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Bacteriological Profile and Antibiotic Resistance Pattern in Respiratory Tract Infection at a Tertiary Care Hospital

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Abstract: ***One of the most prevalent ailments afflicting people worldwide, particularly in underdeveloped nations, is respiratory tract infection (RTI). Public health and the results for patients are seriously threatened by the increasing prevalence of resistant bacteria to antibiotics among the bacterial infections that cause RTIs. The purpose of this study is to ascertain the pattern of antibiotic resistance and bacteriological profile of RTI patients who are admitted to a hospital with tertiary care. Material & Methods: 92 patients with a clinical suspicion of RTI participated in a prospective trial. Clinical samples were collected and processed according to standard microbiological protocols. The isolated pathogenic microbes were identified by biochemical testing, and in accordance with CLSI standards, the Kirby-Bauer disc diffusion technique was employed to test them for antibiotic susceptibility. Result: Out of 92 samples, 50 (54.35%) were culture-negative, 3 (3.26%) had fungal growth, and 39 (42.39%) had bacterial growth. Klebsiella species, Pseudomonas aeruginosa, E. coli, Acinetobacterbaumannii and Staph. Aureus, among others, were the most common bacterial isolates. High resistance to ceftazidime (83.33%) & aztreonam (83.33%) was found in Klebsiella isolates, with piperacillin (66.66%) and tigecycline as (58.33%) following closely behind. Conclusion: The study shows that multidrug-resistant organisms, especially Klebsiella spp., are quite common in RTI cases. For efficient care and to direct empirical therapy, it is essential to regularly evaluate bacterial trends and patterns of antibiotic susceptibility. Strict infection control procedures and the prudent use of antibiotics are required to counteract the growing threat of resistance to antibiotics.***

Keywords: Respiratory tract infections, Antibiotic resistance, Antibiotic sensitivity, Tertiary care hospital, Bacterial profile

1.Introduction

Respiratory tract infections (RTIs) are among the most important infectious disorders in the world. This infection is the principal causes of illness and death among severely ill patients, in developing countries (Reed, 2015). RTIs are the most often reported infection in humans. While some of these illnesses are mild, transient, and often self-limiting, others are serious enough to necessitate medical attention and a prescription for antibiotics (Peters et al., 2011). A diverse and intricate category of illnesses, respiratory infections are brought on by a variety of pathogens, including bacteria, fungi, and viruses (Dasaraju & Liu, 1996). There are two types of acute respiratory tract infections: those that primarily impact the upper and lower respiratory tracts. Acute respiratory infections (ARI), such as pneumonia, one of the greatest, fatal communicable diseases affecting children worldwide (Simoes et al., 2006a). The common signs and symptoms of ARI include blocked or runny nose, cough, ear ache or discharge, sore throat, noisy breathing such as wheeze or strider, and difficult breathing such as chest in-drawing and fast breathing (Simoes et al., 2006b). Anatomically, the vocal cords act as a boundary between these two regions, with the lower upper respiratory tract (bronchial tree and pulmonary parenchyma) situated beneath the vocal cords and the upper respiratory tract (nasopharynx, peri-tonsillar structures, sinuses, larynx, and epiglottis) proximal to the cords. The most common infections of the upper respiratory tract include sinusitis, tonsillitis, otitis media, pharyngitis, and nasopharyngitis (Suárez-Quintanilla et al., 2025). The majority of acute upper respiratory tract infections (UTRIs) are caused by viruses. There are two types of acute lower respiratory tract infections (LRTIs): those that cause bronchitis by affecting the airways and those that cause pneumonia, which is an inflammation of the pulmonary parenchyma (Rogan, 2017). Any infection that occurs in the lungs, trachea, bronchi, bronchioles, alveoli, or below the larynx is considered an LRTI. LRTIs are a group of distinct illnesses with different epidemiologist, pathophysiology, clinical manifestations, and outcomes rather than a single illness. The symptoms and emergence or origin of respiratory disorders depending on age, gender, and the type of population at risk. An LRTI is an infection that typically lasts one to three weeks and manifests as cough, expectoration, dyspnea, wheezing, and chest pain or discomfort (Pavia, 2011). LRTI can be caused by a number of predisposing factors like Smoking, alcohol consumption, diabetes mellitus, immunosuppressive disorders, bronchial asthma, COPD and many more (Kumar et al., n. d.). The causative agents of LRTIs vary from area to area and in their antibiotic susceptibility profile. Gram-positive bacteria such as *Staphylococcus aureus, Streptococcus pneumoniae, etc. and gram-negative bacteria e.g. Pseudomonas spp. Escherichia coli, Klebsiella spp*. are identified commonly in the LRTI patients (Khan et al., 2015). The choice for antimicrobial therapy is usually straight forward when the etiologic agents and their susceptibility patterns are known (Leekha et al., 2011). The primary problem with current antibiotic treatments is that antimicrobial resistance is

