Iranian Journal of Microbiology
Volume 15 Number 4 (August 2023) 492-502

ORIGINAL ARTICLE

Bacterial etiology, antimicrobial resistance and factors associated with community acquired pneumonia among adult hospitalized patients in Southwest Ethiopia

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Received: April 2023**, Accepted:** July 2023

ABSTRACT

Background and Objectives: Antibiotic resistance is a significant problem that restricts the options for treating bacterial pneumonia. This research aimed to determine the bacterial causes of pneumonia and antibiotic resistance among hospitalized patients in southwest Ethiopia.

Materials and Methods: We collected and analyzed 150 sputum samples from individuals with community-acquired pneumonia from April 1st to October 30th, 2019. Standard bacteriological procedures were used to identify the bacteria. Kirby Bauer's disk diffusion method was used to assess the bacteria's susceptibility patterns. Production of carbapenemase and extended-spectrum-lactamase were confirmed phenotypically. Odds ratios and the chi-square test were computed.

Results: On the whole, bacterial pathogens were verified in 50% of the sputum samples. The predominant bacterial isolates were *Klebsiella* species, followed by *Pseudomonas aeruginosa, Staphylococcus aureus* and *Streptococcus pneumoniae.* About 77.5% of isolates were multidrug resistant. Moreover, 40.5% and 10.8% of the isolates were ESBL and carbapenemase producers, respectively. Aging, tobacco smoking, previous history of pneumonia, heart disease, and chronic respiratory disease had association with sputum culture-positivity.

Conclusion: As a result, it is important to regularly monitor the bacterial etiologies and their patterns of resistance. Additionally, sociodemographic and clinical characteristics should all be taken into account while managing patients with pneumonia empirically in this context.

Keywords: Pneumonia; Bacterial; Etiology; Antimicrobial drug resistance; Hospitalized; Ethiopia

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INTRODUCTION

Infections of the trachea, bronchi, and lung parenchyma are known as lower respiratory tract infections (LRTIs). This includes lung abscesses, acute bronchitis, and pneumonia (1, 2). One of the main reasons for hospitalization and death worldwide is pneumonia (3). Hospital-acquired pneumonia (HAP) is an infection obtained after at least 48 hours of hospitalization, whereas community-acquired pneumonia (CAP) is an infection acquired outside of the hospital setting. Numerous microbes, including bacteria, viruses, and fungi, can cause it (4, 5).

According to many studies, a variety of factors, including an increase in patient age, the existence of comorbidities, cigarette and alcohol use, and chronic malnutrition, put the population at risk for pneumonia (6, 7). Additionally, the use of recent antibiotics, corticosteroids, and structural lung disease are risk factors for gram-negative pneumonia infection (8).

The commonest etiologies of pneumonia are viruses to which antibiotics are often unnecessarily prescribed (9, 10). Additionally, there can be significant differences in the microbial flora and antimicrobial resistance patterns between and within nations, regions, hospitals, ICUs within hospitals, and specimen sources through different means (11, 12). As a result, accurate diagnosis of the causes of pneumonia and knowledge of their susceptibility patterns will help to reduce the need for unnecessary antibiotic prescriptions, which could help fight antimicrobial resistance (9, 10, 12).

In Ethiopia, bacterial etiologies of community-acquired pneumonia from outpatients, *Streptococcus pneumoniae*, *Klebsiella species*, *S. aureus*, *H. influenzae*, *Pseudomonas* species and *Acinetobacter* species are frequently isolated with different levels of resistance for different antibiotics (13-16). However, there is no published data on the bacteriological profiles and patterns of antibiotic resistance among hospitalized patients in Ethiopia with community-acquired pneumonia in general and in the research context. Thus, this study was conducted to identify bacterial etiologies and associated antibiotic resistance patterns among hospitalized patients with community-acquired pneumonia at Jimma Medical Center (JMC), Jimma, Ethiopia.

MATERIALS AND METHODS

Study design and setting. From April 1 to October 30, 2019, a cross-sectional study was carried out at Jimma Medical Centre in Jimma Town, southwest Ethiopia. With a bed capacity of 800, it is the only teaching and referral hospital in the country's southwest. With a catchment population of more than 20 million people, it serves over 15,000 inpatients, 160,000 outpatient attendants, 11,000 emergency cases, and 4500 deliveries annually.

Source population. All adult patients clinically diagnosed with community-acquired pneumonia at Jimma Medical Center.

Study population. All adult hospitalized patients diagnosed with community-acquired pneumonia at Jimma Medical Center from April 1 to October 30, 2019.

