BMC Infectious Diseases

RESEARCH

Open Access

Bacterial profile, antimicrobial susceptibility patterns, and associated factors among lower respiratory tract infection patients attending at Debre Markos comprehensive specialized hospital, Northwest, Ethiopia

Osman Yimer[1], Abtie Abebaw[1], Adane Adugna[1*], Fentahun Adane[2] and Ahmed Esmael[1]

Abstract

Background Lower respiratory tract infections are the most common health problem, demanding frequent consultation and hospitalization. Moreover, there has been a dramatic rise in antibiotic resistance among respiratory pathogens.

Objective This study aimed to assess the bacterial profile, antimicrobial susceptibility patterns, and associated factors of lower respiratory tract infection among patients attending at Debre Markos Comprehensive Specialized Hospital, Northwest Ethiopia, in 2023.

Method A hospital-based cross-sectional study was conducted on a total of 305 study participants from May 1 to July 30, 2023. Purulent sputum samples were collected and streaked onto chocolate agar, blood agar, and MacConkey agar. Chocolate agar and blood agar plates were incubated at 35–37 °C for 24 h with 5% carbon dioxide in a candle jar. MacConkey agar was incubated aerobically at 35–37 °C for 24 h. Antimicrobial susceptibility patterns were determined via the disk diffusion method (Kirby–Bauer) on Mueller-Hinton agar. A logistic regression model was used to show the relationship between the outcome and independent variables.

Result Of a total of 305 samples, 33.4% (95% CI: 29.2–38.8%) samples showed growth of various species of bacteria. The predominant pathogens were *Klebsiella pneumoniae* 31/102 (30.4%), *Streptococcus pneumoniae* 21/102 (20.6%), and *Pseudomonas aeruginosa* 16/102 (15.7%). The overall magnitude of multidrug resistance (MDR) was 47.1%. Having > 58 age groups (AOR = 7.180, 95% CI: 1.858–27.743), being illiterate (AOR = 2.76, 95 CI: 1.158–6.578), chronic cough (AOR = 5.26, 95% CI: 1.725–16.038), and alcohol drinking (AOR = 6.542, 95% CI: 2.570-16.654), were determinants of lower respiratory tract infection.

*Correspondence:
Adane Adugna
adaneadugna29@gmail.com

Full list of author information is available at the end of the article

Conclusion *K. pneumoniae* and *S. pneumoniae* were the most predominant pathogens. A high levels antibiotic resistance was present in the majority of the isolates. Therefore, antibiotic susceptibility testing should be applied to guide treatment decisions.

Keywords Bacterial profile, Antimicrobial susceptibility test, LRTIs

Introduction

Lower respiratory tract infections (LRIs) are the leading cause of severe morbidity and mortality around the globe, especially in developing countries [1]. There are 488.9 million cases and 2.4 million deaths worldwide as a result of LRIs [2]. Half of the fatalities take place in sub-Saharan Africa [3]. The prevalence of LRIs in Ethiopia is ranges from 32.1 to 33.5% [4, 5]. *Mycobacterium tuberculosis* (MTB) and *Streptococcus pneumoniae* are important causes of LRTIs and cause tuberculosis (TB) and pneumonia, respectively. Pneumoniae is caused by inhalation of bacterial pathogens that pass through the nose, throat, and lungs [6, 7]. Furthermore, blood and touch can transmit pneumonia, particularly during and after childbirth [8]. Sharing air space with someone who has active tuberculosis and breathing in their droplet aerosols are the main ways that M. tuberculosis infection is transmitted. In poor nations, the great majority of people are afflicted [9].

The common pathogens causing LRTIs other than *M. tuberculosis* and *Streptococcus pneumoniae* are *Klebsiella* species, *Pseudomonas* species, *Staphylococcus* species, *Acinetobacter* species, *H. influenza. K. pneumoniae*, *M.pneumoniae*, *B.pertussis*, and *M.catarrhalis* cause significant community-acquired as well as hospital-acquired LRTIs, including bronchitis, and lung abscess in elderly individuals [10, 11].

The following factors may increase a person's susceptibility to lower respiratory tract infections (LRTIs): advancing age, smoking, alcoholism, pulmonary disease, heart disease, neurological disorders, cystic fibrosis, major surgical interventions (such as transplantation), cancer, the geriatric population, and the use of immunosuppressive medications [1, 12].

Antibacterial drugs are not widely available, but when they are, people tend to overuse them, which has led to the selection and spread of resistant bacteria. Antibacterial drugs have been extensively utilized over the course of several decades. Antibiotics have therefore become less or perhaps useless, leading to a worldwide medical catastrophe that is expanding faster than accessible treatment options [13].

Therefore, this study aimed to assess the bacterial profile, antimicrobial susceptibility patterns, and associated factors among lower respiratory tract infection patients attending at Debre Markos Comprehensive Specialized Hospital, Northwest, Ethiopia.

Materials and methods

Study design, period, and setting

A hospital-based cross-sectional study was conducted among patients with lower respiratory tract infections at Debre Markos Comprehensive Specialized Hospital (DMCSH), Northwest Ethiopia, from May 2023 to July 2023. DMCSH is located in Debre Markos Town, and it provides specialized health services via its clinical, medical, and diagnostic departments for approximately 255,248 per year from a catchment area with a population of about 5 million people [14].

Inclusion and exclusion criteria

All patients who were suspected of lower respiratory tract infections at DMCSH during the study period were considered as the study population. All patients who fulfilled the eligibility criteria, were clinically diagnosed with lower respiratory tract infections, and showed typical clinical signs and symptoms of the disease like chronic cough > 2-week duration, unexpected weight loss, night sweat, purulent sputum, loss of appetite, streaked blood sputum, and the habit of alcohol drinking were included in the study. All patients who took antibiotics in the last 14 days and could not produce sputum were excluded from the study.

Sample size determination and sampling techniques

The sample size was calculated using a single population proportion formula by considering a 95% confidence interval (Zα/2 = 1.96), a 5% margin of error, and a prevalence of lower respiratory tract infection (32.1%) from Addis Ababa, Ethiopia [4].

$$n = \frac{(z\alpha/2)^2 \times P\,(1-P)}{d^2}$$

Where, n = the sample size, $Z_{a/2}$ = the z-value at 95% confidence interval = 1.96.

P = prevalence = 32.1%, d = margin of error = 5%. The total sample size = 334. A convenience consecutive sampling technique was employed to select 334 participants. However, 29 samples have been excluded form statistical analysis as they did not fulfill the acceptance criteria and with Bartlett's scoring of ≤ 0. Hence, the final sample size for this study was 305.

Socio-demographic and clinical data collection

After signed consent/assent agreement from study participants, socio-demographic, clinical, and other associated factors data were collected by trained nurses by using a pretested structured questionnaire from eligible patients.

Sputum specimen collection and transportation

Two up to ten milliliters (2–10 mL) of sputum samples were collected in wide-mouthed sterile containers by standard collection procedures and labeled with patients' medical registration number (MRN) and ID and transported to the Microbiology Laboratory of DMCSH within 2 h of collection for laboratory analysis via amies transport medium. Sputum samples were stable for up to 48 h at refrigeration temperatures (2–8 °C) before processing. If specimens could not be processed within 48 h, they were frozen at or below – 70 °C to maintain viability.

According to the routine procedure, sputum specimens were first examined macroscopically and microscopically (using gram staining) at the DMCSH microbiology laboratory before being subjected to further culture analysis. A thin smear was made on a clean microscope slide by using the collected sputum sample and then allowed to air-dry. The slide was briefly heat-fixed by passing through flame. Crystal violet stain was applied for 1 min, followed by rinsing with distilled water. Iodine solution was added for 1 min for better retention, followed by a rinse. The slide was then decolorized in acetone for 10–30 s and immediately rinsed. Safranin was used as a counterstain for 30 s to 1 min, followed by another rinse and blotting dry. Lastly, the slide was observed under an oil immersion lens (100x) to identify purple (Gram-positive) and pink (Gram-negative) bacteria.

