Section: Microbiology

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STUDY TO UNDERSTAND MICROBIAL PATTERN IN ISOLATES FROM ENDOTRACHEAL TUBE IN THE PATIENTS OF LIFE INTENSIVE CARE UNIT IN UTTER PRADESH, INDIA

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Corresponding Author:
Dr. Manisha Yadav,
Email: yadav.manisha76@gmail.com

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Manisha Yadav[1], Sandhya Niranjan[1] , Jampala Srinivas[2]

[1]Junior Resident, Department of Microbiology, Rajashree Medical Research Institute & Hospital, Bareilly, Uttar Pradesh, India.
[2]Professor and Head of the Department of Microbiology, Rajashree Medical Research Institute & Hospital, Bareilly, Uttar Pradesh, India.

ABSTRACT

Background: Nosocomial infections, particularly in critically ill patients requiring mechanical ventilation in the Life Intensive Care Unit (LICU), pose a significant challenge. This study aimed to identify the bacterial and fungal pathogens and determine their antimicrobial susceptibility profiles to guide effective treatment. **Materials and Methods:** Endotracheal specimens were collected from LICU patients and immediately processed for culture and sensitivity testing. The investigation included **168 samples**, with **64.3%** yielding positive bacterial growth. **Result:** The predominant isolates identified were **Staphylococcus spp. (26.3%)** and **Pseudomonas spp. (21%)** (the most prevalent single species). **Gram-positive isolates** were susceptible to aminoglycosides, fosfomycin, tetracycline, and chloramphenicol. **Gram-negative isolates** were susceptible to tetracycline, tobramycin, meropenem, aminoglycosides, and fosfomycin. **Isolated yeasts** were sensitive to Amphotericin B, ketoconazole, and fluconazole. Crucially, **15.7%** of the isolated species were identified as **multidrug-resistant (MDR)**. **Conclusion:** The high incidence of nosocomial infection and the significant proportion of MDR species in the LICU population necessitate continuous surveillance and strict adherence to infection control protocols. The identified susceptibility patterns are vital for informing empirical and targeted antimicrobial therapy.

INTRODUCTION

Healthcare-associated infections represent a critical challenge in intensive care unit (ICU) settings, where invasive medical interventions necessary for patient survival create opportunities for microbial colonization.[1,2]These infections predominantly arise from opportunistic microorganisms that take advantage of weakened immune systems in critically ill patients. Contemporary research demonstrates that specimens collected from endotracheal sources, including aspirates and tube tips, serve as valuable diagnostic materials for identifying causative pathogens.[3]

Previous investigations conducted by,[2] and colleagues,[1] identified Pseudomonas species and Klebsiella species as predominant bacterial isolates recovered from tracheal aspirate samples in ICU settings. Their findings also documented an alarming escalation in antimicrobial resistance profiles among these healthcare-associated pathogens.[4]Supporting evidence from substantiates the widespread occurrence of multidrug-resistant (MDR) bacterial strains in intensive care environments, with particularly high prevalence among mechanically ventilated patients. This research underscored the urgent requirement for continuous microbiological monitoring and rigorous implementation of infection prevention protocols to control pathogen transmission.

Genomic investigations have uncovered specific molecular mechanisms underlying antibiotic resistance in these organisms. Complete genome sequencing of Pseudomonas aeruginosa clinical isolates has identified resistance-conferring genes including bla_OXA-50 and active efflux mechanisms such as the mexAB-oprMsystem.[5] The capacity of these pathogens to form biofilms represents another crucial factor in their persistence and therapeutic resistance.[6]Biofilm-forming Pseudomonas aeruginosa strains demonstrate markedly increased tolerance to antimicrobial agents, creating substantial treatment challenges. The intricate architecture of biofilms shields bacterial populations from both immunological defences and pharmaceutical interventions, highlighting the need for novel therapeutic strategies.

Standard antimicrobial susceptibility testing through conventional culture methods continues to be fundamental for guiding clinical decision-making. Recent innovations in diagnostic microbiology, encompassing rapid molecular detection platforms and advanced susceptibility assays, have enhanced our ability to identify and characterize resistant microorganisms promptly.

The present investigation seeks to evaluate the bacterial spectrum and antimicrobial resistance profiles of specimens obtained from endotracheal sources in patients admitted to the life Intensive Care Unit.

MATERIALS AND METHODS

A total of 168 endotracheal specimens were obtained from patients aged 11 to 90 years who were admitted to the Life ICU presenting with pyrexia alongside clinical and radiographic indicators of pneumonia. All samples were collected aseptically in sterile collection vessels. The specimens comprised various sample types including endotracheal tube material, aspirated respiratory secretions, catheter segments removed from endotracheal tubes, and suction catheter tips containing tracheal discharge from different patients. Ethical clearance was taken.Following collection, all specimens were promptly transferred to the microbiology laboratory for analysis.

