

The present analysis revealed a substantial degree of resistance to cephalexin (97.29%), ciprofloxacin (84.78%), gentamicin (60.38%), and pipercillin (54.32%) among the predominant P. aeruginosa strain. Tobramycin, meropenem, carbenecillin, and amikacin demonstrated a notable degree of efficacy against Pseudomonas aeruginosa. The observed high resistance of Pseudomonas aeruginosa to cephalexin and quinolones is consistent with findings reported in a separate investigation conducted in Indonesia. The number.13

This study documented the observation that Pseudomonas, K. pneumoniae, and Acinetobacter exhibited resistance to many drugs, specifically ampicillin, cephalosporins (including cefepime), and quinolone antibiotics. Furthermore, these isolates exhibit resistance to gentamicin. The results of experiments conducted in other locations were consistent with the findings of the current study.14,15 The observed phenomenon can be linked to the widespread utilization of cephalosporins and quinolones inside the confines of this medical facility.

The present investigation also noted that amikacin, tobramycin, and meropenem shown favorable sensitivity against all bacteria that were isolated from patients hospitalized to the intensive care unit (ICU). Another study conducted in Pakistan also documented a high sensitivity of gram-negative bacilli from lower respiratory tract specimens of patients admitted to the intensive care unit (ICU) towards aminoglycosides.16 Another study conducted in Jordan also found a high sensitivity rate of meropenem, which aligns with our own observations.17

Numerous reports from various regions worldwide have identified Pseudomonas aeruginosa, Acinetobacter, Klebsiella pneumoniae, and Escherichia coli as the predominant pathogens commonly isolated. A notable observation was made regarding the high resistance rate of frequently identified bacteria to cephalosporins and quinolone medications. These investigations provide further evidence that the indiscriminate use of antibiotics without adhering to antibiotic policies contributes to the development of antimicrobial resistance in both gram-positive and gram-negative bacteria.18-21

CONCLUSION

The current imperative for the management of intensive care unit (ICU) infections caused by resistant organisms necessitates the implementation of antibiotic policies, the establishment of effective surveillance systems, and the careful examination of epidemiological trends associated with these illnesses. There is a clear imperative to investigate both the epidemiological patterns of nosocomial infections and the specific circumstances inside our country. This necessitates the implementation of multicentre studies to facilitate coordination and the development of protocols that are informed by discernible patterns of antibiotic resistance. Modifying and rotating antibiotic prescribing patterns would result in a reduction in antibiotic resistance.

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AUTHORS’ CONTRIBUTION

All the authors have contributed equally.

CONFLICT OF INTEREST

The authors declare no conflicts of interest.

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