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Bacteriological and mycological profile of non-tuberculous lower respiratory tract infections in patients attending a tertiary care centre in eastern Bihar: A prospective observational study.

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Abstract

Introduction

Acute lower respiratory tract infection (LRTI) is a common clinical illness encountered both in community and hospital settings. Worldwide, lower respiratory tract infections are the leading cause of death. Apart from tuberculosis, pneumonia, bronchitis, and bronchiolitis are the important LRTIs. This prospective hospital-based study was undertaken to identify the microbiological profile and antibiogram of LRTI patients attending our institution.

Aim

To determine the bacteriological and mycological profile of suspected cases of LRTI attending a tertiary care center in Eastern Bihar

Materials and methods

This study was carried out over a period of 3 years. A total of 2107 sputum samples were received in the Microbiology laboratory in Katihar Medical College, Katihar, from July 2022 to June 2025. After doing Bartlett scoring, 1665 samples were processed and included in the study. Identification and antibiotic susceptibility testing of isolates were done using automated methods (VITEK 2) for bacteria and yeasts. LPCB preparation was used for the identification of molds.

Results

Out of the 1665 sputum samples processed, 487 showed the growth of pathogenic organisms. 290 bacterial species, 148 yeasts, and 32 molds were isolated. 17 samples showed mixed growth. The male-to-female ratio was 1.4:1. The Maximum patients (43.15%) were aged 61–80 years, followed by 41–60 years (29.46%). The majority were inpatients from the Department of General Medicine (62.65%).

Conclusion

Gram-negative bacilli were identified as the leading cause of LRTI, followed by yeasts and molds. Many of the isolates were found to be multidrug resistant (MDR).

Recommendation

The increasing rate of isolation of yeasts and molds and the rising incidence of antibiotic resistance a matter of grave concern for one and all. Strict implementation of antimicrobial stewardship is the need of the hour.

Keywords: *Lower Respiratory Tract Infection, Bartlett scoring, multidrug resistant, antimicrobial stewardship.*
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Introduction

Acute lower respiratory tract infection (LRTI) is a common condition encountered both in community and hospital settings. LRTIs are the leading infectious disease cause of death and the fifth overall cause of death worldwide. It is estimated that 2.74 million deaths occur each year due to LRTIs worldwide.[1] Pneumonia, bronchitis, and bronchiolitis are among the most important LRTIs. Management of such infections often poses a challenge to clinicians because of the diagnostic difficulty in differentiating infections caused by typical and atypical microorganisms.

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Moreover, the global rise in antimicrobial resistance due to indiscriminate use of antibiotics is a mammoth problem the world is reeling under. Presumably, one of the major factors responsible for it is the irrational use of antibacterial therapy for empirical treatment. Empirical antibiotic treatment is the administration of antibacterials before the availability of culture results. It is a necessity and many times life-saving for critically ill patients in intensive care units. There is an absence of proper guidelines for the start of empirical treatment, as the majority of the hospitals and medical colleges in our country are still working without an antibiotic stewardship program in place. Highly resistant strains of pathogens, gram-negative bacilli in particular, continue to thrive in hospitals in many parts of the world, especially in developing countries. Several factors influence the incidence and mortality associated with LRTI, including characteristics of the population at risk, standard of healthcare facilities available, immunosuppressive drugs, inappropriate antibiotic therapy, distribution of causative agents, and prevalence of antimicrobial resistance. Acute respiratory tract infection continues to be the leading cause of morbidity and mortality in critically ill patients, particularly in developing countries.[2]

The most common bacterial agents of LRTIs are Gram-negative bacteria such as *Acinetobacter* spp., *Klebsiella pneumoniae*, *Pseudomonas* species, and *Haemophilus influenzae*, and Gram-positive bacteria such as *Staphylococcus aureus* and *Enterococcus* spp. [3] Fungal pathogens, especially yeasts, are being increasingly isolated from sputum samples.

Beta-lactams are one of the most commonly used antibiotics for the treatment of infections. Unfortunately, the ongoing spread of beta-lactamases, especially the extended-spectrum beta-lactamases and carbapenemases, among commonly isolated bacterial pathogens has begun to limit the clinical effectiveness of these agents.

Automated antimicrobial susceptibility testing devices, such as VITEK2 Advanced expert system (AES), can be used to generate AST reports. AES incorporates extensive information to recognize certain drug-resistant patterns as indicative of specific resistant phenotypes of bacteria. AES software of the VITEK 2 system analyzes the minimum inhibitory concentration (MIC) data against a database of phenotypes and infers the resistance phenotype while generating results.[4]

This prospective observational hospital-based study was undertaken to identify the bacterial and fungal causes of LRTI in patients attending our hospital, along with their antibiograms. Moreover, the utility of VITEK 2 AES in reporting various resistance patterns among Gram-positive and Gram-negative clinical isolates has also been analyzed. This can, in turn, alert the physicians and enable them to formulate rational empirical treatment regimens in order to curb the menace of rising antimicrobial resistance.