If the specimens had less than 10 epithelial cells per low-power field and at least 25 polymorph nuclear leukocytes, they were allowed for culture [15]. If not, the sputum sample was rejected since it was thought to be tainted with saliva. Only good-quality specimens were used to culture the bacteria in the DMCSH Microbiology Laboratory [16]. The quality of the specimens for bacterial culture was checked through a visual examination by observing the clarity of the specimen, color, and presence of contaminants; the good-quality specimens were clear without any visible impurities. An exact microscopic count of PMNs was also done since the higher the count, the better was the specimen for culture.

Isolation and identifications of bacterial pathogens

The media and chemicals used were first cleared for the experiment according to quality control checks and were within their expiry dates to ensure efficacy. Prior to the procedures, it was necessary to clean all work areas using 10% bleach. For inoculation, sterile inoculation loops were used, which were flame-sterilized before and immediately after the inoculation of each specimen to avoid contamination. The cultures were capped and stored appropriately when not in use. All manipulations were performed inside a biosafety cabinet to minimize aerosol exposure. Following inoculation, incubation conditions were carefully controlled to optimize bacterial growth while addressing safety concerns at every step.

Blood agar plate (Oxoid, Hampshire, UK), Chocolate agar plate (Oxoid, Hampshire, UK), and MacConkey agar plate (Oxoid, Hampshire, UK) were prepared following the manufacturer's instructions. A sample of purulent sputum was streaked over each agar plate using a calibrated wire loop.

The inoculated MacConkey agar plates were incubated aerobically at 37 °C for 24 h whereas Chocolate agar and Blood agar plates were incubated in a candle jar for 24 h at 35–37 °C with 5–10% carbon dioxide [17]. Following incubation, the plates were checked for growth, and those that showed no growth were left to incubate for an additional 48 h to allow for the potential growth of slow-growing or fastidious organisms [17].

The Gram stain, hemolysis patterns on blood agar, colonial features, catalase test, coagulase test, and Optochin susceptibility were used to distinguish Gram-positive cocci. In addition, Gram-negative bacteria were differentiated using colony morphology, triple sugar iron agar (TSI), indole creation, urea hydrolysis, oxidase test, hydrogen sulfur, gas formation, citrate utilization, motility, and lysine decarboxylase (LDC) [18].

Antimicrobial susceptibility testing

Muller-Hinton agar with a uniform agar depth of approximately 4 mm (Oxoid, Hampshire, UK) supplemented with 5% sheep's blood was used for the disk diffusion method (Kirby–Bauer) for fastidious bacterial isolates. To create a uniform suspension, similar pure colonies were subcultured into nutrient broth and well mixed. Mueller-Hinton agar was uniformly inoculated with the suspension. The turbidity of the inoculum was adjusted to 0.5 McFarland standards. Following that, using a sterile cotton swab, the bacterial suspensions were seeded onto the Mueller-Hinton agar's surface. Using sterile forceps, the antimicrobial-impregnated disks were put into the media, and the plate was left to stand for fifteen minutes. After that, the plates were incubated for 18 to 24 h at 35 to 37 degrees Celsius. The zone of inhibition was then measured using a clipper, and according to standard protocol, it was reported as sensitive, intermediate, and resistant.

Antibiotic discs such as Trimethoprim-Sulfamethoxazole (SXT, 1.25/23.75 µg), Erythromycin (ERY, 15 µg), Tetracycline (TET, 30 µg), Chloramphenicol (CHL, 30 µg), Azithromycin (AZM), Clindamycin (CLI, 2 µg),

Ciprofloxacin (CIP, 5 µg), Gentamycin (CN, 10 µg), Cefoxitin (FOX), and Penicillin (PEN, 5 µg) were used for Gram-positive bacteria and Trimethoprim-Sulfamethoxazole (SXT, 1.25/23.75 µg), Ampicillin (AMP, 30 µg), Ciprofloxacin (CIP, 5 µg), Gentamycin (GEN, 10 µg), Tetracycline (TET, 30 µg), Ceftriaxone (CRO, 30 µg), Ceftazidime (CAZ, 30 µg), Tombomycin (TOB, 10 µg), Cefazolin (CZO,), Piperacillin (PIP, 10 µg), Amoxicillin-Clavulanate (AMC, 20/10 µg), and Meropenem (Mem, 10 µg) were used for gram-negative bacteria. All antibiotics were sourced from Abtek Biologicals Ltd., located in Liverpool, UK [19].

Laboratory quality control

The quality of the specimens was checked based on Bartlett's acceptance and rejection criteria. Bartlett's criteria primarily focused on the ratio of squamous epithelial cells (SEC) to white blood cells (WBC) in sputum samples. A sample was considered acceptable if it contained fewer than 25 s per low power field (LPF) and a sufficient number of WBCs, typically more than 10 WBCs per LPF. Alternatively, a Q-score could be calculated, where a score of + 2 was assigned for more than 25 WBCs per LPF, + 1 for 10–25 WBCs per LPF, -2 for more than 25 s per LPF, and − 1 for 10–25 s per LPF; a positive Q-score indicated material from an active infection, categorizing it as acceptable. Conversely, samples that showed more than 25 s per LPF were generally rejected due to the likelihood of contamination from oropharyngeal flora rather than true respiratory pathogens, while a Q-score of 0 or negative suggested low sputum quality, excessive contamination, or insufficient cellular evidence of infection [20].

By incubating 5% of the batch at 35–37 °C overnight and watching for bacterial growth, the prepared culture media's sterility was verified. The performance of all prepared media was checked by inoculating international standard strains, including *E. coli* (ATCC 25922), *P. aeruginosa* (ATCC 27853), *S. aureus* (ATCC 25 923), *S. pneumoniae* (ATCC 49619), *P. mirabilis* (ATCC-12453), and *H. influenzae* (ATCC-49766), during culture and antimicrobial susceptibility testing. The effectiveness of the tested antibiotics was assessed using control strains. In addition, the CLSI M100 and CLSI M2 standards were utilized to establish performance criteria for antimicrobial susceptibility testing and antimicrobial disk susceptibility tests. Moreover, the CLSI M100 S33 standard was utilized to establish performance criteria for the selection of antibiotics based on the specimen type. To standardize the inoculum density of bacterial suspension for the susceptibility test, 0.5 McFarland standards was used.

Table 1 Socio-demographic characteristics of study participants with lower respiratory tract infections among patients attending DMCSH, Debre Markos, Ethiopia, 2023

Variables	Categories	Frequency	Percentage (%)
Sex	Male	183	60
	Female	122	40
Age	18–27	39	12.8
	28–37	77	25.2
	38–47	87	28.5
	48–57	58	19.1
	> 58	44	14.4
Marital status	Single	42	13.8
	Married	240	78.7
	Divorced	11	3.6
	Windowed	12	3.9
Residence	Urban	137	44.9
	Rural	168	55.1
Education	Unable to read and write	108	35.4
	Primary school	69	22.6
	Secondary school	68	22.3
	Collage/university above	60	19.7
Occupation	Merchant	33	10.8
	Government employer	47	15.4
	Student	28	9.2
	Farmer	146	47.8
	Housewife	27	8.9
	Daily labor	24	7.9

Data processing and analysis

Data were entered into EPI data software version 4.6 and analyzed via SPSS version 26 software. Descriptive statistics were performed using frequency. Binary logistic regression models were used to show the association between the dependent and independent variables. Variables with a p-value < 0.25 in the bivariable logistic regression analysis were moved to a multivariable logistic regression analysis model. Adjusted odds ratios with a 95% confidence interval (CI) were used and variables with a p-value less than 0.05 in multivariable analysis were taken as significant predictors.

Results

Socio-demographic characteristics of study participants

A total of 334 lower respiratory tract infection cases were enrolled in this study. Of them, twenty-nine sputum samples, which did not fulfill acceptance criteria and with Bartlett's scoring of ≤ 0 were discarded. Finally, 305 sputum samples were enrolled. The majority (60%) of study participants were males. Moreover, 240 (78.7%) were married, and 158 (55.1%) were from rural areas (Table 1).

