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A Study of Bacteriological Profile and its Antibiogram in Respiratory Tract Infections Among the Patients Attending Tertiary Care Teaching Hospital, Greater Noida

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ABSTRACT
Introduction: *Respiratory tract infections (RTIs) is a major health problem, particularly in developing nations. They include upper and lower RTIs, with bacterial pathogens playing a significant role in lower RTIs. Rising antimicrobial resistance (AMR) necessitates continuous surveillance of local bacterial profiles and their susceptibility patterns.*
Aim and Objective: *A study of bacteriological profile and its antibiogram in respiratory tract infections among the patients attending tertiary care teaching hospital ,greater noida.*
Method: *A cross-sectional study was done over 12 months at a tertiary care hospital in Greater Noida. A total of 108 culture-positive respiratory samples from OPD, IPD, and ICU patients were analyzed. Standard microbiological methods were used for bacterial identification and antimicrobial susceptibility testing via Kirby-Bauer disc diffusion method, following CLSI 2024 guidelines.*
Result: *Of 229 samples, 108 (47.2%) showed bacterial growth. LRTIs accounted for 96 (88.9%) isolates and URTIs 12 (11.1%). Sputum was the most common sample (43.5%). Gram-negative bacilli predominated (71.9%), with* Klebsiella pneumoniae *(27.1%) being the most frequent. MRSA was identified in 10 of 17* Staphylococcus aureus *isolates (58.8%). Among 108 isolates, 41 (38.0%) were multidrug-resistant, mainly Gram-negative organisms.*
Conclusion: *The study shows a high prevalence of LRTIs and multidrug-resistant Gram-negative organisms. Empirical antibiotic policies should consider local resistance patterns, with emphasis on rational antibiotic use to mitigate AMR.*
Keywords: *Respiratory tract infections; Antimicrobial resistance; MRSA; Klebsiella pneumoniae; Multidrug resistance; Kirby-Bauer; CLSI.*

INTRODUCTION

Respiratory tract infections (RTIs) remain a significant public health concern worldwide, contributing to substantial morbidity and mortality, particularly in developing countries. They are broadly classified into upper respiratory tract infections (URTIs) and lower respiratory tract infections (LRTIs), depending on the anatomical site involved. URTIs commonly include pharyngitis, tonsillitis, and sinusitis, whereas LRTIs encompass bronchitis, bronchiolitis, and pneumonia. While viral etiologies are predominant in URTIs, bacterial pathogens play an important role, especially in LRTIs, and can lead to severe complications if not promptly identified and appropriately treated.[1,2]

The empirical use of antibiotics in RTIs, often without microbiological confirmation, has led to an alarming increase in antimicrobial resistance (AMR). This scenario shows a major challenge in the management of respiratory infections, particularly in hospitalized patients and those admitted to intensive care units (ICUs). Timely identification of the causative bacterial pathogens and understanding their antimicrobial susceptibility patterns are require for effective treatment and in formulating antibiotic stewardship policies.[3,4]

With increasing trends in multidrug-resistant (MDR) organisms, it is important to continuously monitor the local bacteriological profile and resistance patterns to guide empirical therapy. With this background present study was done with the aim to determine the spectrum of bacterial isolates from patients with respiratory tract infections presenting to the outpatient department (OPD), inpatient department (IPD), and ICU settings. The study also evaluates the antimicrobial susceptibility patterns of these isolates, thereby providing insight into the burden of MDR organisms and helping to optimize clinical management and antibiotic policy.

METHOD

This cross-sectional study was done in the Department of Microbiology, in tertiary care hospital, Greater Noida, for 12 months. The study included patients of all age groups and both sexes who were admitted in the inpatient department (IPD), intensive care unit (ICU), or visiting the outpatient department (OPD), and had clinical signs and symptoms suggestive of either upper or lower respiratory tract infections.

A total of 108 respiratory samples that showed positive bacterial growth during the study period were included for analysis. The clinical specimens collected were sputum, throat swabs, endotracheal aspirates, bronchial washings, tracheal secretions, and pleural fluids. All specimens were collected under aseptic precautions and transported promptly to the microbiology laboratory for processing.