Materials and methods

Study design

This research focuses on documenting the bacteriological and mycological features and antibiotic resistance tendencies of non-tuberculous lower respiratory tract infections (LRTIs).

Study setting

The study was carried out over three years at Katihar Medical College, Katihar, Bihar, India, in the Department of Microbiology from July 2022 to June 2025.

Study population

The study population consisted of suspected non-tuberculous lower respiratory tract infections for whom microbiology laboratory culture and sensitivity testing was performed.

Participants (inclusion and exclusion criteria)

Inclusion criteria: Sputum samples were taken from patients clinically suspected to have non-tuberculous LRTIs and showing acceptable quality as per Bartlett scoring (score ≥1). Exclusion criteria: Samples showing poor quality (Bartlett score <1), samples contaminated with saliva, and those positive for *Mycobacterium tuberculosis.*

Method of data collection and tools

In the years of the study, 2107 sputum samples were received, and microbiological quality control was performed; Bartlett's grading system was also implemented. For the 1665 samples deemed suitable, standard microbiological sample processing was performed. The VITEK 2 automated system was used for bacterial and yeast identification as well as antibiotic susceptibility testing. The VITEK 2 Advanced Expert System (AES) was used to detect 'resistance' phenotypes. Mold identification was performed using the Lactophenol cotton blue (LPCB) technique.

Statistical analysis

Data were entered into Microsoft Excel and analyzed using descriptive statistics. Results were expressed in frequencies and percentages.

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Ethical consideration

Ethical approval for this prospective study was obtained from the Institutional Ethics Committee of Katihar Medical College, Katihar, Bihar, India. Informed consent was obtained from all participants before sample collection. All procedures followed institutional and international ethical guidelines to ensure patient confidentiality and data protection.

Results

The study included 1665 sputum samples that met Bartlett's quality criteria. The male-to-female ratio in the study population was 1.4:1. The Maximum number of patients (43.15%) were within the age group 61–80 years, followed by 41–60 years (29.46%). The least number of patients were from the age group >80 years (3.32%), followed by 0–20 years (5.39%). Patients from the inpatient department accounted for a major fraction of the samples as compared to the outpatient department. The maximum number of patients was from the department of General Medicine (62.65%), followed by Emergency Medicine (14.46%) and Neurosurgery (9.64%).

Out of the 1665 samples that were processed, 487 (29.25%) showed the growth of pathogenic organisms.

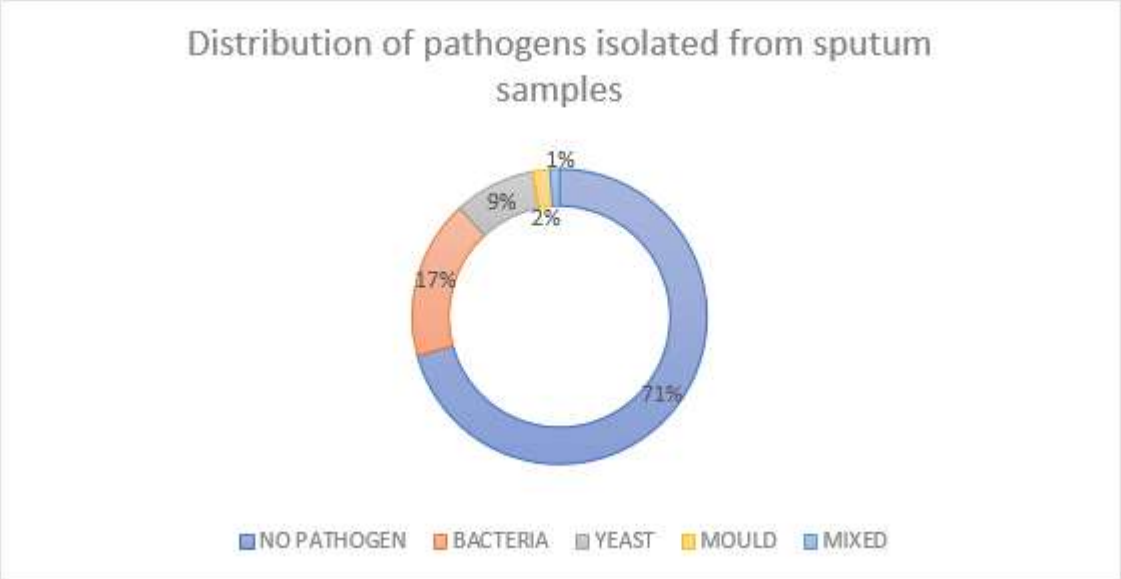

Fig.1: distribution of pathogens isolated from sputum samples

No pathogenic organism was isolated from 1178 (70.75%) samples. Out of the 487 samples that yielded pathogenic organisms, 290 (17.42%) were bacterial isolates, 148 (8.89%) were yeasts, 32 (1.92%) were molds, while 17 (1.02%) samples showed a mixed or polymicrobial growth.