Clinical characteristics of study participants

Among 305 individuals, the majority 262 (85.9%), 250 (82%), 233 (76.4%), and 216 (70.8%) had a night sweat, a chronic cough > 2 weeks, purulent sputum, and habit of drinking alcohol, respectively.

Prevalence of bacterial isolates of lower respiratory tract infections among study participants

The overall prevalence of bacterial isolates among study participants was 33.4% (102/305) (95% CI: 29.2–38.8%). Furthermore, the prevalence of *K.pnuemoniae*, *S. pneumoniae*, *P. aeruginosae*, *E.coli*, *S. aureus*, *P.mirabilis*, and *P. vulgaris* were 31/102 (30.4%), 21/102 (20.6%), 16/102 (15.7%), 15/102 (14.7%), 14/102 (13.7%), 3/102 (9%), and (2/102) (2%), respectively. The most prevalent bacterial isolates were *K. pneumoniae* 31/102 (30.4%) and *S. pneumoniae* 21/102 (20.6%) (Fig. 1).

Antimicrobial susceptibility patterns of bacterial isolates

From Gram-positive isolates (22.39%), *S.aureus* showed high sensitivity to clindamycin, trimethoprim-sulfamethoxazole, and ciprofloxacilin, with 87.7%, 78.6%, and 78.6%, respectively. In contrast, a high level of resistance was observed to penicillin (64.3%). Moreover, *S. pneumoniae* showed a high sensitivity to clindamycin (85.7%) and trimethoprim-sulfamethoxazole (73.7%). While a high level of resistance was observed to tetracycline (76.2%) (Table 2).

Among Gram-negative isolates, *K. pneumoniae* showed a high sensitivity rate to meropenem (93.5%), ceftriaxone (83.9%), ciprofloxacin (74.2%), chloramphenicol (61.3%), and ceftazidime (61.3%). While high resistance rate was noted for ampicillin (83.9%). *E. coli* showed high sensitivity to meropenem (86.7%) and trimethoprim-sulfamethoxazole (80%). While a high level of resistance was observed to ampicillin (71.4%). *Pseudomons aeruginosa* showed a high sensitivity to gentamaycin (81.7%), and tombomaycin (75%) (Table 3).

Multidrug resistance (MDR) patterns of bacterial isolates

Resistance to three or more antimicrobials was observed in 48/102 (47.1%) of the isolates and a high level of MDR was observed among *K.pneumoniae* 17/31 (54.9%), *E.coli* 8/15 (53.3%), and *S.aureus* 7/14 (50%) (Table 4).

Factors associated with lower respiratory tract infections

Patients with age groups of > 58 years (AOR = 7.180, 95% CI: 1.858–27.743, $P < 0.004$), who were alcohol consumers (AOR = 6.542, 95% CI: 2.570-16.654, $P < 0.000$), who had chronic cough (AOR = 5.26, 95% CI: 1.725–16.038, $P < 0.004$), and who were illiterate (AOR = 2.76, 95 CI: 1.158–6.578, $P < 0.022$) were more likely to be exposed to bacterial infections as compared to their counterparts (Table 5).

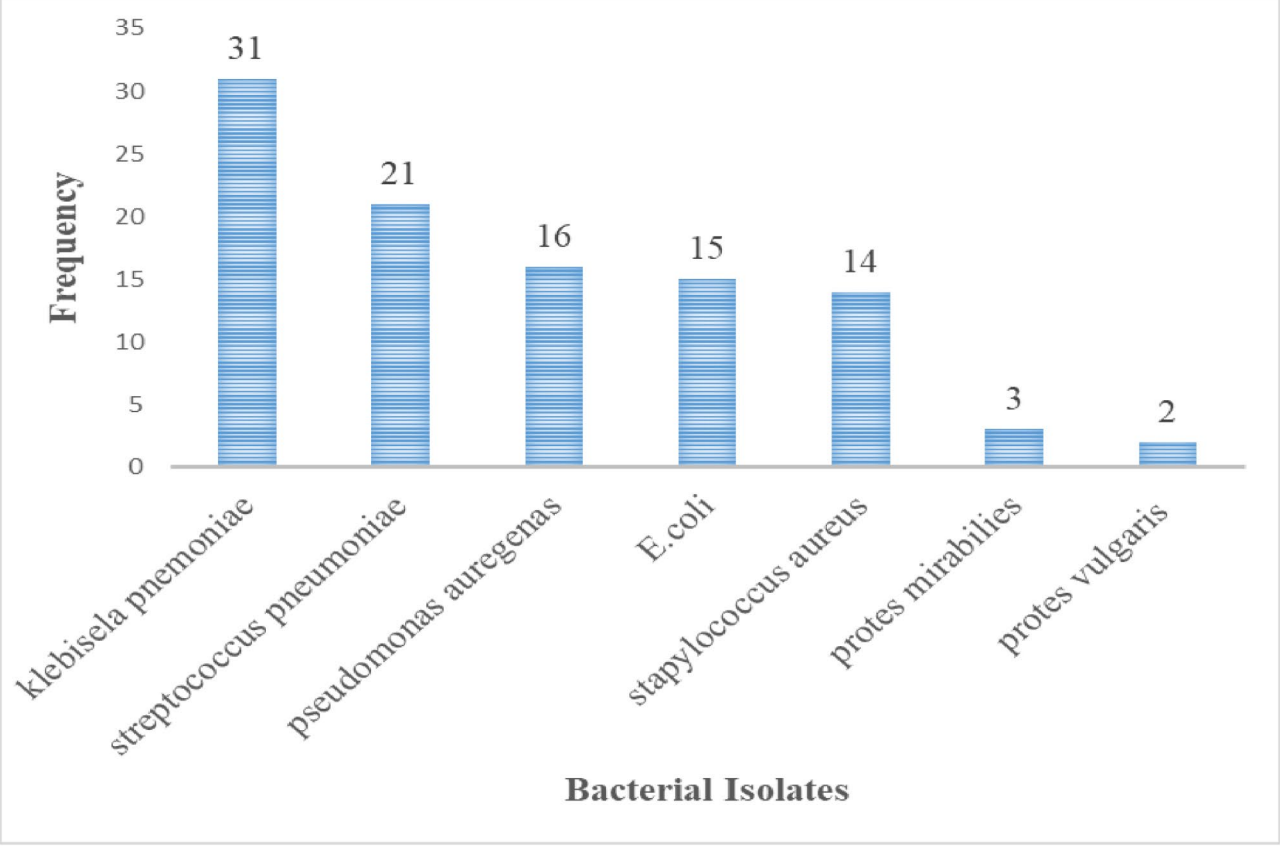

Fig. 1 Frequency of bacterial isolates of study participants of lower respiratory tract infection among patients attending DMCSH, Debre Markos, Ethiopia, 2023

Table 2 Antimicrobial susceptibility patterns of Gram-positive isolates

Isolates		Antimicrobial susceptibility patterns								
S. pneumoniae (N = 21)		PEN (%)	AZM (%)	TET (%)	CD (%)	CIP (%)	ERY (%)	SXT (%)	CTX (%)	C (%)
	S	NA	NA	3(14.3)	18(85.7	NA	8(38.1)	15(71.5	NA	NA
	I	NA	NA	2(9.5)	2(9.5)	NA	5(23.8)	3(14.2)	NA	NA
	R	NA	NA	16(76.2)	1(4.8)	NA	8(38.1)	3(14.3)	NA	NA
S. aureus (*N* = 14)	S	9(64.3)	10(71.42)	4(28.6)	12(85.7)	11(78.6	NA	11(78.6	10(71.4	9(64.3
	I	0	2(14.3)	6(42.9)	2(14.3)	2(14.3)	NA	1(7.1)	0	4(28.6
	R	5(35.7)	2(14.23)	4(28.6)	0	1(7.1)	NA	2(14.3)	4(28.6)	1(7.1)
Overall (*N* = 35)	S	9(64.3)	10(71.42)	7(20)	30(85.73	11(78.6	8(38.1)	26(74.3	10(71.4	9(64.3
	I	0	2(14.28)	8(22.9)	4(11.42)	2(14.3)	5(23.8)	4(11.4)	0	4(28.6
	R	5(35.7)	2(14.28)	20(57.1)	1(2.85)	1(7.1)	8(38.1)	5(14.3)	4(28.6)	1(7.1)