rapidly spreading in hospitals and communities (Kushwaha et al., 2025). Soil microorganisms are among the most diverse and significant groups of found in terrestrial ecosystems (Dubey, n. d.). It is important to know commonly involved pathogens and current antibiotic sensitivity patterns to treat respiratory infections. Knowledge of current patterns of pathogens involved in respiratory infection and antibiotic sensitivity patterns may help greatly in treating infections, avoiding complications, and reducing mortality as well as in making antibiotic policy at departmental, institutional, or regional level (Agmy et al., 2013). Keeping this in mind, the purpose of this study is to determine the prevalence of bacteriological profile and antibiotic resistance pattern in respiratory tract infection at a tertiary care hospital. Compiling the incidence and correlating it with sociodemographic data and risk factors would aid in understanding and controlling infection prevalence.

2.Material and Method

Study Design and Period - This prospective study received ethical clearance from the Institutional Research Committee and Institutional Ethical Committee on 8 march 2025 (MGUG/GGIMS$MDAC/IEC (HS)/2025/010). It was conducted at the Department of Microbiology, Shri Gorakshnath Medical College Hospital and Research Centre, Mahayogi Gorakhnath University Gorakhpur, Uttar Pradesh, over a period of six month (January 2025 to June 2025).

Data Collection-We evaluated 92 sputum sample for antibiotic sensitivity which were received from Mahant Digvijayanath Ayurveda Chikitsalaya, Shri Guru Gorakhnath Chikitsalaya Gorakhpur and Baba Raghav Das Medical College, Gorakhpur over a period of six months (January 2025 to June 2025).

Inclusion criteria:

(1) Patients of all age groups and both genders (Male/Female) with clinical symptoms of respiratory tract infections.
(2) Patients attending the tertiary care hospital outpatient's department and inpatients department.
(3) Patients who consent to participate in the study.

Exclusion criteria:

(1) Duplicate samples from same patients.
(2) Samples showing mixed growth or contamination.
(3) Patients who decline to give consent for participation in the study.

Laboratory Method -

Sample collection: Aseptic conditions were used to collect Sputum and fluid samples.

Microscopy:

Gram staining-Gram staining will be performed for the differentiation of gram positive and gram-negative (Tripathi et al., 2025). Gram positive bacteria appear purple color shown figure 1 after Gram's staining. Gram negative bacteria appear pink color after Gram's staining in shown figure 2.