Upon arrival at the laboratory, each specimen underwent immediate inoculation onto multiple sterile culture media, including Nutrient agar, MacConkey agar, Cetrimide agar, and Potato Dextrose Agar plates, maintaining aseptic conditions throughout the process. The inoculated plates were then placed in an incubator maintained at 37°C and examined after a 24-hour incubation period for evidence of bacterial proliferation. Plates demonstrating growth with distinct isolated colonies were subsequently processed for morphological characterization and Gram staining procedures.

Bacterial identification was accomplished through a comprehensive panel of conventional biochemical assays. These included carbohydrate fermentation tests utilizing glucose, sucrose, lactose, maltose, and mannitol as substrates, along with Indole production assay, Methyl Red reaction, Lysine Decarboxylase activity test, Citrate utilization assay, Urease production test, and Triple Sugar Iron (TSI) agar test. All biochemical identification procedures followed established microbiological protocols as described in previous literature.[7]

RESULTS

This investigation encompassed 168 patients admitted to the Neurological Intensive Care Unit at a suburban tertiary care facility located in Makrandpur, Thakuran, Uttar Pradesh, India. Microbiological analysis revealed that 108 specimens (64.3%) yielded positive cultures, whereas 60 specimens (35.7%) demonstrated no microbial growth. The study population exhibited a male predominance with 136 participants (81%), compared to 32 female participants (19%). The age distribution analysis indicated that the largest patient subset, comprising 48 individuals (28.5%), belonged to the 61–70 years age bracket (Table 1).

Microbiological characterization of the culture-positive specimens revealed that 102 samples (94.5%) harbored monomicrobial infections, while 6 samples (5.5%) demonstrated polymicrobial growth patterns, including mixed bacterial and fungal colonization, yielding a cumulative total of 114 pathogenic isolates.

The microbial spectrum comprised nine distinct pathogenic species, categorized as follows:

a) Gram-negative organisms: Yersinia pseudotuberculosis, Enterobacter spp., Pseudomonas spp., Neisseria spp., and Klebsiella spp.

b) Gram-positive organisms: Staphylococcus spp., Streptococcus spp., Enterococcus spp., and yeast species.

The distribution of isolates based on Gram staining characteristics revealed that Gram-positive organisms constituted 54 isolates (47.4%), while Gram-negative organisms accounted for 60 isolates (52.6%) of the total microbial population. *Staphylococcus* spp. emerged as the predominant pathogen, representing 26.3% of all isolates recovered.

Table1: Demographic Data

Age Group	Total No of	Gender		Growth No	
Year	Patients	Male	Female		Growth
11–20	01	01	00	01	00
21–30	03	03	00	02	01
31–40	08	06	02	05	03
41–50	08	04	04	02	06
51–60	22	17	05	16	06
61–70	24	22	02	18	06
71–80	10	08	02	06	04
81–90	08	07	01	04	04
Total	84	68	16	54	30
Percentage		81%	19%	64.3%	81%

Pseudomonas spp. represented the second most frequently isolated pathogen, accounting for 21% of the total microbial isolates (Table 2). Gender-based analysis of culture-positive cases revealed that 86 male patients (79.62%) yielded positive cultures, in contrast to 22 female patients (20.37%).

A panel of 32 antimicrobial agents for bacterial isolates and 5 antifungal agents for yeast isolates. The susceptibility profiles of the isolated organisms are detailed below.

Streptococcus spp. demonstrated complete susceptibility (100%) to Fosfomycin. The solitary Enterococcus isolate exhibited susceptibility to both Tetracycline and Chloramphenicol. Fungal isolates displayed sensitivity to Fluconazole, Ketoconazole, and Amphotericin B.

Staphylococcus spp. exhibited broad-spectrum sensitivity to Aminoglycosides, β-lactam antibiotics, Quinolones, and Nitrofurantoin. However, susceptibility rates were notably lower for Tetracycline and Chloramphenicol (33.3% each) and Vancomycin (40%). Cephalosporin susceptibility among staphylococcal isolates remained markedly limited, not exceeding 20%. Similarly, other Gram-positive organisms demonstrated resistance to cephalosporin derivatives.

Pseudomonas spp. and Klebsiella spp. exhibited sensitivity to Aminoglycoside antibiotics while manifesting resistance to Ciprofloxacin. Enterobacter spp. demonstrated heterogeneous susceptibility patterns: Fosfomycin (42.8%), Amikacin (42.8%), Gentamicin and Tobramycin (14.2% each), and Tetracycline (57.1%).

Comprehensive analysis revealed that all Gram-positive bacterial species maintained susceptibility to Tetracycline and Chloramphenicol. Among Gram-negative organisms, Tetracycline and Fosfomycin retained activity against all isolates, with the exception of multidrug-resistant (MDR) strains.