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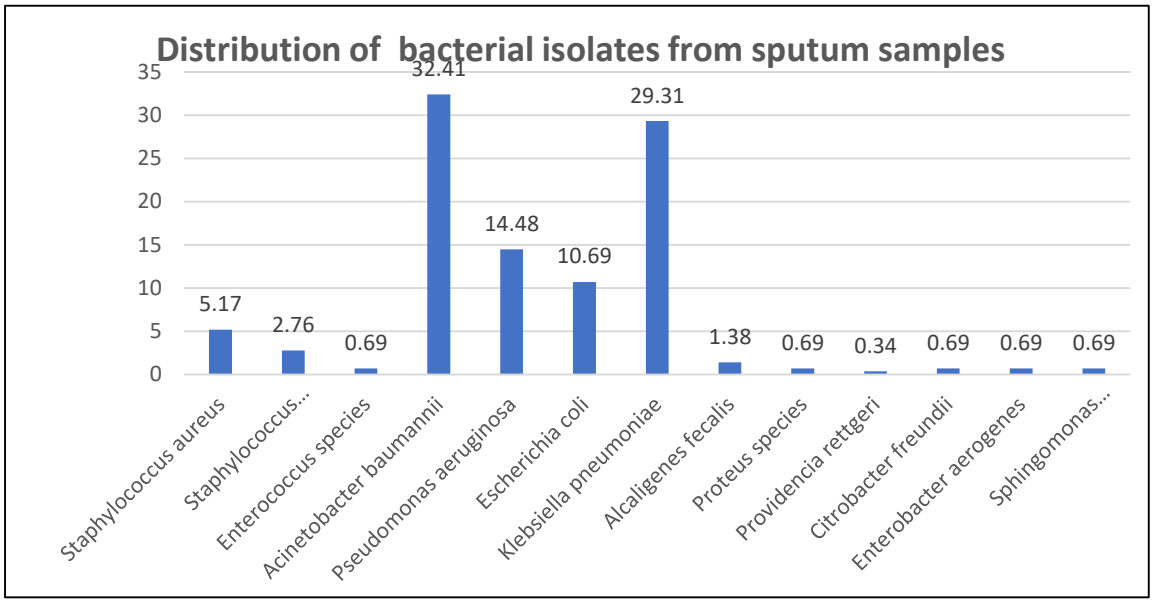

Fig. 2: distribution of bacteria isolated from sputum samples

There was a preponderance of Gram-negative isolates. *Acinetobacter baumannii* (32.41%) was the commonest isolate, followed by *Klebsiella pneumoniae* (29.31%), *Pseudomonas aeruginosa* (14.48%), and *Escherichia coli* (10.69%). Among the Gram-positive isolates, *Staphylococcus aureus* (5.17%) was the commonest, followed by *Staphylococcus haemolytic* (2.76%)