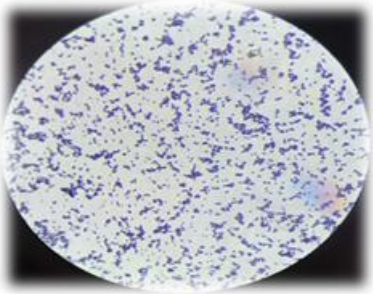

Figure 1: Gram Positive Bacteria

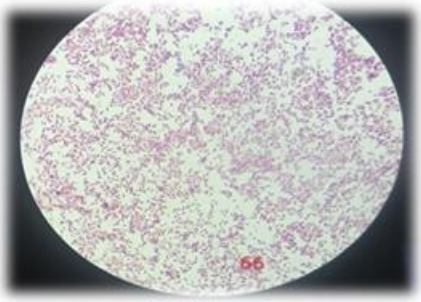

Figure 2: Gram Negative Bacteria

Culture Media-Specimens were analyzed at the Microbiology Laboratory of Mahayogi Gorakhnath University, Gorakhpur, over a six-month period. Each sample was inoculated onto MacConkey in shown NLF bacterial colony figure 3 and Lf colony in shown figure 4, and Blood agar shown hemolysis in figure 5 and Mannitol salt agar shows Staphylococcus bacterial colony in figure 6, while Chocolate agar was incubated at 37°C for 24-48 hours in 5-10% CO_2. Other plates were incubated aerobically at 37°C for 24-48 hours. Isolates were identified using conventional microbiological methods and biochemical tests on selective and differential media (Franco-Duarte et al., 2019).

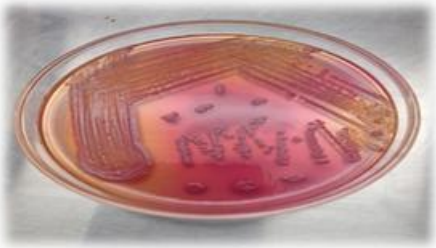

Figure 3: NLF bacterial colony

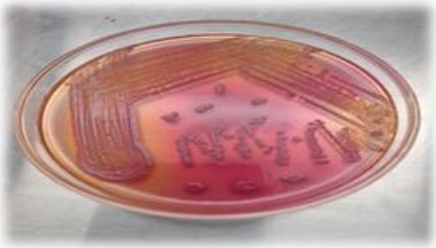

Figure 4: LF bacterial colony

Figure 5: Hemolysis on Blood Agar

Figure 6: Staphylococcus on Mannitol salt Agar

Species Identification:

Biochemical Tests -Biochemical tests are tests that identify the bacteria on the basis of the presence of certain enzymes and differences in the biochemical activities of different bacteria. They are among the most important methods for microbial identification. E.g. Catalase, coagulase, oxidase, indole, methyl red, citrate and triple sugar iron test.

Catalase test: Bubbles that produce catalase appear when a colony of bacteria is combined with the peroxide solution (3% H2O2). Because the catalase enzyme in this reaction breaks down H2O2 and creates nascent oxygen (Iwase et al., 2013). Catalase positive test shows bubbles and catalase negative shows not bubbles in figure 7.

Figure 7: Shows Catalase test Positive & Negative

Coagulase Test: To distinguish Staphylococcus aureus among other Staphylococcus species (which generate the enzyme coagulase), the coagulase test is used. Coagulase in plasma changes fibrinogen to fibrin in this test, which causes a clot or clump to develop. Staphylococcus was separated into coagulase positive and coagulase negative groups by this test (Foster, 1996).

Oxidase test: Oxidase test detects the presence of cytochrome oxidase enzyme in the bacteria, which catalysis the oxidation of reduced cytochrome by atmospheric oxygen. Due to this reaction the positive disc will turn into deep purple in color in shown figure 8 and oxidase negative test shown colorless in figure 9 (Hederstedt, 2022).

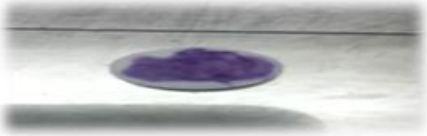

Figure 8: Oxidase positive result

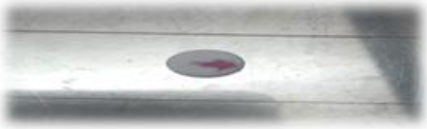

Figure 9: Oxidase negative result

Indole Test: Indole test detects the ability of some bacteria which produce enzyme tryptophan's that break down the Amino acid, tryptophan's present into indole medium (Ferrer et al., 2024). Indole test positive shown red color ring formed in figure 10 and negative result shown yellow color ring formed in figure 11.