Samples were processed using standard microbiological procedures. In cases where immediate processing was not possible, samples were stored at 4°C. Culture media such as Blood Agar, Chocolate Agar, MacConkey Agar, and Nutrient Agar were used for inoculation. These were prepared according to the manufacturer's guidelines. The inoculated plates were incubated aerobically at 37°C for 24 hours, and bacterial growth was observed and recorded.

Identification of bacterial isolates was initially done by observing colony characteristics, hemolysis patterns, Gram staining, and growth on differential media. Further biochemical tests were conducted for confirmation. When required, uncertain isolates were confirmed using the automated VITEK 2-Compact system.

Antimicrobial susceptibility testing (AST) was performed using the Kirby–Bauer disc diffusion method on Mueller-Hinton Agar, following the guidelines provided by the Clinical and Laboratory Standards Institute (CLSI 2024).

To standardize bacterial inoculum, a 0.5 McFarland turbidity standard was prepared, equivalent to approximately 1×10^8 CFU/mL. This was verified using a spectrophotometer or a viable plate count method using E. coli ATCC 25922 as the control strain. Colonies from pure cultures were suspended in sterile peptone water and adjusted to match the McFarland standard. The suspension was then uniformly swabbed onto Mueller-Hinton agar plates, and antibiotic discs were placed on the surface. After 24 hours of incubation at 37°C, zones of inhibition were measured using a sliding caliper and interpreted according to CLSI 2024 criteria.

The antibiotics tested against Gram-positive bacteria included: penicillin, cefoxitin, vancomycin, linezolid, teicoplanin, gentamicin, amikacin, erythromycin, levofloxacin, ciprofloxacin, and ampicillin. For Gram-negative bacteria, the antibiotics tested were: ampicillin, amoxicillin-clavulanate, ampicillin-sulbactam, ceftazidime, cefotaxime, ceftriaxone, cefepime, gentamicin, tobramycin, amikacin, levofloxacin, aztreonam, ticarcillin, ticarcillin-clavulanic acid, tetracycline, and imipenem. For Pseudomonas species, drugs such as ceftazidime, gentamicin, amikacin, piperacillin, piperacillin-tazobactam, aztreonam, cefepime, ciprofloxacin, levofloxacin, imipenem, ticarcillin, and ticarcillin-clavulanic acid were tested.

RESULT

A total of 229 clinical specimens were collected from patients with signs and symptoms of respiratory tract infections (RTIs), comprising both upper and lower respiratory tract infections. Of these, 108 samples yielded significant bacterial isolates.

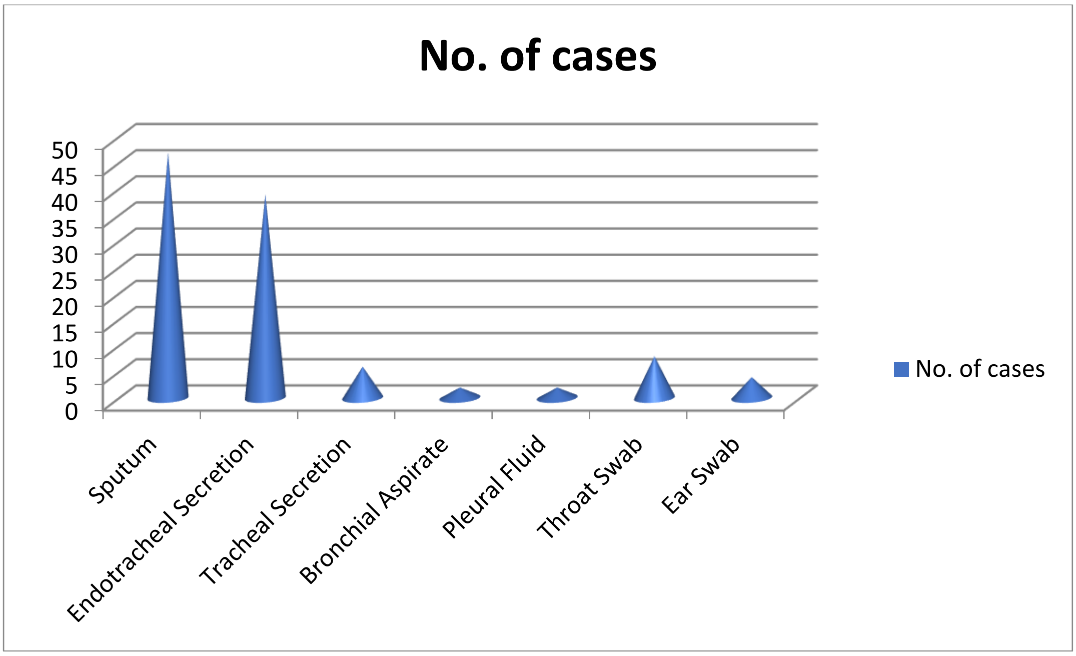
Out of the 108 isolates, 96 (88.89%) were from lower respiratory tract infections (LRTIs) and 12 (11.11%) from upper respiratory tract infections (URTIs), showing a higher burden of LRTIs.