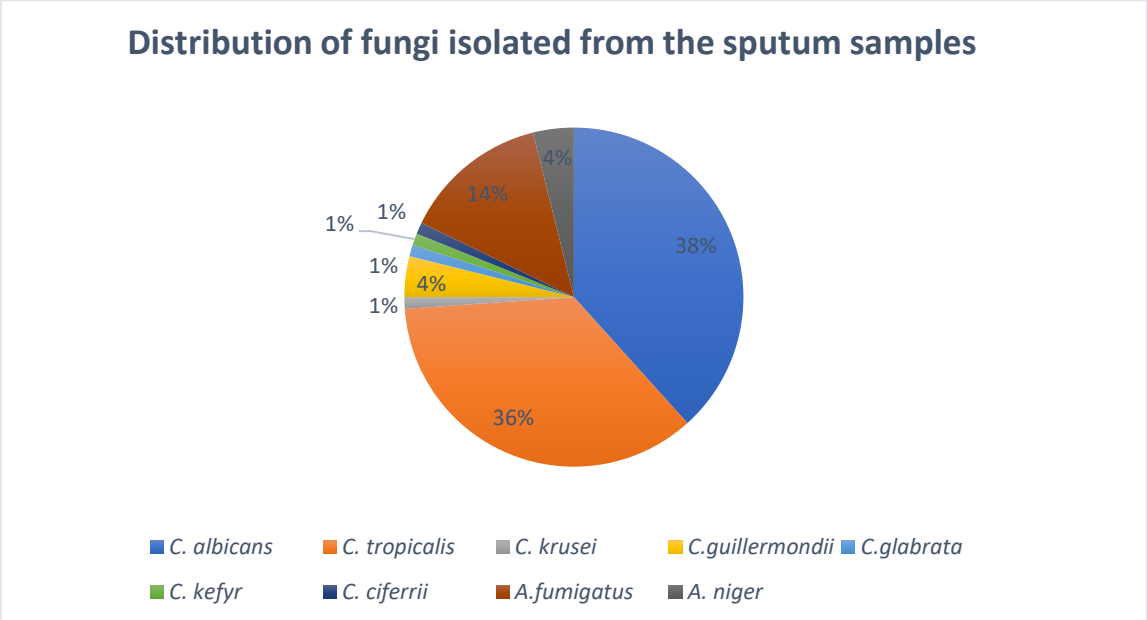

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Fig. 3: distribution of fungal isolates in sputum samples

Among the fungal isolates, *Candida albicans* (38.33%) was the most common organism, followed by *Candida tropicalis* (35.56%) and *C. guillermondii* (3.89%). Among the molds, *Aspergillus fumigatus* (13.89%) was the most common, followed by *Aspergillus niger* (3.89%)

Antibiotics	*S. aureus* (n=15)	*S. hemolyticus* (n=8)	*Enterococcus species* (n=2)
	No. of strains susceptible (%)	No. of strains susceptible (%)	No. of strains susceptible (%)
Benzylpenicillin	0/15 (0)	0/8 (0)	
Trimethoprim/ Sulfamethoxazole	5/15 (33.33)	4/8 (50)	-
Oxacillin	8/15 (53.33)	3/8 (37.5)	-
Gentamicin	7/15 (46.67)	0/8 (0)	-
Ciprofloxacin	0/15 (0)	0/8 (0)	0/2 (0)
Levofloxacin	0/15 (0)	0/8 (0)	0/2 (0)
Erythromycin	4/15 (26.67)	0/8 (0)	0/2 (0)
Clindamycin	8/15 (53.33)	1/8 (12.5)	-
Linezolid	15/15 (100)	8/8 (100)	2/2 (100)
Daptomycin	15/15 (100)	8/8 (100)	1/2 (50%)
Teicoplanin	15/15 (100)	8/8 (100)	2/2 (100)
Vancomycin	15/15 (100)	8/8 (100)	0/2 (0)
Tetracycline	2/15 (13.33)	8/8 (100)	0/2 (0)
Tigecycline	15/15 (100)	8/8 (100)	2/2 (100)
Rifampicin	15/15 (100)	3/8 (37.50)	-
High-level gentamicin	-	-	1/2 (50%)

Table 1: Antibiotic susceptibility pattern of Gram-positive isolates

Among the *S. aureus* isolates, maximum susceptibility was seen to Linezolid, Daptomycin, Teicoplanin, Vancomycin, Tigecycline, and Rifampicin (100%). Least susceptibility (0%) was seen to Benzylpenicillin and fluoroquinolones. 7/15 (46.67%) strains were oxacillin resistant (MRSA).

Among the *S. hemolyticus isolates*, maximum susceptibility (100%) was seen to Linezolid, Daptomycin, Teicoplanin, Vancomycin, Tigecycline, and Rifampicin. Least susceptibility (0%) was seen to the aminoglycosides and fluoroquinolones. 5/8 (62.5%) isolates were resistant to oxacillin (MRSH).

7/15 (46.67%) strains were resistant to both erythromycin and clindamycin, all showing inducible clindamycin resistance (MLSB i phenotype), 4/15 (26.67%) were sensitive to both erythromycin and clindamycin, and 4/15 (26.67%) were erythromycin resistant but clindamycin sensitive.

7/8 (87.5%) of the *S. hemolyticus* isolates were resistant to both erythromycin and clindamycin, showing constitutive MLS_B resistance (MLS_B c phenotype). One strain of *S. hemolyticus* was resistant to erythromycin but sensitive to clindamycin (inducible clindamycin resistance negative).