Figure 10: Shows Indole Positive

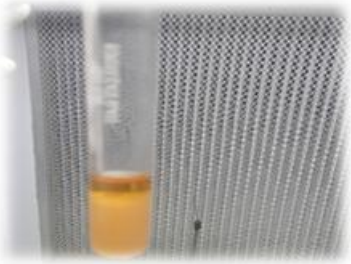

Figure 11: Shows Indole Negative

Methyl Red Test: In glucose phosphate broth, certain bacteria ferment the glucose to produce stronger acids (lactic, acetic or formic) that maintain the pH below 4.4, which turn the methyl (Konieczna et al., 2012) red indicator to yellow to red**.** MR positive shows red color in figure 12 and MR negative no color change in figure 13.

Figure 12: MR positive

Figure 13: MR negative

Urease Test: Urea producing bacteria can split the urea present in the medium to produce ammonia that makes the medium alkaline. The test was done on Christensen's urea medium, which contain phenol red indicator that change to pink in alkaline medium due to ammonia production (Konieczna et al., 2012). Urease positive shows pink color in figure 14 and urease negative shows no color change in figure 15.

Figure 14: Urease positive

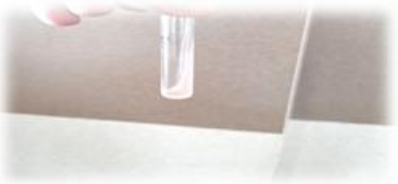

Figure 15: Urease Negative

Citrate test: Citrate test detects ability of a few bacteria that utilize citrate as the sole source of carbon for their growth, with production of alkaline metabolic products. Citrate lest is performed on a citrate containing medium, like Simmon's (solid) citrate medium. Citrate positive shows in blue color in figure 16 and citrate negative shows green color in figure 17.

Figure 16: Citrate positive

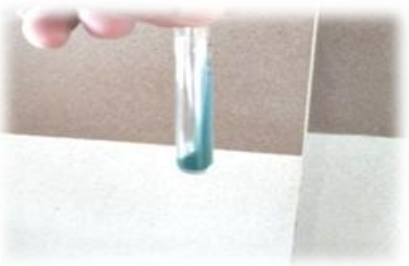

Figure 17: Urease positive

Triple Sugar Iron (TSI) Test: TSI is a very important medium employed widely for identification of gram-negative bacteria. It detects 3 properties of bacteria, such as: fermentation of sugars, produce acid and/or gas and Production of H_2S. The medium contains phenol red as a pH indicator. Fermentation of sugars lowers the pH and changes the medium color to yellow, while protein utilization (alkaline reaction) turns it red. Sodium thiosulfate and ferric ammonium citrate allow detection of H_2S (black precipitate formation) in shown table 1 and figure 18.

Table 1: Displaying interpretation of TSI

Slant	Butt	Gas	H_2S	Interpretation
Yellow	Yellow	±	±	Glucose, lactose, and/or sucrose fermentation
Red	Yellow	±	±	Glucose fermentation only
Red	Red	-	-	No fermentation; peptone catabolized aerobically and anaerobically
Black precipitate in butt	-	-	H_2S production (requires acidic butt)	
Cracks or bubbles	-	+	Gas production	