Table 1. Distribution of Respiratory Samples by Site (n = 108)

Sample Type	Number (%)
Sputum	47 (43.5%)
Endotracheal Secretion	39 (36.1%)
Tracheal Secretion	6 (5.6%)
Bronchial Aspirate	2 (1.9%)

Pleural Fluid	2 (1.9%)
Throat Swab	8 (7.4%)
Ear Swab	4 (3.7%)

Sputum was the most frequently collected sample (43.5%), followed by endotracheal secretions (36.1%). URTI samples (throat and ear swabs) constituted 11.1% of total isolates.Of the 108 isolates, 72 (66.7%) were from male patients and 36 (33.3%) from female patients, showing a higher prevalence of RTIs among males.Age-wise analysis showed that the majority of bacterial isolates were recovered from the 21–30 year age group (n=20), followed by 41–50 years (n=19) and 61–70 years (n=17), showing that both younger and older adults are more susceptible to RTIs.



Graph No. 1: Graphical Representation of Distribution of Respiratory Samples by Site (n = 108)

Table 2. Age-wise Distribution of Samples (n = 108)

Age Group (years)	Number (%)
0–10	11 (10.2%)
11–20	6 (5.6%)
21–30	20 (18.5%)
31–40	8 (7.4%)
41–50	19 (17.6%)
51–60	14 (13.0%)
61–70	17 (15.7%)
71–80	9 (8.3%)
81–90	4 (3.7%)

Regarding the spectrum of organisms, Gram-negative bacilli were more frequently isolated than Gram-positive cocci, particularly in LRTIs.

Table 3. Distribution of Bacterial Pathogens by Site and Gram Stain Reaction

Infection Type	GPC	GNB (Fermenter)	GNB (Non-Fermenter)
URTI (n=12)	9 (75.0%)	1 (8.3%)	2 (16.7%)
LRTI (n=96)	27 (28.1%)	52 (54.2%)	17 (17.7%)

In URTI samples, Staphylococcus aureus (50%) was the predominant pathogen, followed by Enterococcus spp. (25%). In LRTI samples, Klebsiella pneumoniae (27.08%) was the most commonly isolated organism.

Table 4. Bacteriological Profile of URTI and LRTI

Organism	URTI n (%)	LRTI n (%)
Staphylococcus aureus	6 (50%)	11 (11.5%)
Enterococcus sp.	3 (25%)	2 (2.1%)

Pseudomonas aeruginosa	2 (16.7%)	14 (14.6%)
Citrobacter sp.	1 (8.3%)	8 (8.3%)
Klebsiella pneumoniae	0 (0%)	26 (27.1%)
Escherichia coli	0 (0%)	15 (15.6%)
CONS	0 (0%)	14 (14.6%)
Proteus mirabilis	0 (0%)	3 (3.1%)
Acinetobacter sp.	0 (0%)	3 (3.1%)

Most isolates were obtained from inpatients (n=86, 79.6%), with only 22 (20.4%) from OPD cases. This shows that hospitalized patients are more likely havepathogenic isolates, may be due to the severity of illness or increased risk of hospital-acquired infections.