Table 2: antibiotic susceptibility pattern of Lf gram-negative bacilli

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Antibiotics	*Klebsiella pneumoniae* n = 85	*Escherichia coli* n =31
	No of strains susceptible (%)	No of strains susceptible (%)
Amoxicillin/ clavulanic acid	24/85 (28.24)	3/31(9.68)
Piperacillin /Tazobactam	36/85 (42.35)	5/31(16.13)
Cefuroxime	8/85 (9.41)	3/31(9.68)
Ceftriaxone	14/85 (16.47)	3/31 (9.68)
Cefoperazone/ Sulbactam	36/85 (42.35)	10/31 (32.26)
Cefepime	14/85 (16.47)	5/31 (16.13)
Ertapenem	40/85 (47.06)	13/31 (41.94)
Imipenem	36/85 (42.35)	13/31 (41.94)
Meropenem	40/85 (47.06)	13/31 (41.94)
Amikacin	40/85 (47.06)	15/31 (48.39)
Gentamicin	28/85 (32.94)	14/31 (45.16)
Ciprofloxacin	18/85 (21.18)	5/31 (16.13)
Tigecycline	60/85 (70.59)	28/31 (90.32)
Fosfomycin	28/85 (32.94)	20/31 (64.52)
Colistin	82/85 (96.47)	29/31(93.59)
Trimethoprim/ Sulfamethoxazole	36/85 (42.35)	12/31 (38.71)
Minocycline	8/85 (9.41)	25/31 (80.64)

Klebsiella pneumoniae showed maximum susceptibility to colistin (96.47%), followed by tigecycline (70.59%), ertapenem/meropenem (47.06%), and piperacillin tazobactam/ cefoperazone sulbactam (42.35%). Least susceptibility was seen to cefuroxime (9.41%), followed by ceftriaxone and cefepime (16.47%).

Escherichia coli showed maximum susceptibility to colistin (93.59%), followed by tigecycline (90.32%) and fosfomycin (64.52%). Least susceptibility was seen to cefuroxime/ ceftriaxone (9.68%), followed by cefepime (16.13%).

Antibiotic	*A. baumannii* (n = 94) No. susceptible (%)	*P. aeruginosa* (n = 42) No. susceptible (%)
Piperacillin + Tazobactam	8 (8.51)	20 (47.61)
Cefuroxime	0 (0)	–
Ceftriaxone	5 (5.32)	–
Cefoperazone + Sulbactam	36 (38.30)	28 (66.67)
Cefepime	6 (6.38)	30 (71.43)
Ceftazidime	0 (0)	16 (38.10)
Imipenem	6 (6.38)	26 (61.90)
Meropenem	6 (6.38)	26 (61.90)
Amikacin	9 (9.57)	30 (71.43)
Gentamicin	9 (9.57)	30 (71.43)
Ciprofloxacin	7 (7.45)	28 (66.67)
Colistin	92 (97.87)	40 (95.24)
Trimethoprim + Sulfamethoxazole	20 (21.28)	–
Minocycline	9 (9.57)	–

Table 3: antibiotic susceptibility pattern of non-fermenting gram-negative bacilli (*Acinetobacter baumannii* and *Pseudomonas aeruginosa*) isolated from sputum samples

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In *Acinetobacter baumannii*, maximum susceptibility was seen to colistin (97.87%), followed by cefoperazone-sulbactam (38.30%) and trimethoprim-sulfamethoxazole (21.28%). Least susceptibility was seen to ceftazidime/cefuroxime (0%), followed by ceftriaxone (5.32%).

In *Pseudomonas aeruginosa,* maximum susceptibility was seen to colistin (95.24%), followed by amikacin/gentamicin (71.43%), cefoperazone-sulbactam, and ciprofloxacin (66.67%). Least susceptibility was seen to ceftazidime (38.10%), followed by piperacillin-tazobactam (47.61%).

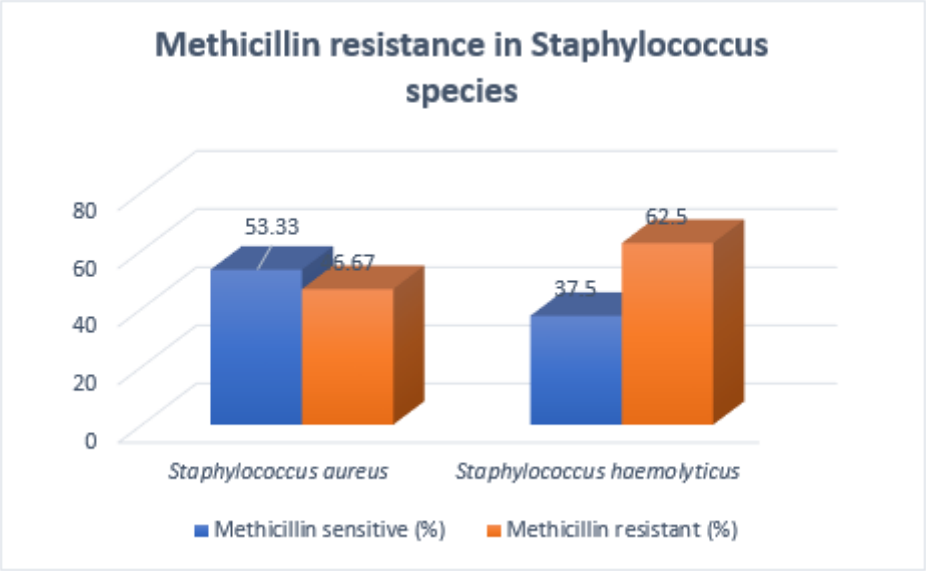

Fig. 4: Methicillin resistance in Staphylococcal isolates

46.67% of *Staphylococcus aureus* and 62.5% of the *Staphylococcus hemolyticus* isolates were found to be methicillin-resistant. Resistance to oxacillin was mediated by modification of the penicillin-binding protein (PBP) by the acquired mecA gene.