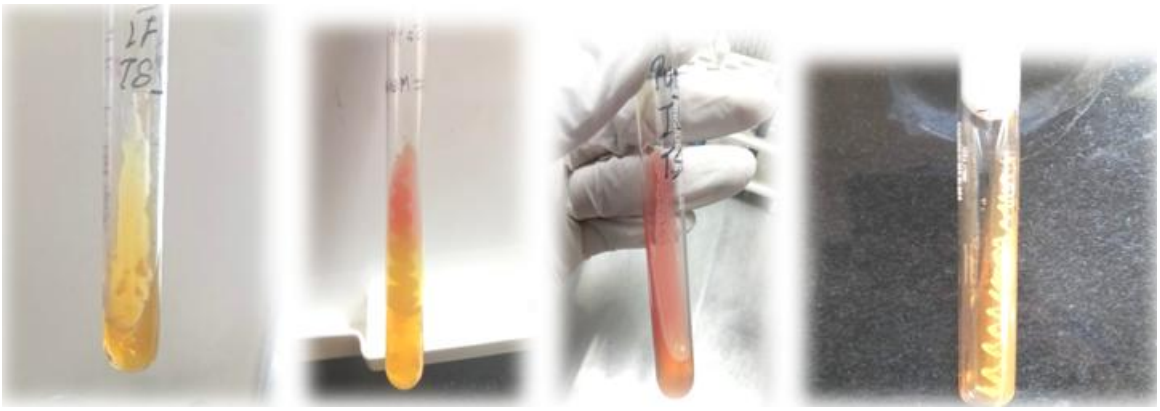

Figure 18: Interpretation of TSI Test

Antimicrobial susceptibility test-Antimicrobial susceptibility testing is performed on Muller Hinton agar (MHA) media by disc diffusion method (Kirby-Bauer method) according to CLSI guideline in shown figure 19 (Bayot & Bragg, 2025).

Figure 19: Antimicrobial susceptibility test

3.Observation and Result

Out of 92 samples collected from clinically suspected patients of respiratory tract infection, 39 samples showed bacterial growth and 03 samples showed growth of fungal species and the remaining 50 sample were culture-negative in shown table 2 and figure 20.

Table 2: Displaying the distribution of infection among total suspected Patients

Total	Disease		
92	Bacteria	fungus	No growth
	39 (35.88%)	3 (2.76%)	50 (46%)

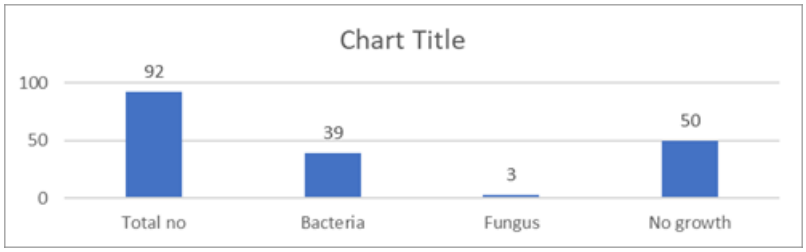

Figure 20: Columns displaying distribution of infection among total suspected Patients

Gender-wise distribution of Respiratory Tract Infection: Among the male patients include in this study, (64.10%) were found to have Respiratory Tract Infection. Among the female patients include in this study, (35.89%) were found to be affected with respiratory tract infection in shown table 3 and figure 21.

Table: 3 Shows Gender wise distribution of Respiratory Tract Infection

Gender	Frequency	Percentage
Male	25	64.10%
Female	14	35.89%
Total	39	100%

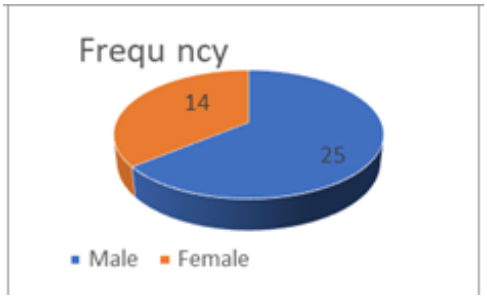

Figure 21: Displaying Pie chart Gender wise distribution of RTI

According to no. of isolates:

Table 4: Shows Gender wise distribution of Respiratory Tract Infection

Bacterial Species	No. of isolates	Percentage
Klebsiella	12	30.76
E. coli	7	17.94
Pseudomonas	5	12.82
Acinetobacter	5	12.82
Staph. Aureus	3	7.69
Proteus	2	5.12
Streptococcus	1	2.56
Enterobacter	1	2.56
Providencestuartii	1	2.56
CONS	1	2.56
Bacillus cereus	1	2.56
Total	39	97.39

A total of 39 bacterial isolates were identified. The most frequently isolated organism was Klebsiella spp., accounting for 12 isolates (30.76%), followed by Escherichia coli with 7 isolates (17.94%). Pseudomonas spp. and Acinetobacterbaumannii were each found in 5 isolates (12.82%). Other organisms included Staphylococcus aureus (3 isolates, 7.69%), Proteus spp. (2 isolates, 5.12%), and single isolates (2.56% each) of Streptococcus spp., Enterobacter spp., Providencestuartii, coagulase-negative Staphylococci (CONS), and Bacillus cereus in shown table 4.