Among the 17 total isolates of Staphylococcus aureus, 10 (58.8%) were Methicillin-Resistant Staphylococcus aureus. MRSA was most commonly isolated from sputum (7 isolates) and throat swabs (3 isolates).

Table 5. Antibiotic Susceptibility Pattern of MRSA Isolates (n = 10)

Antibiotic	Sensitive n (%)	Resistant n (%)
Vancomycin	10 (100%)	0 (0%)
Linezolid	10 (100%)	0 (0%)
Teicoplanin	10 (100%)	0 (0%)
Amikacin	6 (60%)	4 (40%)
Gentamicin	4 (40%)	6 (60%)
Ciprofloxacin	2 (20%)	8 (80%)
Erythromycin	3 (30%)	7 (70%)
Clindamycin	5 (50%)	5 (50%)
Penicillin	0 (0%)	10 (100%)
Cefoxitin	0 (0%)	10 (100%)

Glycopeptides and oxazolidinone group antibiotics were found to be the most effective against MRSA. Similarly, Imipenem showed 100% sensitivity across all Gram-negative isolates including Klebsiella, E. coli, and Pseudomonas.

Out of 108 total isolates, 41 (37.96%) were multidrug-resistant. MDR was more common in Gram-negative bacilli (41.09%) compared to Gram-positive cocci (30.55%).

Table 6. Distribution of Multidrug-Resistant Organisms

Organism	MDR n (%)
E. coli (n=15)	8 (53.3%)
Citrobacter sp. (n=9)	5 (55.6%)
Klebsiella pneumoniae	9 (34.6%)
Pseudomonas aeruginosa	6 (37.5%)
Staphylococcus aureus	10 (58.8%)
Proteus sp.	1 (33.3%)
Acinetobacter sp.	1 (33.3%)
Enterococcus sp.	1 (20.0%)
CONS	0 (0%)

DISCUSSION

In our study, a total of 229 respiratory specimens were analyzed, of which 108 (47.2%) yielded significant bacterial isolates. Among these, lower respiratory tract infections (LRTIs) predominated, accounting for 88.89% of cases, while upper respiratory tract infections (URTIs) represented 11.11%. This trend is similar to several prior studies that have consistently showed a higher burden of LRTIs among hospitalized patients.[5–7]

Our analysis showedmajority of Gram-negative bacilli (GNB), especially fermenters like Klebsiella pneumoniae (27.1%) and Escherichia coli (15.6%), and non-fermenters like Pseudomonas aeruginosa (14.6%). This is similar to findings from Choudhury et al. (2025), where GNB fermenters and non-fermenters together accounted for 85.56% of LRTI isolates.[8]. Similarly, Vishwanath et al. (2013)