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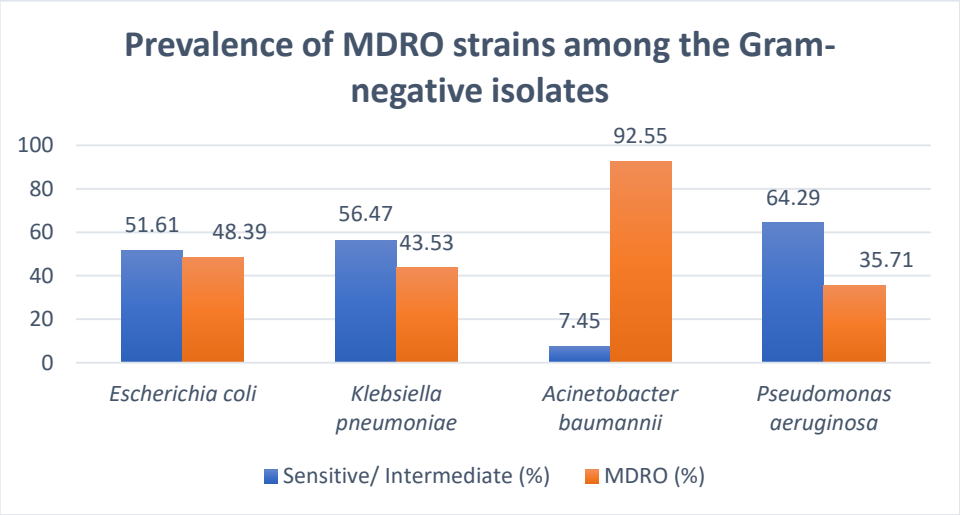

Fig. 5: prevalence of MDRO strains among gram-negative isolates.

92.55% (87/94) of *Acinetobacter baumannii*, 48.39% (15/31) of *Escherichia coli*, 43.53% (37/85) of *Klebsiella pneumoniae,* and 35.71% (15/42) of *Pseudomonas aeruginosa* were found to be multidrug resistant.

Phenotypic mechanism of resistance	***Klebsiella pneumoniae* No. (%)**	***Escherichia coli* No. (%)**	***Acinetobacter baumannii* No. (%)**	***Pseudomonas aeruginosa* No. (%)**
ESBL producer				1 (6.67)
Carbapenemase production			84 (96.55)	
ESBL+ carbapenemase		3 (20)		
ESBL+ Impermeability to carbapenems				2 (13.33)
ESBL+ carbapenemase+ Impermeability to carbapenems				12 (80)
ESBL+ cephalosporinase+ carbapenemase			3 (3.45)	
Impermeability to carbapenems+ ESBL+ AmpC+ carbapenemase	33 (89.19)	12 (80)		
ESBL+ impermeability to cephamycins	4 (10.81)			
Total MDRO	37 (100)	15 (100)	87 (100)	15 (100)

Table 4: drug-resistant phenotypes among MDR Gram-negative isolates using Vitek2 AES

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Among the lactose-fermenting Gram-negative bacilli, 43.53% (37/85) of *K. pneumoniae* and 15/31 (48.39%) *E. coli* isolates were multidrug resistant. All the MDR isolates showed a high level of resistance to β-lactam antibiotics. 89.19% (33/37) of *K. pneumoniae* and 80% (12/15) of *E. coli* isolates possessed four resistance mechanisms, viz. impermeability to carbapenems, ESBL production, AmpC production, and carbapenemase production.

10.81% (4/37) of *K. pneumoniae* showed a combination of two resistance mechanisms, viz. ESBL production and impermeability to cephamycins, while 20% (3/15) of *E. coli* showed a combination of ESBL+ carbapenemase production.