SXT- Trimethoprim-sulfamethoxazole, AZM- Aztromaycin, CIP–Ciprofloxacin, CD - Clindamycin, ERY - Erytromicin, TET-Tetracyclin, PEN– Penicillin, C - Chloraphinicole, OXA- Oxacilin, CTX-Cefoxitin and NA- not applicable

Discussion

In this study, the overall prevalence of culture-confirmed bacterial isolates among patients with lower respiratory tract infections was 102 (33.4%) (95%CI: 29.2–38.8%). This result is in line with studies done in Ethiopia: Hawassa (33.5%) [5], and Addis Abeba (32.1%) [4]. But it is higher than the study conducted in Nigeria (24.24%) [21], and India (26.34%) [22]. These variations in prevalence between different places could be explained by several variables. First, differences in the number of study participants may have an impact on the prevalence rates that are detected. This is because larger sample sizes may yield more accurate estimates of the infection rates within the population [23]. The possibility of detecting and validating bacterial illnesses through culture tests may also be impacted by variations in infection control procedures among nations or areas [24].

Moreover, variations in study design may also be a factor in the disparities in prevalence rates; for instance, variations in inclusion criteria or sampling techniques may have an impact on the makeup of the patient groups under investigation [25]. Finally, geographic locations may matter because of regional differences in environmental conditions that could affect the presence of pathogens and the spread of disease [26].

In this study, gram-negative bacteria were the major isolates (65.7%). This result is in good agreement with a previous study from Nigeria that found a higher percentage of isolates of gram-negative bacteria than gram-positive bacteria (82.5 vs. 17.5%) [21]. This might be due to differences in their cell wall structures. For instance, Gram-negative bacteria have an outer cell wall beyond the peptidoglycan membrane as compared to Gram-positive bacteria, and this makes them resistant to various antibiotics. However, Gram-positive isolates are vulnerable to different antibiotics [27].

In the current study, *K. pneumoniae* was the most common isolate from Gram-negative bacteria (30.4%) (95% CI: 22.2–40.2%). This is because *K. pneumoniae*, the most commonly known bacterial-induced community, acquired a lower respiratory infection [28]. This finding is consistent with the previous results reported from Nigeria (34.29%) [29], Tanzania (29.9%) [30], and Ethiopia (25.4–39.5%) [4, 31]. However, this is lower than the result reported from Nigeria (70%) [21], and higher than the result from Cameroon (9.2%) [32]. The spread of *K. pneumoniae* can be influenced by variations in sanitation standards and hygiene practices, especially in healthcare settings. Additionally, *K. pneumoniae* may spread more quickly and be more common in countries with larger population densities. In other words, the prevalence of *K. pneumoniae* in various locations can also be influenced by environmental factors like pollution, climate, and other ecological characteristics. Furthermore, disparities in socioeconomic status may affect the availability of healthcare services and be a factor in the national variances in the prevalence rates of *K. pneumoniae* infections [33, 34].

Furthermore, *P. aeruginosae* was the 2nd most common isolate from Gram-negative bacteria, accounting for 16 (15.7%) (95% CI: 9.5 to 22.5). It is consistent with the results from various nations; China (10.3%) [35], Ghana (15.2%) [36], and Tanzania (11.7%) [30], and lower than the result reported from Nigeria (25.71%) [29]. This may be due to differences in medical facilities, environmental factors, population density, sanitation standards, and hygiene practices [37].

From the total Gram-negative isolates, *E. Coli* accounted for 14.7% (95% CI: 7.8 to 21.6%), which is in line with studies conducted in China (17.9%) [35], and Ethiopia (16%) [4]. *More*over, the prevalence of *P. mirabilis and P. vulgaris* was 3 (2.9%) (95% CI: 0.0 to 6.9%) and 2 (2%) (95% CI: 0.0 to 4.9%), respectively.

In this study, Gram-positive bacteria comprise 22.39% of all isolated bacteria, with S. pneumoniae being the most frequently isolated (20.6%) (95% CI: 12.7 to 22.5%) and this is one of the most responsible bacterial agents for community-acquired pneumonia [38]. Similar results

Table 3 Antimicrobial susceptibility patterns of Gram-negative isolates

Isolates	Antimicrobial susceptibility patterns												
K. pneumoniae (*n* = 31)		MER%	TOB%	PRL%	TET %	CAZ %	CIP %	SXT %	AMC %	AMP %	C %	CN %	CTR%
	S	29(93.5	NA	NA	23(74.2	19(61.3)	23(74.2)	18(58.1)	16(51.6)	1(3.2)	23(74.2	NA	26(83.9)
	I	1(3.2)	NA	NA	4(12.9)	4(12.9)	4(12.9)	8(25.8)	6(19.4)	4(12.9)	1(3.2)	NA	1(3.2)
	R	1(3.2	NA	NA	4(12.9)	8(25.8)	4(12.9)	5(16.1)	9(29)	26(83.9)	7(22.6	NA	4(12.9)
p.aeruginosa(*n* = 16)	S	11(68.8	12(75)	7(43.8	NA	9(56.3)	11(68.8)	NA	NA	NA	NA	13(81.3)	NA
	I	4(25)	2(12.5	6(37.5	NA	3(18.7)	4(25)	NA	NA	NA	NA	2(12.5)	NA
	R	1(6.3)	2(12.5	3(18.7	NA	4(25)	1(6.3)	NA	NA	NA	NA	1(6.3)	NA
E.coli = 15	S	13(86.7	NA	NA	6(40)	10(66.7)	9(60)	12(80)	5(33.3)	3(20)	10(60)	NA	9(60)
	I	1(6.7)	NA	NA	2(13.3)	3(20)	4(26.7)	2(13.3)	4(26.7)	2(13.3)	4(26.7)	NA	4(26.7)
	R	1(6.7)	NA	NA	7(46.7)	2(13.3)	2(13.3)	1(6.7)	6(40)	10(66.7)	1(6.7)	NA	2(13.3)
Pm (*n* = 3)	S	2(66.7	NA	NA	2(66.7)	1(33.3)	2(66.7)	1(33.3)	2(66.7)	2(66.7)	0(0%)	NA	1(33.3)
	I	1(33.3	NA	NA	1(33.3)	1(33.3)	1(33.3)	2(66.7)	1(33.3)	1(33.3)	1(33.3)	NA	2(66.7)
	R	0(0%)	NA	NA	0(0%)	1(33.3)	0(0%)	0(0%)	0(0%)	0(0%)	2(66.7)	NA	0(0%)
P. vulgaris = 2	S	2(100)	NA	NA	1(50)	1(50)	1(50)	1(50)	1(50)	1(50)	0	NA	NA
	I	0	NA	NA	1(50)	1(50)	1(50)	1(50)	1(50)	0	1(50	NA	NA
	R	0	NA	NA	0	0	0	0	0	1(50)	1(50	NA	NA
Overall (*n* = 67)	S	57(85.1	12(75)	7(43.8	29(56.9	39(52.2)	46(68.7)	32(62.7)	22(43.2)	5(9.8)	36(70.6	13(81.3)	36(73.5)
	I	7(10.4	2(12.5	6(37.5	8(15.7)	12(17.2)	14(20.9)	13(25.5)	12(23.5)	7(13.7)	7(13.7	2(12.5	5(10.2)
	R	3(4.5)	2(12.5)	3(18.7	16(27.4)	16(23.8)	7(10.4)	6(11.8)	17(33.3	39(76.5)	8(15.7)	1(6.3)	8(16.3)

TOB-Tobramycin, SXT, Trimethoprim-sulfamethoxazole, CAZ-Ceftazidime, TET-Tetracycline, AMC-Amoxicillin-clavulanate, CTR- Ceftriaxone, CN - Gentamycin, CIP - Ciprofloxacin, MEM - Meropenem and AMP- Ampicillin, NA- not applicable