reported a high incidence of Klebsiella pneumoniae (37%) and Pseudomonas aeruginosa (28.6%) in LRTI cases, showing their continued dominance in nosocomial settings.[9]
In contrast, Gram-positive cocci (GPC) were more frequently isolated from URTI samples in our study, with Staphylococcus aureus comprising 50% and Enterococcus spp. 25% of the isolates. This is similar to the findings of Dutta et al. (2017).[10] and Zelelie et al. (2019),[11] who also reported GPC predominance in URTI cases, particularly Staphylococcus aureus and Streptococcus pneumoniae. Our results show that GPC are the major pathogens in community-acquired URTIs, while GNB dominate in LRTIs and hospital-acquired infections.
Regarding age distribution, the highest number of isolates in our study were from the 21–30 and 41–50-year age groups, consistent with literature noting increased vulnerability in both younger adults (due to exposure) and older adults (due to comorbidities).[6,12]In our study Male were more common (66.7%) similarly seen inMiriti et al. (2023)[13] and Bajpai et al. (2013),[7] who reported a higher prevalence of RTIs among males.
The antibiotic susceptibility pattern in our study showed that all Staphylococcus aureus isolates were sensitive to vancomycin, linezolid, and teicoplanin. These results are similar to several studies.[14–16]which consistently showed high susceptibility of MRSA isolates to glycopeptides and oxazolidinones, confirming their continued role as mainstay treatments for MRSA infections. However, high resistance rates to penicillin (100%), cefoxitin (100%), erythromycin (70%), and ciprofloxacin (80%) were noted, comparable to global reports.[17,18]
Out of the 17 total S. aureus isolates, 10 (58.8%) were Methicillin-Resistant Staphylococcus aureus (MRSA). This is higher than some international averages but similar to figures reported by Bajpai et al. (2013)[7] and Shahin et al. (2018)[19], showing a significant MRSA burden in respiratory infections within healthcare facilities.
Multidrug resistance (MDR) was a major concern in our study, with 41 out of 108 isolates (37.96%) being MDR. This is comparable to the MDR rates reported by Vishwanath et al. (2013)[9] (~37%) and supports findings from Souza et al. (2020)[20] and de Oliveira et al. (2023)[21], where MDR prevalence among LRTI pathogens like Acinetobacter baumannii, Klebsiella pneumoniae, and Pseudomonas aeruginosa was frequently above 50%.In our study, MDR rates for E. coli (53.3%), Citrobacter spp. (55.6%), and Klebsiella pneumoniae (34.6%) were comparable to the meta-analysis data, showing widespread resistance among Enterobacterales. For Acinetobacter spp., the MDR rate was 33.3% in our study, lower than that reported by Raut et al. (2020)[22] and Huang et al. (2018),[23] who found rates above 60–70%. These differences show difference in infection control practices and antibiotic stewardship policies across institutions.
Our findings of Gram-negative bacilli predominance in lower respiratory tract infections (LRTIs), particularly Klebsiella pneumoniae and Pseudomonas aeruginosa, are consistent with recent studies highlighting their role as major pathogens in hospital-acquired infections. A 2024 [24] multicentric study by Mahale et al. similarly demonstrated Klebsiella as the leading isolate in LRTIs, with high multidrug resistance rates necessitating careful antimicrobial stewardship. Furthermore, Carrel et al. (2024) [25] reported continued susceptibility of MRSA to glycopeptides and oxazolidinones, supporting our observation of vancomycin and linezolid efficacy. More recently, Choudhury et al. (2025) [26] reported that non-fermenting Gram-negative bacilli accounted for over 80% of LRTI isolates, reinforcing the increasing clinical importance of these organisms. Similarly, Tobin et al. (2025) [27] emphasized that bacterial pathogens remain significant contributors to respiratory infections despite widespread viral etiologies in URTIs. Collectively, these findings highlight the urgent need for sustained local surveillance, judicious antibiotic use, and strengthened infection control measures to limit the burden of multidrug-resistant respiratory pathogens.

Overall, our findings show the continued dominance of Gram-negative bacilli in LRTIs, the significant burden of MRSA and MDR organisms, and the importance of ongoing surveillance, rational antibiotic use, and infection control measures to mitigate the spread of resistant pathogens.

CONCLUSION

Overall, our findings align with global trends showing Gram-negative bacilli predominance in LRTIs and Gram-positive cocci in URTIs, with a troubling burden of MDR pathogens including MRSA. The resistance profiles necessitate ongoing surveillance and antibiotic stewardship to preserve therapeutic efficacy.

Limitations and Future Directions

This study was done in single-center and there was lack of molecular typing for resistance mechanisms, which could show deeper insights into epidemiology and transmission dynamics. Future multicentric research with molecular epidemiology and resistance gene profiling would increase understanding and guide targeted interventions.

DECLARATIONS

Conflicts of interest: There is no any conflict of interest associated with this study

Consent to participate: There is consent to participate.

Consent for publication: There is consent for the publication of this paper.

Authors' contributions: Author equally contributed the work.

REFERENCES

[1] Calderaro A, Buttrini M, Farina B, Montecchini S, De Conto F, Chezzi C. Respiratory Tract Infections and Laboratory Diagnostic Methods: A Review with A Focus on Syndromic Panel-Based Assays. Microorganisms 2022, Vol 10, Page 1856 2022;10:1856. https://doi.org/10.3390/MICROORGANISMS10091856.

[2] Tobin EH, Thomas M, Bomar PA. Upper Respiratory Tract Infections With Focus on The Common Cold. StatPearls 2025.