Sample Wise Distribution:

Table5: Shows Sample wise distribution of RTI

Sample	Positive	Negative	Total no of Sample
Pleural Fluid	14	36	50
Sputum	22	12	34
Broncho alveolar Lavage	3	4	7
Tracheal aspirate	1	0	1
Total			92

A total of 92 respiratory samples were processed to assess bacterial growth. Out of 50 pleural fluid samples, 14 (28%) were culture-positive, while 36 (72%) were negative. Among 34 sputum samples, the majority 22 (64.7%) were positive, and 12 (35.3%) were negative. Of the 7 Broncho alveolar lavage (BAL) samples, 3 (42.9%) showed positive cultures, while 4 (57.1%) were negative. Only 1 tracheal aspirate sample was received, which tested 100% positive for bacterial growth. These results indicate that sputum samples had the highest number of positive cultures, whereas pleural fluid samples had the highest number of negative cultures in shown table 5.

Age Wise Distribution:

Table 6: Shows Age wise frequency of Respiratory Tract Infection

Age (Years)	Total	Disease		Total
		Positive	Negative	
01-10	92	1	5	6
11-20		8	11	19
21-30		5	13	18
31-40		8	4	12
41-50		2	7	9
51-60		6	1	7
61-70		7	10	17
71-80		3	1	4

A total of 92 samples were collected from patients with clinically suspected respiratory tract infections. The age-wise distribution of positive and negative cases is presented in Table 6. The highest number of positive cases was reported in the 11-20 years and 31-40 years age groups, with 8 positive cases each. This was followed by 7 positive cases in the 61-70 years group and 6 cases in the 51-60 years age group. The 21-30 years group had the highest number of negative cases (13), followed by 11 cases in the 11-20 years group and 10 cases in the 61-70 years group. Interestingly, the 1-10 years age group had only 1 positive case and 5 negative cases, indicating a relatively low prevalence of respiratory tract infections in young children. In contrast, elderly individuals (71-80 years) also showed 3 positive and 1 negative case, highlighting moderate susceptibility in older adults. Out of the total 92 cases, 40 (43.47%) were positive for respiratory tract infection, and 52 (56.53%) were negative. This distribution suggests that respiratory tract infections are more commonly observed in younger adults (11-20 years) and middle-aged individuals (31-40 and 61-70 years).

Antibiotic Resistance Patterns:

Table 7: Shows Antibiotic resistance patterns

Bacterial Isolate	Most Resistant Antibiotic (s) (Highest % Resistance)	Least Resistant Antibiotic (s) (Lowest % Resistance)
Klebsiella	Nitrofurantoin (100%), CIP/LE/CTR/CZ/TE (91.6%)	Tigecycline (58.3%), Piperacillin (66.6%)
E. coli	Teicoplanin (100%), CAZ/CIP/CTR (85.7%)	Tigecycline (14.2%), A/S/IPM/GEN/CPM (57.1%)
Pseudomonas	Teicoplanin (100%), Aztreonam/A/S (80%)	Amikacin & Gentamicin (20%), others ~40%
S. aureus	Clindamycin & Levofloxacin (100%), E/CIP/TE (66%)	Linezolid & Vancomycin (0%), GEN/DO (33.3%)
CONS	TEI/E/CD/LE/DO/CX (100%)	Linezolid, Amikacin, Tobramycin, Gentamicin (0%)
Bacillus cereus	TEI/CD/LE/CX (100%)	Linezolid, Amikacin, Ciprofloxacin, Gentamicin (0%)
Enterobacter	TE/A/S/DOR/AT/LE/MRP/IPM/CTR (100%)	Gentamicin, PIT, TOB, CPM, NX, CIP (0%)
Providence	Almost all tested (100%)	Norfloxacin, Ciprofloxacin, Levofloxacin (0%)
A. baumannii	NX, NIT, CTR (100%)	Amikacin & Gentamicin (40%), MRP (40%)