Table 4 Multi-drug resistance patterns of bacterial isolates

Antimicrobials	Drug classeResistance	S.aurues (*n* = 14)	S. pnemoniae (*n* = 21)	*P.* aerugi-nosa (*n* = 16)	*K. pneu-moniae* (*n* = 31)	E.coli (*n* = 15)	*P.* mirabiles (*n* = 3)	Total
PEN, SMX, FOX	3	1(12.9%)	-	-	-	-	-	1(12.9%)
PEN, TET, FOX		1(12.9%)	-	-	-	-	-	1(12.9%)
PEN, AZM, FOX		2(28.6%)	-	-	-	-	-	2(28.6%)
CIP, SMX, C		1(12.9%)	-	-	-	-	-	1(12.9%)
CIP, TET, SMX, C	4	1(12.9%)	-	-	-	-	-	1(12.9%)
PEN, AZM, FOX, SMX		1(12.9%)	-	-	-	-	-	1(12.9%)
TET, AZM, SMX	3	-	1(10%)	-	-	-	-	1(10%)
CD, TET, AZM		-	1(10%)	-	-	-	-	1(10%)
CD, TET, SMX		-	1(10%)	-	-	-	-	1(10%)
ERY, TET, AZM		-	6(60%)	-	-	-	-	6(60%)
CD, TET, AZM, SMX	4	-	1(10%)	-	-	-	-	1(10%)
CAZ, TOB, CIP	3	-	-	2(40%)	-	-	-	2(40%)
CAZ, TOB, TZP		-	-	1(20%)	-	-	-	1(20%)
MEM, CIP, CAZ		-	-	1(20%)	-	-	-	1(20%)
MEM, TOB, TZP, CAZ	4	-		1(20%)	-	-	-	1(20%)
CAZ, C,AMP	3	-	-	-	2(11.8%)	-	-	2(11.8%)
AMP, CAZ, TET		-	-	-	2(11.8%)	-	-	2(11.8%)
AMP, TET, CAZ, AMC	4	-	-	-	2(11.8%)	-	-	2(11.8%)
AMP, TET, SMX, CTR		-	-	-	1(5.9%)	-	-	1(5.9%)
AMP, TET, SMX, CAZ		-	-	-	1(5.9%)	-	-	1(5.9%)
AMC, TET, CTR, CAZ, AMP	5	-	-	-	1(5.9%)	-	-	1(5.9%)
CIP, TET, SMX, CTR,	4	-	-	-	1(5.9%)	-	-	1(5.9%)
CIP, AMC, TET, CAZ, AMP	5	-	-	-	1(5.9%)	-	-	1(5.9%)
MEM, CIP, SMX, C,AMP	5	-	-	-	1(5.9%)	-	-	1(5.9%)
AMC, TET, SMX, CAZ, AMP	5	-	-	-	1(5.9%)	-	-	1(5.9%)
CIP, TET, SMX, CAZ, AMP	5	-	-	-	1(5.9%)	-	-	1(5.9%)
CIP, TET, SMX, CRO, AMP	5	-	-	-	1(5.9%)	-	-	1(5.9%)
AMP, AMC, TET, SMX, CTR, CAZ	6	-	-	-	1(5.9%)	-	-	1(5.9%)
AMP, CIP, AMC, SMX, CTR, CAZ	6	-	-	-	1(5.9%)	-	-	1(5.9%)
AMP, AMC, TET	3	-	-	-	-	3(37.5%)	-	3(37.5%)
AMP, C, AMC	3	-	-	-	-	1(12.5%)	-	1(12.5%)
TET, SMX, AMP	3	-	-	-	-	1(12.5%)	-	1(12.5%)
CAZ, CIP, AMC, TET	4	-	-	-	-	1(12.5%)	-	1(12.5%)
AMP, CIP, AMC, TET, CTR	5	-	-	-	-	1(12.5%)	-	1(12.5%)
AMP, AMC, TET, CTR, CAZ		-	-	-	-	1(12.5%)	-	1(12.5%)
CAZ, AMC, AMP	3	-	-	-	-	-	1(100%)	1(100%)
Total		7(50%)	10(47.7%)	5(31.3%)	17(54.9%)	8(53.3%)	1(33.3)	48(47.1%)

SXT- Trimethoprim-sulfamethoxazole, AZM- Aztromaycin, CIP–Ciprofloxacin, CD - Clindamycin, ERY - Erytromicin, PEN- Penicilin, C - Chloraphinicole, FOX-Cefoxitin TOB-Tobramycin, CAZ-Ceftazidime, TET-Tetracycline, AMC-Amoxicillin-clavulanate, CTR - Ceftriaxone, CN - Gentamycin, MEM–Meropenem, AMP- Ampicillin

were reported from Pakistan (18.11%) [39], and Nigeria (17.5%) [21]. However, this finding is relatively higher than the previous result from Vietnam (12.6%) [40]. On the other hand, the culture positivity of *S. aureus* was14 (13.7%) (95% CI: 7.8 to 20.6%), which is consistent with the findings from Ethiopia (8.8–18.6%) [41–43], and another country; China (12%) [35]. Whereas a higher finding was found in Jordan (7.7%) [44]. However, a higher result was reported from Spain (82.3% [45]. Numerous factors, such as healthcare infrastructure, public health regulations, socioeconomic situations, and the environment, might affect the prevalence of gram-positive bacteria across the world [46].

In the current study, *K. pneumoniae* showed high resistance to ampicillin (83.9%) and sensitivity to meropenem (93.5%) and ceftriaxone (73.5%). One possible explanation for the increased resistance of K. pneumoniae to ampicillin could be that the bacteria naturally develop extended-spectrum beta-lactamases (ESBLs), which render beta-lactam medications ineffective [47]. These results are similar to the study done in Ethiopia, which found that the resistance and sensitivity profiles of *K. pneumoniae* were 83.0% and 98%, respectively [4]. Our

Table 5 Multivariable logistic regression analysis of associated factors

Variables	Categories	Culture positivity		COR(95%,CI)	P-value	AOR(95%,CI)	P-value
		Yes	No				
Residence	Rural	74	94	3.065(1.831, 5.129)	0.000*		
	Urban	28	109	1			
Age	18–27	4	33	1		1	
	28–37	24	55	3.6(1.148, 11.291)	0.028		
	38–47	32	54	4.889(1.586,15.074)	0.006*		
	48–57	18	45	3.3(1.021,10.663)	0.046		
	> 58	24	16	12.375(3.671,41.719)	0.000*	7.180(1.858,27.743)	0.004**
Educations	Unable to R and W	53	49	4.867(2.214,10.699)	0.000*	2.760(1.158,6.578)	0.022**
	Primary School	30	49	2.755(1.211,6.269)	0.016*		
	Secondary School	9	60	0.675(0.253,1.798)	0.432		
	College /university	10	49	1			
Number of families	< 5	52	131	1			
	> 5	50	72	1.749(1.079,2.836)	0.023*		
chronic cough > 2 weeks	Yes	98	155	7.587(2.653,21.701)	0.000*	5.260(1.725,16.038)	0.004**
	No	4	48	1		1	
Sputum production	Yes	92	141	4.045(1.974,8.292)	0.000*		
	No	10	62	1			
Alcohol drinking	Yes	96	123	10.407(4.353,24.877)	0.000*	6.542(2.570,16.654)	0.000**
	No	6	80	1		1	

R and W = read and write, COR = crude odds ratio, AOR = adjusted odds ratio, CI = confidence interval, *=Candidate variable for multivariate analysis at $P < 0.25$, **=statistically significant, 1 = reference category

study also demonstrated that E. coli showed resistance to ampicillin (66.7%) and comparable results were reported from Bangladesh (100%) [48] and Tanzania (100%) [30]. However, it was highly sensitive to meropenem (86.7%), trimethoprim-sulfamethoxazole (80%), and ceftazidime (66.7%).