[3] Murray CJ, Ikuta KS, Sharara F, Swetschinski L, Robles Aguilar G, Gray A, et al. Global burden of bacterial antimicrobial resistance in 2019: a systematic analysis. The Lancet 2022;399:629–55. https://doi.org/10.1016/S0140-6736(21)02724-0.

[4] Basu S, Copana R, Morales R, Anugulruengkitt S, Puthanakit T, Maramba-Lazarte C, et al. Keeping It Real: Antibiotic Use Problems and Stewardship Solutions in Low- and Middle-income Countries. Pediatr Infect Dis J 2022;41:S18. https://doi.org/10.1097/INF.0000000000003321.

[5] Chawla K, Vishwanath S, Munim FC. Nonfermenting Gram-negative Bacilli other than Pseudomonas aeruginosa and Acinetobacter Spp. Causing Respiratory Tract Infections in a Tertiary Care Center. J Glob Infect Dis 2013;5:144. https://doi.org/10.4103/0974-777X.121996.

[6] PayalRahangdale AAG, Shaikh AmbreenFatema JAI, Nashrah Khan AH. Microbiological Profile of Lower Respiratory Tract Infections in MICU in a Tertiary Care Hospital. Int J CurrMicrobiolApplSci 2021;10:1450–9. https://doi.org/10.20546/ijcmas.2021.1002.174.

[7] Bajpai T, Bhatambare G, Shrivastava G, Deshmukh A, Chitnis V. Microbiological profile of lower respiratory tract infections in neurological intensive care unit of a tertiary care center from Central India. J Basic Clin Pharm 2013;4:51. https://doi.org/10.4103/0976-0105.118789.

[8] Choudhury S, Pathi BK, Sahoo JP, Mohanty S, Panigrahi K, CHOUDHURY S, et al. Prevalence and Antimicrobial Susceptibility Patterns of Non-fermenting Gram-Negative Bacteria Causing Lower Respiratory Tract Infections: A Retrospective Study. Cureus 2025;17. https://doi.org/10.7759/CUREUS.88844.

[9] Shashidhar Vishwanath, Kiran Chawla, AnushaGopinathan. (PDF) Multidrug resistant Gram-negative bacilli in lower respiratory tract infections. Researchgate 2013;5.

[10] Dutta AP, Dutta SE, Mazumdar R, Chatterjee M, Sarkar A. Bacteriological Profile of Recurrent Upper Respiratory Tract Infection in Children Attending a Tertiary Care Hospital. Int J CurrMicrobiolApplSci 2017;6:2561–7. https://doi.org/10.20546/ijcmas.2017.608.303.

[11] Zelelie TZ, Mekonnen YT, Abebe TA. Bacterial Profile and Antimicrobial Resistance Patterns In Patients With Upper Respiratory Tract Infections In DebreBerhan Referral Hospital, Ethiopia. Egyptian Journal of Ear, Nose, Throat and Allied Sciences 2019;20:9–15. https://doi.org/10.21608/EJENTAS.2018.4422.1026.

[12] Mahale RP, DarpanSheth P, Murthy NS. Evaluating the Sputum Bacteriological Profile of Lower Respiratory Tract Infections With Bartlett Score Analysis in a Tertiary Care Hospital in Southern Karnataka. Cureus 2024;16. https://doi.org/10.7759/CUREUS.61924.

[13] Miriti DM, Muthini JM, Nyamache AK. Study of bacterial respiratory infections and antimicrobial susceptibility profile among antibiotics naive outpatients visiting Meru teaching and referral hospital, Meru County, Kenya in 2018. BMC Microbiol 2023;23. https://doi.org/10.1186/S12866-023-02905-X,.

[14] Gurung RR, Maharjan P, Chhetri GG. Antibiotic resistance pattern of Staphylococcus aureus with reference to MRSA isolates from pediatric patients. Future Sci OA 2020;6. https://doi.org/10.2144/FSOA-2019-0122,.

[15] Carrel M, Smith M, Shi Q, Hasegawa S, Clore GS, Perencevich EN, et al. Antimicrobial Resistance Patterns of Outpatient Staphylococcus aureus Isolates. JAMA Netw Open 2024;7:e2417199–e2417199. https://doi.org/10.1001/JAMANETWORKOPEN.2024.17199.