Klebsiella spp. exhibited the highest resistance to Nitrofurantoin (100%), Ciprofloxacin (91.6%), Levofloxacin (91.6%), and Ceftriaxone (91.6%). Carbapenem resistance was also significant (75%). E. coli showed 100% resistance to Teicoplanin and high resistance to Ceftriaxone (85.7%) and Ciprofloxacin (85.7%). Tigecycline, however, was effective (only 14.2% resistance). Pseudomonas spp. demonstrated universal resistance to Teicoplanin (100%) and high resistance to Aztreonam (80%) and Ampicillin/Sulbactam (80%). Aminoglycosides (Amikacin, Gentamicin) showed relatively low resistance (20%). S. aureus isolates were fully sensitive to Linezolid and Vancomycin, but showed 100% resistance to Clindamycin and Levofloxacin. CONS isolates displayed complete resistance to Teicoplanin, Erythromycin, Clindamycin, Levofloxacin, Doxycycline, and Cefuroxime (all 100%). Linezolid and Amikacin remained effective. Bacillus cereus isolates were resistant to Teicoplanin, Clindamycin, Levofloxacin, and Cefuroxime (100% each), but sensitive to Linezolid, Amikacin, Ciprofloxacin, and Gentamicin**.** Enterobacter spp**.** demonstrated resistance to multiple agents including Ampicillin/Sulbactam, Doripenem, Ciprofloxacin, Levofloxacin, Imipenem, and Meropenem (100%). Gentamicin, Piperacillin, and Tobramycin showed effectiveness (0% resistance). Providence spp. showed extreme resistance, with 100% resistance to almost all antibiotics tested (Piperacillin, Tigecycline, Ceftriaxone, Meropenem, Imipenem, Nitrofurantoin, etc.), with sensitivity retained only to Norfloxacin and Ciprofloxacin. Acinetobacterbaumannii showed complete resistance to Norfloxacin and Nitrofurantoin (100%), and high resistance to Piperacillin, Ciprofloxacin, Imipenem, and Cefepime (60%). Amikacin and Gentamicin retained partial sensitivity (40% resistance).

4.Discussion

Three samples (3.26%) and 39 samples (42.39%) of the 92 respiratory samples were taken from individual with clinically suspected RTIs in the current investigation revealed fungal growth and bacterial growth, respectively. These results are in line with earlier research that show that between 35% and 60% of RTI patients have culture positivity, suggesting that although bacterial causes account for a large share of respiratory infections, nonbacterial causes or non-cultivable pathogens may also play a role (D et al., 2021). The detected infection ratios were 64.10% for males and 35.89% for females. Studies by Gupta et al. (2021) and Sharma et al. (2019) also found that RTI prevalence was higher in men, which may be because men are more likely to be exposed to risk factors such smoking, occupational exposure, and outdoor activities (Chaudhary et al., 2019; Sharma et al., 2018). In this study male predominance is consistent with their findings. Klebsiella spp. (30.76%) was the most prevalent pathogen among the 39 bacterial isolates, followed by E. coli (17.94%), Pseudomonas spp. (12.82%), and Acinetobacterbaumannii (12.82%). According to (Worku et al., 2024) and (Neelambike Sumana et al., 2025), Klebsiella and Acinetobacter are the most common Gram-negative bacteria in lower respiratory tract infections (Vishwanath et al., 2013). The most positive clinical specimens were sputum samples (64.7%), BAL (42.9%), and pleural fluid (28%). This lends credence to the idea that sputum is still a very valuable specimen for the microbiological diagnosis of respiratory diseases, particularly in situations when invasive sampling or bronchoscopy may not be practical (Shen et al., 2025). The largest number of positive cases (8 each) occurred in the age groups of 11-20 and 31-40 years, followed by 61-70 years. These results are in line with those of (Ng et al., 2025), Who found that teens and middle-aged people had a high incidence of RTI, possibly as a result of increasing exposure in settings connected to employment or