Numerous variables influence the development of antibiotic resistance in *K. pneumoniae*. Resistance can be exacerbated by the overuse or improper use of antibiotics. *K. pneumoniae* is subject to selective pressure from environmental factors, such as the use of antimicrobial drugs in healthcare settings, which fosters resistance. The ability of *K. pneumoniae* to develop resistance mechanisms against antimicrobial drugs is also influenced by its genetic makeup. Infections produced by resistant strains of *K. pneumoniae* are also more likely to occur in patients with certain features, including age, underlying medical problems, and prior antibiotic exposure [49].

As well, *P. arogenesae* exhibited a high sensitivity to gentamycin (81.3%), tobramycin (75%), meropenem (68.8%), and resistance to ceftazidime (28.6%). Comparatively, a study from the USA shows that *P. arogenesae* is sensitive to meropenem (86.2%) [50]. The high level of ampicillin resistance in different bacterial isolates may be brought on by the drugs' easy availability, unrestricted use, empirical therapy, and careless use. Moreover, from Gram-positive isolates, *S. pneumoniae showed* high levels of sensitivity to trimethoprim-sulfamethoxazole (73.7%) and clindamycin (85.7%) and resistance to tetracycline (76.2%). The genetic determinants may affect the sensitivity of *S. pneumoniae to* tetracycline [51]. These findings are lower than the result from Pakistan, with 90% sensitivity to sulfamethoxazole-trimethoprim [52].

The resistance pattern of *S. pneumoniae* to tetracycline is higher than the result from Felege Hiwot, Ethiopia (45%) [53]. *S. aureus* exhibited sturdy resistance to penicillin (64.3%), and tetracycline (28.6%). Resistance of *S. aureus* to various antibiotics could arise from mutations in chromosomal genes or from the horizontal transfer of resistance determinants encoded by transposons, plasmids, and the staphylococcal cassette chromosome. Enzymatic drug modification, inactivation, alteration of the drug binding site, drug efflux, bypass mechanisms including the acquisition of a novel drug-resistant target, and drug displacement to protect the target are all examples of how horizontally acquired resistance might arise. Mutations that cause the drug target to change such that the inhibitor cannot bind derepression of chromosomally encoded multidrug resistance efflux pumps and a series of stepwise mutations that change the composition and structure of the cell wall and/or membrane to decrease drug access to the target can all lead to the acquisition of resistance through mutation [54].

In contrast, it was highly sensitive to clindamycin (85.7%), trimethoprim-sulfamethoxazole (78.6%), and ciprofloxacin (78.6%). In the current study, the resistance

pattern of *S. aureus to* penicillin and tetracycline is relatively lower than the findings reported from Kenya (91.9%) and (33.15%), respectively [55]. Moreover, the overall magnitude of multidrug resistance (MDR) in the current study was 47.1%. In contrast, a higher result of MDR profile was reported from another study in Ethiopia, Gondar (72.2%) [56].

Several causes, including improper and excessive use of antibiotics, treatment noncompliance, inadequate infection control in healthcare and community settings, and inadequate hygiene and sanitation, may contribute to the occurrence of MDR variation. Furthermore, MDR in bacteria can be caused by the activity of multidrug efflux pumps, which are capable of pumping out several drug types, or by the accumulation of genes that code for resistance to a particular agent in on-resistance (R) plasmids or transposons [57].

In our study, factors like alcohol use ($p < 0.001$), educational status ($p = 0.022$), chronic cough ($p = 0.004$), and age ($p = 0.004$) were significant contributors to patients with lower respiratory tract infections. This is analogous to the studies conducted in India, Nigeria, Turkey, and Indonesia [58–61], and also comparable with another study done in Ethiopia; Mekelle [62]. According to this study, illiterate participants were 2.76 times more likely to be subjected to bacterial illnesses than participants who had completed their elementary, secondary, as well as higher-level education, and this might be because human health is directly impacted by illiteracy. It makes it impossible for people to read the directions on a bottle of medication. This indicates that fewer people are likely to be aware of information regarding infectious diseases, such as how they spread, what causes them, and how to avoid getting lower respiratory tract infections brought on by bacteria [63].

In the present study, participants who were found to be in the age group of > 58 years had a 7.18-fold higher chance of being exposed to lower respiratory bacterial infections as compared to their counterparts. An immune system deterioration, especially cell-mediated immunity, and declines in efficiency with aging could be the possible reason. However, this modification by itself is unable to account for the rise in infection rates. The infections that most commonly affect the elderly are those of specific organ systems, such as the lung, for which aging-related changes in the anatomical structure and function account for a major portion of the increased vulnerability. A situation such as malnourishment, degenerative illness, or the extent of prior infection exposure can potentially cause an infection in old age [64].

As compared to non-consumers, alcohol users had a 6.542 times greater chance of contracting bacterial illnesses. People with a history of alcohol use have weakened immune systems, which makes them more vulnerable to this lung illness. Innate immune response cells, neutrophils, lymphocytes, and alveolar macrophages are the main immune cells that fight lower respiratory tract infections. For instance, drinking too much alcohol might alter the way alveolar macrophages operate, which weakens the lungs' defenses against infections [65]. According to this study, patients with a persistent cough had a 5.26-fold increased risk of coming into contact with bacterial infections compared to those without one. Suspected lung patients who have a chronic cough may be more susceptible to the spread of bacterial pathogens, which could explain their heightened vulnerability to these pathogens.

Limitations of the study

Despite the significant importance of this study for public health, we only characterized the bacterial isolates phenotypically. Moreover, *Mycobacterium tuberculosis* has not been detected due to resource and time constraints. In addition, *methicillin-resistant Staphylococcus aureus* (MRSA), inducible clindamycin-resistant *S. aureus*, Extended-spectrum beta-lactamases (ESBLs)-producing gram-negative bacteria and carbapenemase-producing Enterobacteriaceae (CPE) have not been detected due to resource constraints.

Conclusions

The prevalence of lower respiratory tract infections was high in the study area. Gram-negative bacteria were the major isolates. *Klebsiella pneumoniae* was the most predominant bacteria isolated from patients with lower respiratory tract infections. Gram-negative bacilli were highly sensitive to meropnem, while Gram-positive cocci were highly sensitive to clindamaycin. However, this study found a significant rate of antibiotic resistance and most of the isolates were highly resistant to ampicillin and penicillin. In other words, selecting targeted and effective antibiotic therapy for LRTIs and preventing the establishment of multidrug-resistant bacteria depend heavily on accurately identifying the causative bacteria and their patterns of antibiotic susceptibility. In addition, the findings of this study underscore the need for ongoing surveillance and targeted interventions, such as antimicrobial stewardship programs, to combat the rising threat of multidrug-resistant bacterial agents in LRTIs and to ensure effective treatment options.

Furthermore, associated factors were also assessed in this study and the ages of study participants, alcohol consumption, chronic cough, and being illiterate are determinants of lower respiratory infections.

To avoid the spread of lower respiratory tract infection and drug resistance pathogens, there should be appropriate infection prevention measures, periodic antimicrobial

surveillance, an effective antibiotic policy, and regular monitoring of the antimicrobial resistance patterns.

In addition, there should be several initiatives to combat antibacterial drug resistance in hospital settings, including research into new treatment options, collaboration with public health agencies, the adoption of rapid and accurate diagnostic tools, and antibiotic stewardship programs. Future research is also needed on the molecular characterization of the isolates and the detection of *Mycobacterium tuberculosis*, methicillin-resistant *Staphylococcus aureus* (MRSA), inducible clindamycin-resistant *S. aureus*, extended-spectrum beta-lactamases (ESBLs)-producing gram-negative bacteria, and carbapenemase-producing Enterobacteriaceae (CPE).

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s12879-025-10633-y.

Supplementary Material 1

Acknowledgements
We thank the Debre Markos Comprehensive Specialized Hospital staff and all of the study participants.