[16] Pai V, Rao VI, Rao SP. Prevalence and Antimicrobial Susceptibility Pattern of Methicillin-resistant Staphylococcus Aureus [MRSA] Isolates at a Tertiary Care Hospital in Mangalore, South India. J Lab Physicians 2010;2:082–4. https://doi.org/10.4103/0974-2727.72155.

[17] Almutairi H, Albahadel H, Alhifany AA, Aldalbahi H, Alnezary FS, Alqusi I, et al. Prevalence and antimicrobial susceptibility pattern of methicillin-resistant Staphylococcus aureus (MRSA) at a maternity and children hospital in Saudi Arabia: A cross-sectional study. Saudi Pharmaceutical Journal 2024;32. https://doi.org/10.1016/J.JSPS.2024.102001,.

[18] Ahmed SMA-Z, Abdelrahman SS, Saad DM, Osman IS, Osman MG, Khalil EAG. Etiological Trends and Patterns of Antimicrobial Resistance in Respiratory Infections. Open Microbiol J 2018;12:34–40. https://doi.org/10.2174/1874285801812010034,.

[19] Shahin M, Moghim S, Havaei SR, Ghanbari F, Havaei SA. Determination of antimicrobial resistance pattern and molecular characteristics of methicillin-resistant Staphylococcus aureus strains isolated from patients in a teaching hospital of Isfahan, Iran. Gene Rep 2018;12:289–93. https://doi.org/10.1016/J.GENREP.2018.07.004.

[20] Souza RR de, Nascimento MA, Ederli RB, Santos ECM, Santos IA dos, Ederli JPB. Multi-resistant Acinetobacter baumannii emergence associated with healthcare infections: Meta-analysis. Research, Society and Development 2020;9:e1889108270. https://doi.org/10.33448/rsd-v9i10.8270.

[21] de Oliveira ABS, Sacillotto GH, Neves MFB, da Silva AHN, Moimaz TA, Gandolfi JV, et al. Prevalence, outcomes, and predictors of multidrug-resistant nosocomial lower respiratory tract infections among patients in an ICU. JornalBrasileiro de Pneumologia 2023;49:e20220235–e20220235. https://doi.org/10.36416/1806-3756/E20220235.

[22] Raut S, Rijal KR, Khatiwada S, Karna S, Khanal R, Adhikari J, et al. Trend and Characteristics of Acinetobacter baumannii Infections in Patients Attending Universal College of Medical Sciences, Bhairahawa, Western Nepal: A Longitudinal Study of 2018. Infect Drug Resist 2020;13:1631. https://doi.org/10.2147/IDR.S257851.

[23] Huang H, Chen B, Liu G, Ran J, Lian X, Huang X, et al. A multi-center study on the risk factors of infection caused by multi-drug resistant Acinetobacter baumannii. BMC Infect Dis 2018;18:11. https://doi.org/10.1186/S12879-017-2932-5.

[24] Mahale RP, Sheth PD, Murthy NS. Evaluating the sputum bacteriological profile of lower respiratory tract infections with Bartlett score analysis in a tertiary care hospital in Southern Karnataka. Cureus. 2024;16:e61924. https://doi.org/10.7759/cureus.61924

[25] Carrel M, Smith M, Shi Q, Hasegawa S, Clore GS, Perencevich EN, et al. Antimicrobial resistance patterns of outpatient Staphylococcus aureus isolates. JAMA Netw Open. 2024;7(6):e2417199. https://doi.org/10.1001/jamanetworkopen.2024.17199

[26] Choudhury S, Pathi BK, Sahoo JP, Mohanty S, Panigrahi K, Choudhury S, et al. Prevalence and antimicrobial susceptibility patterns of non-fermenting Gram-negative bacteria causing lower respiratory tract infections: A retrospective study. Cureus. 2025;17:e88844. https://doi.org/10.7759/cureus.88844

[27] Tobin EH, Thomas M, Bomar PA. Upper respiratory tract infections with focus on the common cold. StatPearls. Treasure Island (FL): StatPearls Publishing; 2025.