Inclusion criteria. All adult hospitalized patients diagnosed with community-acquired pneumonia agreed to the study and provided written informed consent.

Exclusion criteria. The study excluded patients who were seriously unwell, known cases of tuberculosis, a history of hospital admission in the previous two weeks, those who were admitted to the hospital for at least 48 hours prior to data collection and who were unable to provide adequate sputum sample. Finally, a total of 150 study participants who provided good quality of sputum (<10 SECs per LPF and >25 PMNs per LPF on gram stain), recruited using the purposive sampling technique (17).

Data and sample collection. By using a face-to-face administered structured questionnaire, socio-demographic traits, clinical, and behavioral aspects of the patients were collected. The questionnaire had a pretested to ensure its reliability and necessary modifications were made as a result. Other important medical data of the patient were obtained from the patient medical record. Expectorated sputum specimens were collected under possible aseptic conditions. All samples were delivered to the medical center's microbiology lab, where a bacteriological study was carried out.

Bacterial isolation and identification. Quality of expectorated sputum samples were approved (17).

Sputum washing technique was performed and the specimen was inoculated onto 5% sheep blood agar, chocolate agar, and MacConkey agar and then incubated aerobically at 37°C for 48 hours. The inoculated chocolate agar was incubated at 35-37°C for 72 hours in a candle jar to provide a 5-10% CO_2 concentration for isolation of *Streptococcus pneumoniae*, and *Hemophilus influenzae*. After the indicated time, quantitative sputum culture was employed (18, 19). Finally, the bacterial identification was done using standard microbiological techniques including colony characterization, series of biochemical tests (20).

Antimicrobial susceptibility test. Following the recommendations of the Clinical Laboratory Standards Institute (CLSI), the antimicrobial susceptibility pattern of the isolates for different antibiotic was determined using the Kirby Bauer disc diffusion method on Mueller Hinton agar (Oxoid Ltd., England) (21). Following an overnight incubation period, the diameter of the zone of inhibition was measured in millimeter and, in accordance with the CLSI guideline, interpreted as susceptible, intermediate, or resistant (21). Multidrug-resistant (MDR) bacteria were classified as isolated bacteria that are resistant to at least one antimicrobial drug in three or more antimicrobial categories (22).

Extended spectrum β-lactamase and carbapenemase detection. Using the MASTTM D68C and D73C combination disc sets, respectively, ESBL and carbapenemase production were assessed in gram-negative isolates. The zone of inhibition was measured and recorded on an excel sheet following an overnight incubation at 35-37°C. It was then transferred to Mast Group's ESBL/AmpC and CARBA plus calculator spreadsheet (Mast Group, UK) and classified as either positive or negative for ESBL/AmpC and/or carbapenemase.

Quality control. The specimen's quality was assessed using Bartlett's acceptance and rejection criteria. Furthermore, sputum washing technique and quantitative sputum culture were employed to reduce the heavy growth of commensal organisms from sputum culture (18, 19). The CLSI guideline was followed while using the control strains from the American Type Culture Collection (ATCC): *P. aeruginosa* ATCC 27853, *E. coli* ATCC 25922, and *S. aureus* ATCC 25923. As a control for ESBL detection, ESBL-positive ATCC 700603 *K. pneumoniae* and ESBL-negative ATCC 25922 *E. coli* control strains were also employed.

Data management and statistical analysis. Before being loaded into EpiData version 3.1 and exported to IBM® SPSS® version 25 for analysis, the data were examined for consistency and accuracy. The results of the descriptive statistics computation were presented in tables and graphs. Fisher's exact test, chi-square test, odds ratios with corresponding confidence intervals, and patient clinical and demographic data and outcome variables were calculated to examine the link between them. The cutoff for statistical significance was set at p-values below 0.05.

Ethical considerations. The Jimma University Institute of Health's institutional review board granted ethical approval (Ref No. IHRPGD/565/2019). Each participant in the study, or their legal guardian, provided written informed consent. The study participants' privacy was protected while the data were collected, analyzed, and interpreted. Patients in the study had their test findings communicated to their attending physicians for case management.

RESULTS

Socio-demographic and clinical characteristics. A total of 150 patients diagnosed with community acquired pneumonia for a period of seven months were enrolled. More than half, 52.7% (79/150) of the participants were females (Table 1).

Bacterial profile among hospitalized patients with community acquired pneumonia. In this study, the magnitude of potentially pathogenic bacterial isolates was 50% (75/150). About 80 bacteria were identified which were grouped under 12 different bacterial types, where 80% of them were gram-negative bacilli. The predominant bacterial isolates were *Klebsiella* spp. 23.8% (19/80), followed by *P. aeruginosa* 21.3% (17/80), *S. aureus* 11.25% (9/80), and *S. pneumoniae* 8.75% (7/80) (Fig. 1).