Author contributions
OY: Involved in conception, study design, investigation, data acquisition, analysis, methodology, Software, interpretation, funding, and writing -original draft, AAB: Involved in conception, study design, methodology, writing-original draft, review, supervision, and editing, AA: Involved in conception, study design, data acquisition, methodology, writing-original draft, review, and editing, FA: Involved in conception, study design, methodology, visualization, and writing-original draft, AE: Involved in conception, study design, data acquisition, analysis, methodology, software, interpretation, writing -original draft, validation, and supervision.

Funding
The Amhara Regional Health Bureau is funded only for material support.

Data availability
The datasets generated and/or analysed during the current study are available from corresponding author on reasonable request.

Declarations

Ethics approval and consent to participate
The study was conducted in accordance with the Declaration of Helsinki, and approved by the Institutional Review Board of Debre Markos University, College of Health Science (Protocol number Ref: HSC/RCS/139/11/12). Written informed consent was acquired from all study subjects.

Consent for publication
Since this specific manuscript did not include any individual data, such as pictures or videos, consent for publication is not applicable.

Competing interests
The authors declare no competing interests.

Author details
[1]Department of Medical Laboratory Sciences, College of Health Sciences, Debre Markos University, Debre Markos, Ethiopia
[2]Department of Biomedical Sciences, School of Medicine, College of Health Sciences, Debre Markos University, Debre Markos, Ethiopia

Received: 4 April 2024 / Accepted: 13 February 2025
Published online: 24 February 2025

References

1. Kandi V. Management of lower respiratory tract infections (LRTI's): clinical microbiologists' perspective. Int J Res Med Sci. 2014;2:10–2.
2. Safiri S, Mahmoodpoor A, Kolahi AA, Nejadghaderi SA, Sullman MJM, Mansournia MA, Ansarin K, Collins GS, Kaufman JS, Abdollahi M. Global burden of lower respiratory infections during the last three decades. Front Public Health. 2022;10:1028525.
3. Seidu AA, Dickson KS, Ahinkorah BO, Amu H, Darteh EKM, Kumi-Kyereme A. Prevalence and determinants of Acute Lower Respiratory infections among children under-five years in sub-saharan Africa: evidence from demographic and health surveys. SSM - Popul Health. 2019;8:100443.
4. Nurahmed N, Kedir S, Fantahun S, Getahun M, Mohammed A, Mohammed A, Mohammed F, F T, Desta K. Bacterial profile and antimicrobial susceptibility patterns of lower respiratory tract infection among patients attending selected health centers of Addis Ababa, Ethiopia. Egypt J Chest Dis Tuberculosis 2020, 69.
5. Gebre AB, Begashaw TA, Ormago MD. Bacterial profile and drug susceptibility among adult patients with community acquired lower respiratory tract infection at tertiary hospital, Southern Ethiopia. BMC Infect Dis. 2021;21(1):440.
6. Lin PL, Flynn JL. Understanding latent tuberculosis: a moving target. J Immunol (Baltimore Md: 1950). 2010;185(1):15–22.
7. Agwu E. Incidence of Streptococcus pneumoniae infections among patients attending tuberculosis clinics in Ekpoma, Nigeria. Shiraz E Med J 2006, 7.
8. Zhang ZX, Sng LH, Yong Y, Lin LM, Cheng TW, Seong NH, Yong FK. Delays in diagnosis and treatment of pulmonary tuberculosis in AFB smear-negative patients with pneumonia. Int J Tuberculosis lung Disease: Official J Int Union against Tuberculosis Lung Disease. 2017;21(5):544–9.
9. Oxlade O, Murray M. Tuberculosis and poverty: why are the poor at greater risk in India? PLoS ONE. 2012;7(11):e47533.
10. Akter S, Shamsuzzaman SM, Jahan F. Community acquired bacterial pneumonia: aetiology, laboratory detection and antibiotic susceptibility pattern. Malays J Pathol. 2014;36(2):97–103.
11. Attia EF, Pho Y, Nhem S, Sok C, By B, Phann D, Nob H, Thann S, Yin S, Noce R et al. Tuberculosis and other bacterial co-infection in Cambodia: a single center retrospective cross-sectional study. 2019, 19(1):60.
12. Millett ER, Quint JK, Smeeth L, Daniel RM, Thomas SL. Incidence of community-acquired lower respiratory tract infections and pneumonia among older adults in the United Kingdom: a population-based study. PLoS ONE. 2013;8(9):e75131.
13. Shilpa K, Ramyashree A. Isolation and antimicrobial sensitivity pattern of Klebsiella pneumoniae from sputum samples in a tertiary care hospital. Int J Biomedical Adv Res. 2016;7:53.
14. Gedefaw A. Journal of Geography and Regional Planning Monitoring the urban growth of Debre Markos Town (1984–2012), Ethiopia: Using satellite images and GPS. 2017.
15. Lee YJ, Shin S, Roh EY, Yoon JH, Kim DK, Chung HS, Lee CH. Acceptability of sputum specimens for diagnosing pulmonary tuberculosis. 2015, 30(6):733–6.
16. M C: District laboratory practice in tropical countries, part 2 2nd edition *New York: Cambridge university press;* 2006 *45–143 p, Accessed on 3/27/2024.*
17. Amissah I, Pappoe F. Prevalence of bacterial pathogens isolated from sputum cultures of hospitalized adult patients with community-acquired pneumonia at the cape coast teaching hospital, Ghana. *E3 Journal of Medical Research* 2014, 3:058–061.
18. Institute CaLs. Performance standards for antimicrobial susceptibility testing. CLSI M100. 2020;30th edition(January):40. accessed on 3/27/2024.
19. Institute CaLS: Performance Standards for Antimicrobial Susceptibility Testing. 32nd edition. 2022, accessed on 3/27/2024.
20. Mahale RP, Darpan Sheth 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(6):e61924.
21. Ogiogwa AA, Okerentugba J, Innocent-Adiele P, Onoh C, Nwanze C, Okonko J. I: Prevalence of Antibiotic Susceptibility Pattern of bacterial agents involve in lower respiratory tract infection in Abeokuta,Ogun State, Nigeria. Report and Opinion; 2012.