education (Belachew et al., 2022). Notably, older patients (71-80 years old) also displayed vulnerability, underscoring the significance of immunological senescence in the elderly. One of the study's main conclusions is that respiratory infections are highly likely to be multidrug resistant (MDR). 100% resistance to nitrofurantoin and over 90% resistance to ceftriaxone, ampicillin/sulbactam, tetracycline, ciprofloxacin, and levofloxacin were shown by Klebsiella species. As reported by (Farheen et al., 2021), These results are concerning and indicative of the growing issue of ESBL and carbapenemase-producing strains in India. In addition, isolates of E. coli shown strong resistance (>85%) to fluoroquinolones and beta-lactams, as well as 100% resistance to Teicoplanin. With a resistance rate of just 14.28%, tigecycline continued to be the most effective antibiotic, which is in accordance with consistent with its demonstrated effectiveness against MDR Gram-negative disease (Govindaswamy et al., 2019). *Pseudomonas* spp. displayed complete resistance (100%) to Teicoplanin and high resistance (80%) to Aztreonam and Ampicillin/Sulbactam. However, aminoglycosides such as Gentamicin and Amikacin showed low resistance (20%), suggesting their retained effectiveness. These patterns are similar to findings reported by (Shbaita et al., 2023). *Staphylococcus aureus* isolates were 100% resistant to Clindamycin and Levofloxacin, but fully sensitive to Vancomycin, Linezolid, and Teicoplanin, which remains in line with standard treatment for MRSA and resistant Gram-positive cocci (Hamwi & Salem-Sokhn, 2025). Coagulase-Negative Staphylococci (CoNS) were highly resistant to commonly used drugs (100% resistance to Erythromycin, Clindamycin, Teicoplanin), but completely sensitive to Linezolid, Amikacin, and Gentamicin. This resistance pattern reinforces the necessity of culture-guided therapy (Ma et al., 2011).

Bacillus cereus, although less common, showed 100% resistance to four antibiotics but was sensitive to the majority (61.53%) tested, including Linezolid and Ciprofloxacin, in line with findings from (Fiedler et al., 2019).

5.Conclusion

The bacteriological profile and pattern of antibiotic resistance among patients with RTIs in a tertiary care hospital setting are highlighted in the present study. A considerable percentage (42.39%) of the 92 clinical samples tested positive for bacterial infections, indicating that bacterial etiology is the most common cause of RTIs, particularly in male patients and those aged 11-20 and 31-40. The most common pathogen was found to be Klebsiella species, which was followed by Acinetobacterbaumannii, Pseudomonas species, and E. coli. High levels of multidrug resistance (MDR) were seen in these Gram-negative bacteria, especially to widely used antibiotics fluoroquinolones, and occasionally even carbapenems. The importance of using antibiotics sensibly was highlighted by Klebsiella's notable 100% resistance to nitrofurantoin and over 90% resistance to a number of broad-spectrum drugs. Among Gram-positive bacteria, *Staphylococcus aureus* and Coagulase-Negative Staphylococci (CoNS) exhibited resistance to multiple antibiotics including macrolides and fluoroquinolones, but remained sensitive to glycopeptides and oxazolidinones such as Vancomycin and Linezolid. The study also demonstrated that sputum was the most reliable clinical specimen for diagnosis, while age and gender distribution offered insight into epidemiological trends of RTIs. Overall, the findings reflect an alarming rise in antibiotic resistance among respiratory pathogens, which calls for regular surveillance, judicious prescription practices, and implementation of hospital infection control policies. Empirical therapy must be continuously updated based on local antibiogram data, and culture-based treatment should be emphasized to ensure effective clinical outcomes and prevent further emergence of resistant strains.

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