Antimicrobial resistance patterns of the isolates. Gram-negative isolates tested resistant for ampicillin (100%), cefuroxime (87.2%), and trimethoprim-sulfamethoxazole (89.1%) in antibiogram tests. A signif-

Table 1. Socio-demographic and clinical characteristics of hospitalized patients with community acquired pneumonia at Jimma Medical center, Southwest Ethiopia, 2019 (n=150).

Variable	Categories	Number	Percent (%)
Age	18-35	55	36.7
	36-49	46	30.7
	50-64	27	18
	≥65	22	14.6
Sex	Female	79	52.7
	Male	71	47.3
Residence	Urban	64	42.7
	Rural	86	57.3
Occupation	Employed	10	6.7
	Farmer	44	29.3
	Merchant	9	6.0
	Housewife	68	45.3
	Daily laborer	10	6.7
	Others	9	6.0
History of tobacco smoking	Yes	20	13.3
	No	130	86.7
Alcohol consumption	Yes	17	11.3
	No	133	88.7
Comorbidities	Chronic renal disease	31	20.7
	Chronic heart disease	32	21.3
	Chronic respiratory disease*	31	20.7
	Diabetes	22	14.7
	HIV/AIDS	27	18.0
	Others**	16	10.7
	No comorbidities	20	13.3
History of pneumonia	Yes	34	22.7
	No	116	77.3
History of antibiotic treatment***	Yes	110	76.3
	No	40	26.7

Abbreviations: Chronic respiratory disease*: COPD + Asthma + Bronchiectasis **: Malignancy + Gastritis + Chronic liver disease; ***: Use of antibiotics in the previous three months

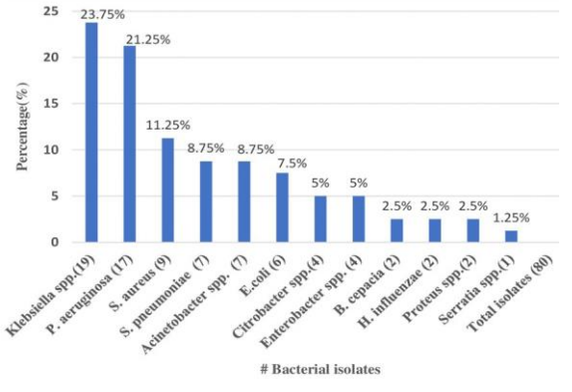

Fig. 1. Profile of bacterial isolates among hospitalized patients with community acquired pneumonia in Jimma Medical Center, Southwest Ethiopia, 2019.

icant percentage of resistance to ampicillin (100%), trimethoprim-sulfamethoxazole (78.9%), and doxycycline (73.9%) was demonstrated by *Klebsiella* spp. Additionally, it was shown that third- and fourth-generation cephalosporin resistance was present in 47.4% to 68.4% of isolated *Klebsiella* species. 88.5% of isolated *P. aeruginosa* were found to be resistant to ceftazidime, cefepime, and augmentin. In addition, 29.4% of the isolated *P. aeruginosa* were meropenem-resistant (Table 2).

Likewise, among Gram-positive bacterial isolates, *S. aureus* showed high resistance to penicillin (100%), trimethoprim-sulfamethoxazole (88.9%), and tetracycline (77.8%). While 77.8% of isolated *S. pneumoniae* was oxacillin-resistant, and 88.9% of

isolated *S. aureus* was methicillin-resistant (MRSA) (Table 3).

Prevalence of multidrug-resistant bacterial isolates. Overall, multidrug resistance was observed in 62/80 (77.5%) of the isolates. The MDR level among frequent isolates was as follows, *Klebsiella* spp. 10 (52.6), *P. aeruginosa* 1 (88.2%), *S. aureus* 9 (100%), *Acinetobacter* spp. 7 (100%), and *E. coli* 4 (66.7) (Table 4). In this study, a history of antibiotic use within three months before the current admission was statistically associated with MDR bacterial isolates 68/80 (85%) ($P < 0.05$) (Table 4).

Prevalence of ESBL and AmpC β-lactamase producing gram-negative isolates. Of the isolated enterobacteriacae, 41.7% (15/36) was found ESBL producers, 22.2% (8/36) were AmpC β-lactamase producers and 11.1% (4/36) of isolates were carbapenemase producer. In *Klebsiella* species, a high percentage of ESBL and Carbapenemase production were confirmed (31.6% and 15.8%, respectively) (Table 5).