22. B RR. Bacteriological profile and antibiotic susceptibility patterns of lower respiratory tract infections in a tertiary care hospital, Central Kerala. IP Int J Med Microbiol Trop Dis. 2018;4:186–90.
23. Serdar CC, Cihan M, Yücel D, Serdar MA. Sample size, power and effect size revisited: simplified and practical approaches in pre-clinical, clinical and laboratory studies. Biochemia Med. 2021;31(1):010502.
24. Ryu S, Chun JY, Lee S. Epidemiology and Transmission Dynamics of Infectious Diseases and Control Measures. 2022, 14(11).
25. Wing C, Simon K, Bello-Gomez RA. Designing Difference in Difference studies: Best Practices for Public Health Policy Research. Annu Rev Public Health. 2018;39:453–69.
26. Mirkarimi M, Alisamir M. Clinical and Epidemiological Determinants of Lower Respiratory Tract Infections in Hospitalized Pediatric Patients. 2020, 2020:8844420.
27. Breijyeh Z, Jubeh B, Karaman R. Resistance of Gram-negative Bacteria to current Antibacterial agents and approaches to resolve it. 2020, 25(6).
28. Rammaert B, Goyet S, Beauté J, Hem S, Te V, Try PL, Mayaud C, Borand L, Buchy P, Guillard B, et al. Klebsiella pneumoniae related community-acquired acute lower respiratory infections in Cambodia: clinical characteristics and treatment. BMC Infect Dis. 2012;12:3.
29. Usman AD, Amina M. Isolation and Identification of Bacteria Associated with Lower respiratory tract infection among patients attending General Hospital Katsina. UMYU J Microbiol Res (UJMR). 2017;2:97–101.
30. Kishimbo P, Moremi N, Kalokola F, Mshana S. Prevalence of gram negative bacteria causing community acquired pneumonia among adults in Mwanza City, Tanzania. Pneumonia. 2020;12:7.
31. Gebre A, Begashaw T, Ormago M. Bacterial Profile and Drug susceptibility among adult patients with Community Acquired Lower respiratory tract infection at Tertiary Hospital. Southern Ethiopia; 2021.
32. Tchatchouang S, Nzouankeu A, Kenmoe S, Ngando L, Penlap V, Fonkoua MC, Pefura-Yone EW, Njouom R. Bacterial Aetiologies of Lower Respiratory Tract Infections among Adults in Yaoundé, Cameroon. 2019, 2019:4834396.
33. Chang D, Sharma L, Dela Cruz CS, Zhang D. Clinical epidemiology, risk factors, and control strategies of Klebsiella pneumoniae infection. Front Microbiol. 2021;12:750662.
34. Effah CY, Sun T, Liu S, Wu Y. Klebsiella pneumoniae: an increasing threat to public health. Ann Clin Microbiol Antimicrob. 2020;19(1):1.
35. Luan Y, Sun Y, Duan S, Zhao P, Bao Z. Pathogenic bacterial profile and drug resistance analysis of community-acquired pneumonia in older outpatients with fever. J Int Med Res. 2018;46:030006051878691.
36. Deberu NO, Nkrumah B, Annan A, Sambian D, Acheampong G, Amuasi J, Stebleson A, Agboyie D, Yenbaree M, Mensah S et al. Common bacteria in sputum or gastric lavage of patients presenting with signs and symptoms of lower respiratory tract infections. Pan Afr Med J 2021, 38.
37. Reynolds D, Kollef M. The epidemiology and Pathogenesis and treatment of Pseudomonas aeruginosa infections: an update. 2021, 81(18):2117–31.
38. Khan S, Priti S, Ankit S. Bacteria Etiological agents causing lower respiratory tract infections and their resistance patterns. Iran Biomed J. 2015;19(4):240–6.
39. Irfan M, Gilani SA, Mahmood E, Qureshi A. IDENTIFICATION OF BACTERIAL ISOLATES AND CLINICAL PROFILE IN SLOW RESOLVING PNEUMONIA IN PATIENTS ATTENDING TERTIARY CARE HOSPITAL, LAHORE. 2022, 7.
40. Tran H, Nguyen Y, Tran T, Le T, Nguyen H, Nguyen C, Le H, Phan T, Vo T, Bui H, et al. Community-acquired pneumonia-causing bacteria and antibiotic resistance rate among Vietnamese patients: a cross-sectional study. Medicine. 2022;101:e30458.
41. Regassa B. Aetiology of Bacterial Pathogens from Adult Patients with Community-Acquired Pneumonia in Arba Minch Hospital, South Ethiopia. 2014.
42. Beyene G, Regassa B, Yilma D, Sewunet T. Antimicrobial susceptibility pattern of bacterial isolates from community-acquired pneumonia patients in Jimma University Specialized Hospital, Jimma, Ethiopia. Saudi J Health Sci 2015, 4.
43. Dessie T, Jemal M, Maru M, Tiruneh M. Multiresistant bacterial pathogens causing bacterial pneumonia and analyses of potential risk factors from Northeast Ethiopia. Int J Microbiol. 2021;2021:1–9.
44. Obeidat N, Bsisu I, Parvez F, Islam Z, Obeidat Z, Altous M, Obeidat N, Ababneh N, Wahbeh A, Farah R. Prevalence of bacterial Lower Respiratory Tract infections at a Tertiary Hospital in Jordan. Int Arabic J Antimicrob Agents. 2019;9:11.
45. Lacoma A, Gomes-Fernandes M, Mesalles E, Arméstar F, Villar Hernández R, Casas I, Molinos S, Giménez M, Ausina V, Prat Aymerich C. Persistence of staphylococcus aureus in lower respiratory tract in patients undergoing mechanical ventilation. Eur Respir J. 2015;46:PA2640.
46. Gnimatin JP, Weyori EW, Agossou SM, Adokiya MN. Bacterial infections epidemiology and factors associated with multidrug resistance in the northern region of Ghana. 2022, 12(1):22069.
47. Heidary M, Nasiri MJ, Dabiri H, Tarashi S. Prevalence of drug-resistant Klebsiella pneumoniae in Iran: a review article. Iran J Public Health. 2018;47(3):317–26.
48. Ullah B, Ahmed S, Shahriar M, Yesmine S. Current Trend of Antibiotic Resistance in Lower Respiratory Tract infections (LRTIs): an experience in a Teaching Hospital in Bangladesh. Bangladesh Pharm J. 2016;19:85–91.
49. Li Y, Kumar S. Characteristics of antibiotic resistance mechanisms and genes of Klebsiella pneumoniae. 2023, 18(1):20230707.
50. Sader HS, Huband MD, Castanheira M, Flamm RK. Pseudomonas aeruginosa Antimicrobial susceptibility results from four years (2012 to 2015) of the International Network for Optimal Resistance Monitoring Program in the United States. Antimicrob Agents Chemother 2017, 61(3).
51. Ousmane S, Diallo BA, Ouedraogo R. Genetic determinants of Tetracycline Resistance in Clinical Streptococcus pneumoniae serotype 1 isolates from Niger. Antibiot (Basel Switzerland) 2018, 7(1).
52. Mansoor S, Qadir S, Javed S, Jehan FS, Kundi M. Antimicrobial susceptibility of organisms isolated from sputum culture of Karachi, Pakistan. Pak J Pharm Sci. 2017;30(6):2247–52.
53. Temesgen D, Bereded F, Derbie A, Biadglegne F. Bacteriology of community acquired pneumonia in adult patients at Felege Hiwot Referral Hospital, Northwest Ethiopia: a cross-sectional study. Antimicrob Resist Infect Control 2019, 8.
54. Foster TJ. Antibiotic resistance in Staphylococcus aureus. Current status and future prospects. FEMS Microbiol Rev. 2017;41(3):430–49.
55. Gitau W, Masika M, Musyoki M, Museve B, Mutwiri T. Antimicrobial susceptibility pattern of Staphylococcus aureus isolates from clinical specimens at Kenyatta National Hospital. BMC Res Notes. 2018;11:226.
56. Assefa M, Tigabu A, Belachew T, Tessema B. Bacterial profile, antimicrobial susceptibility patterns, and associated factors of community-acquired pneumonia among adult patients in Gondar, Northwest Ethiopia: a cross-sectional study. PLoS ONE. 2022;17:e0262956.
57. Nikaido H. Multidrug resistance in bacteria. Annu Rev Biochem. 2009;78:119–46.
58. Jayaraj MM, Limaye B, Chaya S, Dhar S. P A M: factors influencing severity of community-acquired pneumonia. Lung India. 2018;35:284.
59. Iliyasu G, Habib A, Aminu B, Borodo M. Epidemiology and clinical outcomes of Community Acquired Pneumococcal infection in North-West Nigeria. Subsaharan Afr J Med. 2015;2:79–84.
60. Aydin M, Şaylan B, İşcanlı İ. Factors associated with mortality in younger and older (≥ 75 years) hospitalized patients with community-acquired pneumonia. Ann Saudi Med. 2022;42:45–51.
61. Sitompul P, Indriani R, Rusli A, Sundari T, Rosamarlina R, Hartono T, Maemun S, Syahril M, Rudiatmoko D, Setiawaty V. Antimicrobial sensitivity pattern from hospitalized pneumonia patients in National Referral Infectious Disease Hospital in Indonesia. Adv Med. 2022;2022:1–5.
62. Adhanom G, Gebreegziabiher D, Weldu Y, Wasihun A, Araya T, Legese H, Lopes B, Muthupandian S. Species, risk factors, and Antimicrobial susceptibility profiles of bacterial isolates from HIV-Infected patients suspected to have Pneumonia in Mekelle Zone, Tigray, Northern Ethiopia. Biomed Res Int. 2019;2019:1–9.
63. Nations U. https://press.un.org/en/2008/sgsm11746.doc.htm. 2008, Accessed on 4/1/2024.
64. Kline KA, Bowdish DM. Infection in an aging population. Curr Opin Microbiol. 2016;29:63–7.
65. Simet SM, Sisson JH. Alcohol's effects on Lung Health and Immunity. Alcohol Research: Curr Reviews. 2015;37(2):199–208.

Publisher's note