Notably, Neisseria spp. and Yersinia pseudotuberculosis exhibited complete multidrug resistance (100% MDR phenotype). Third- and fourth-generation cephalosporins demonstrated minimal efficacy against Pseudomonas spp. (16.6% susceptibility) and Klebsiella spp. (11.1% susceptibility), while Enterobacter spp. displayed complete resistance to all cephalosporin agents tested.

Table 2: Microorganisms isolated from current study

Microorganism Isolated	Total No Growth	Age Groups (Year)							
		11-20	21-30	31-40	41-50	51-60	61-70	71-80	81-90
Staphylococcusspp.	30	2	2	6	0	12	4	2	2
Pseudomonasspp.	24	0	0	2	2	6	10	2	2
Enterobacterspp.	14	0	2	0	0	4	4	2	2
Klebsiellaspp.	18	0	0	2	0	2	12	2	0
Streptococcusspp.	12	0	0	0	0	6	4	2	0
Yeast	10	0	0	2	1	2	0	2	2
Enterococcusspp.	2	0	0	0	0	0	2	0	0
Neisseriaspp.	2	0	0	0	0	2	0	0	0
Yersiniapseudotuberculosis	2	0	0	0	0	2	0	0	0

DISCUSSION

The microbiological profile observed in the present investigation demonstrates concordance with established global epidemiological patterns of intensive care unit-associated infections, wherein Staphylococcus spp. and Pseudomonas spp. emerge as predominant causative agents. This distribution pattern has been consistently documented across multiple international studies, reinforcing the universal significance of these pathogens in the etiology of healthcare-associated infections,[8]

Interestingly, the complete absence of Acinetobacter spp. in our study population diverges from previously published literature, where Acinetobacter species have been frequently identified as prominent ICU,[2] pathogens.[9] This discrepancy potentially reflects geographical variations in microbial colonization patterns, differences in nosocomial infection dynamics, and the impact of institution-specific infection prevention and control strategies employed at our facility.

The documented prevalence of multidrug-resistant organisms (15.7%) in our cohort aligns with the escalating global burden of antimicrobial resistance (AMR), a phenomenon that has been consistently emphasized in surveillance reports published by the World Health Organization.[10]Our observations corroborate the worldwide trajectory of intensifying resistance patterns, driven by multiple contributing factors including injudicious antimicrobial usage, inadequate stewardship programs, and sustained selective evolutionary pressures within nosocomial environments.[2,3,11,10]

The gender-based differential in culture positivity rates, with male patients demonstrating significantly higher infection prevalence, parallels findings from comparable investigations that have documented enhanced susceptibility to ICU-acquired infections among males,[3,12,13,14] This phenomenon may be attributable to multifactorial determinants, including gender-specific variations in healthcare-seeking behaviors, differential prevalence of comorbid conditions, and inherent immunological response disparities between sexes.[15]

Antimicrobial susceptibility analysis revealed several noteworthy patterns. Streptococcus isolates demonstrated universal susceptibility to

Fosfomycin, while fungal isolates-maintained sensitivity to conventional antifungal agents including Fluconazole, Ketoconazole, and Amphotericin B. However, the markedly diminished susceptibility of Staphylococcus spp. to cephalosporin antibiotics underscores a persistent global challenge associated with β-lactam resistance mechanisms.[16,1]

The resistance profiles exhibited by Gram-negative organisms, particularly Pseudomonas spp. and Klebsiella spp., toward fluoroquinolones (ciprofloxacin) and extended-spectrum cephalosporins, mirror observations documented in international antimicrobial resistance surveillance networks, which have consistently reported progressive resistance evolution in these pathogenic species.[17,10]

Collectively, our findings underscore the imperative for implementing robust, continuous microbiological surveillance systems coupled with evidence-based antimicrobial stewardship initiatives to effectively manage the dynamic threat posed by multidrug-resistant microorganisms in intensive care and neurological intensive care settings globally.[18]

The data generated through this investigation reinforce the fundamental necessity for enhanced international collaborative frameworks in both research endeavors and policy formulation to comprehensively address the antimicrobial resistance crisis, as delineated in the Global Action Plan on Antimicrobial Resistance.[19]

CONCLUSION

The present investigation elucidates the microbiological spectrum and antimicrobial resistance profiles of pathogens isolated from endotracheal specimens obtained from patients admitted to the Neurological Intensive Care Unit of a suburban healthcare facility in Ratnagiri. Microbiological analysis revealed Staphylococcus spp. as the predominant Gram-positive pathogen, while Pseudomonas spp. emerged as the most frequently isolated Gram-negative organism in this study cohort.

The escalating prevalence of antimicrobial resistance among nosocomial pathogens underscores the critical necessity for implementing standardized, evidence-based infection control protocols within healthcare institutions. The comprehensive bacteriological data generated through this investigation provides valuable insights for formulating targeted antimicrobial stewardship strategies and optimizing empirical therapeutic interventions in the Life ICU setting.

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