Among the non-fermenting Gram-negative bacilli, 92.55% (87/94) of *A. baumannii* and 35.71% (15/42) of *P. aeruginosa* isolates were multidrug resistant. 96.55% (84/87) of the *A. baumannii* isolates were carbapenemase producers, while 3.45% (3/87) showed a combination of resistance mechanisms, viz. ESBL, cephalosporinase, and carbapenemase production. 80.00% (12/15) of *P. aeruginosa* isolates possessed three resistance mechanisms, viz. ESBL production, carbapenemase production, and impermeability to carbapenems, 13.33% (2/15) of isolates showed a combination of ESBL production and impermeability to carbapenems, and one strain of P. aeruginosa (6.67%) was a lone ESBL producer.

Discussion

This study was undertaken to determine the bacteriological and mycological profile of non-tuberculous LRTI in patients attending a tertiary care center in Eastern Bihar. In the study, 29.25% culture positivity was observed. Singh J et al reported a positivity of 39.7% whereas Santella B et al reported a sputum positivity of 24.96%.[5,3] In a study from Nepal, Khan S et al have reported a culture positivity of 49.3%.[6] These variations in culture positivity may be because of a difference in sample size, geographical area, and use of antibiotics at different levels of patient care before the patients reach a teaching hospital, where such studies are conducted.

The male-to-female ratio in our study population was 1.4:1. LRTIs were more common in male patients than in female patients. Many Indian authors, Singh J et al, Singh S et al, Gupta E et al, and Dhivya G et al have reported similar findings.[5,7,8,9] Santella B et al, who conducted a similar study in Salerno, Italy, have also reported a male preponderance.[3] This higher prevalence of LRTI in males may be related to the presence of risk factors like smoking, alcoholism, more outdoor exposure, and a higher incidence of COPD.

The maximum number of patients were from the age group 61-80 years (43.15%), followed by 41-60 years (29.46%). The least number of patients were from the age group >80 years (3.32%), followed by 0-20 years (5.39%). Gupta E et al have also reported the highest percentage of patients in the age group 60-79 years.[8] Singh S et al in their study have stated that 35% of patients were above 61 years and 30% were in the 41-60 years age group.[7] These findings are very similar to those in our study. Weakening of the immune system with advancing age appears to be the most likely explanation for this preponderance of infection in old age.

In the present study, patients from the inpatient department accounted for a major fraction of the samples as compared to the outpatient department. The maximum number of patients was from the department of General Medicine (62.65%), followed by Emergency Medicine (14.46%) and Neurosurgery (9.64%). In a study by Singh J et al, 48.9% patients were from ICUs, 38.8% from wards, and 31.1% from OPDs.[5] Dhivya G et al reported that 88.8% of sputum-positive patients were from IPD.[9] Out of the 1665 samples that were processed, 1178 (71%) did not grow any pathogenic organism. Among the 29% that showed the growth of pathogens, around 17% were bacteria, 9% were yeasts, 2% were molds, and 1% samples gave a mixed or polymicrobial growth.

Overall, there was a preponderance of Gram-negative isolates in our study. *Acinetobacter baumannii* (32.41%) was the most common GNB, closely followed by *Klebsiella pneumoniae* (29.31%), *Pseudomonas aeruginosa* (14.48%), and *E. coli* (10.69%). Gram-positive cocci accounted for a small fraction of LRTI cases. *Staphylococcus aureus* (5.17%) was the most common Gram-positive cocci, followed by *S. hemolyticus* (2.76%). Other infrequently isolated bacterial pathogens were *Alcaligenes fecalis, Proteus species, Enterobacter species, Sphingomonas paucimobilis, Citrobacter species, Enterococcus species, and Providencia rettgeri.*

In a study from Baroda, Gujarat, by Singh J et al, *Klebsiella* spp. (39.5%) was the most common isolate, followed by *E. coli (*23.97%), *Pseudomonas* spp. (16.9%), *Acinetobacter* spp. (14.61%), *S. aureus* (3.04%) and *Enterococcus* spp. (1.87%).[5] In a study by Debnath S et al, Klebsiella spp. (52.16%) was the most common organism, followed by Acinetobacter spp. (13.49%) and Pseudomonas spp. (13.23%).[10]

Among the fungal isolates, non albicans *Candida* species (43.89%) were most commonly isolated, followed by *Candida albicans* (38.33%) and *Aspergillus* species (17.78%). *Candida albicans* (38.33%) was the most common species, followed by *Candida tropicalis* (35.56%) and *C. guillermondii* (3.89%). Among the

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molds, *Aspergillus fumigatus* (13.89%) was the most common, followed by *Aspergillus niger* (3.89%).

Dhivya G et al, in their study conducted in Puducherry, reported *Candida albicans* (66.67%) as the most common species, followed by non-albicans *Candida* species (28.57%) and *Aspergillus niger* (4.76%).[9] This difference in distribution of isolates may be due to different geographical areas and different sample sizes.

46.67% of *Staphylococcus aureus* and 62.5% of the *Staphylococcus hemolyticus* isolates were found to be methicillin resistant (MRSA and MRSH, respectively). 92.55% of *Acinetobacter baumannii*, 48.39% of *Escherichia coli*, 43.53% of *Klebsiella pneumoniae*, and 35.71% of *Pseudomonas aeruginosa* were found to be multidrug resistant. Majhi S et al reported 61.7%, Singh S et al reported 56.9% while Singh J et al reported 33% MRSA in their respective studies. [11,7,5]

Teeraputon S et al in their study from Thailand reported 47.59% of the *Staphylococci hemolyticus* were methicillin resistant (MRSH).[12]

Drug-resistant phenotypes among MDR Gram-negative isolates were analyzed using the VITEK 2 Advanced expert system. All the MDR isolates showed a high level of resistance to β-lactam antibiotics. 89.19% (33/37) of *K. pneumoniae* and 80% (12/15) of *E. coli* isolates possessed four resistance mechanisms, viz. impermeability to carbapenems, ESBL production, AmpC production, and carbapenemase production.

10.81% (4/37) of *K. pneumoniae* showed a combination of two resistance mechanisms, viz. ESBL production and impermeability to cephamycins, while 20% (3/15) of *E. coli* showed a combination of ESBL+ carbapenemase production.

96.55% (84/87) of the *A. baumannii* isolates were carbapenemase producers, while 3.45% (3/87) showed a combination of resistance mechanisms, viz. ESBL, cephalosporinase, and carbapenemase production. 80.00% (12/15) of *P. aeruginosa* isolates possessed three resistance mechanisms, viz. ESBL production, carbapenemase production, and impermeability to carbapenems, 13.33% (2/15) of isolates showed a combination of ESBL production and impermeability to carbapenems, and one strain of P. aeruginosa (6.67%) was a lone ESBL producer.

Dinakaran S et al in their study analyzed 50 MDR Gram-negative isolates, viz. 58% (29/50) *Acinetobacter baumannii*, 20% (10/50) *Klebsiella pneumoniae,* 12% (6/58) *Pseudomonas aeruginosa, and* 10% (5/58) *Escherichia coli*. [13]

Advanced expert system analysis (AES) grouped the resistance mechanisms into Carbapenemase (n=29, 58%), Carbapenemase with AmpC (n=5, 10%), Carbapenemase with ESBL (n=6, 12%), Carbapenemase± ESBL (n=7, 14%), and ESBL (n=3,6%)

Generalizability

The findings of this study are generalizable to similar tertiary care hospitals in India, particularly in resource-limited settings in Eastern India. The pattern of multidrug resistance and organism prevalence may reflect trends in comparable regions.

Conclusion

Yeasts and moulds are being increasingly isolated from clinical samples. *Acinetobacter baumannii* and *Klebsiella pneumoniae* were the most common bacterial isolates, and *Candida albicans* was the most common fungal isolate recovered from LRTI patients in our study. About one-half of the Staphylococcus species isolated were methicillin-resistant. A high level of resistance to β-lactam antibiotics was seen among the Gram-negative isolates. Some colistin-resistant strains were also isolated. Development of resistance to reserve drugs like colistin is an alarming sign, and curbs must be put in place to limit their indiscriminate use.

More than half of the Gram-negative isolates were found to be multidrug resistant. Moreover, many of them demonstrated the presence of multiple resistance mechanisms. The coexistence of several resistance mechanisms in a bacterium can significantly increase its resistance profile, making it challenging to treat infections caused by it. The development and introduction of new antibiotics has, unfortunately, not kept pace with the development of bacterial resistance. With each passing day, the availability of antimicrobials in a clinician's armamentarium for successfully treating infections caused by MDR organisms is constantly depleting.

Limitations

The study was limited by its **single-center design** and reliance on **phenotypic identification** of resistance mechanisms. Molecular confirmation of resistance genes was not performed. Additionally, since only sputum samples were analyzed, deeper infections such as bronchial washings or BAL samples were not included.

Recommendations

This rising antibiotic resistance is a matter of grave concern for one and all. Antibiotic stewardship is the need of the hour in all large healthcare setups. Such studies will help in the formulation of proper antibiotic stewardship programmes to curb the menace of antimicrobial resistance, which is gradually becoming a threat to human existence.

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Data availability
Data supporting the findings of this study are available from the corresponding author upon reasonable request.

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List of acronyms
LRTI: Lower Respiratory Tract Infection
MDR: Multidrug Resistant
AES: Advanced Expert System
AST: Antimicrobial Susceptibility Testing
IPD: Inpatient Department
OPD: Outpatient Department
LPCB: Lactophenol Cotton Blue
ESBL: Extended-Spectrum Beta-Lactamase

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The authors declare no conflict of interest.

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All authors contributed equally.

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