Factors associated with culture-positive sputum among adult hospitalized patients community acquired pneumonia. Selected variables that are suitable for logistic regression analysis were subjected to bivariate and multivariate analyses (Table 6). In the bivariate logistic analysis's overall set of variables, six variables such as age, tobacco smoking status, history of pneumonia, history of antibiotic use, heart disease, and chronic respiratory disease were associated with sputum culture positivity at a P value <0.25. The multivariable logistic regression analysis included all the factors that were associated with sputum culture positivity at a P value <0.25 in the bivariate logistic regression analysis. Sputum culture positivity had a significant association with age 65 years (AOR: 4.11; 95% CI: 1.04 -16.27), tobacco smoking (AOR: 7.00; 95% CI: 1.36 -36.18), prior history of pneumonia (AOR: 6.58; 95% CI: 2.11-20.54), chronic heart disease (AOR: 3.01; 95% CI: 1.34 -7.97), and chronic respiratory disease (AOR: 4.04; 95% CI: 1.40 -11.67) (Table 6).

DISCUSSION

Pneumonia is among the leading causes of hospitalization and mortality in the world (3). Reduced occurrence of these consequences can be achieved through early diagnosis, awareness of the main bacterial etiologies, and understanding of the distribution of antibiotic resistance. As a result, this study was carried out to provide details on the bacterial etiological agents of pneumonia acquired in the community in hospitalized patients and its pattern of antibiotic resistance. In this investigation, hospitalized

Table 2. Gram-negative bacterial isolates' antibiotic resistance patterns from hospitalized patients with community acquired pneumonia in Jimma University Medical Center, Southwest Ethiopia, 2019.

List of Isolates	Pattern	Antibiotic resistance pattern (%)												
		TOB	CN	AMK	CAZ	CRO	FEP	AMC	CAF	SXT	CXM	AMP	CIP	MRP	DOX
Klebsiella spp. (19)	R	3 (15.8)	3 (15.8)	3 (15.8)	12 (63.2)	13 (68.4)	9 (47.4)	10 (52.6)	12 (63.2)	15 (78.9)	14 (73.7)	19 (100)	7 (36.8)	3 (15.8)	14 (73.9)
E. coli (6)	R	1 (16.7)	1 (16.7)	1 (16.7)	4 (66.7)	4 (66.7)	4 (66.7)	4 (66.7)	4 (66.7)	5 (83.3)	6 (100)	6 (100)	4 (66.7)	1 (16.7)	6 (100)
Citrobacter spp. (4)	R	1 (25)	1 (25)	0	4 (100)	4 (100)	3 (75)	2 (50)	3 (75)	4 (100)	4 (100)	4 (100)	2 (50)	0	3 (75)
Proteus spp. (2)	R	1 (50)	1 (50)	1 (50)	1 (50)	1 (50)	1 (50)	1 (50)	1 (50)	2 (100)	2 (100)	2 (100)	2 (100)	0	2 (100)
Enterobacter spp. (4)	R	2 (50)	2 (50)	0	3 (75)	4 (100)	3 (75)	3 (75)	2 (50)	3 (75)	4 (100)	NT	2 (50)	0	4 (100)
Serratia spp. (1)	R	0	0	0	1 (100)	1 (100)	1 (100)	1 (100)	1 (100)	1 (100)	1 (100)	1 (100)	1 (100)	0	1 (100)
P. aeruginosa (17)	R	6 (35.3)	4 (23.5)	5 (29.4)	15 (88.2)	17 (100)	15 (88.2)	15 (88.2)	14 (82.4)	17 (100)	NT	NT	9 (52.9)	5 (29.4)	NT
Acinetobacter spp. (7)	R	2 (28.6)	2 (28.6)	2 (28.6)	7 (100)	7 (100)	6 (85.7)	6 (85.7)	6 (85.7)	7 (100)	7 (100)	NT	5 (71.4	3 (42.6)	5 (71.4)
B. cepacia (2)	R	0	0	1 (50)	2 (100)	2 (100)	2 (100)	2 (100)	2 (100)	2 (100)	2 (100)	NT	2 (100)	2 (50)	2 (100)
H. influenzae (2)	R	NT	NT	NT	NT	1 (50)	0	0	0	1 (50)	1 (50)	2 (100)	0	0	2 (100)
Total (64)	R	16 (25.8)	14 (22.6)	13 (21)	49 (79.0)	54 (84.4)	44 (68.8)	44 (68.8)	45 (70.3)	57 (89.1)	41 (87.2)	34 (100)	34 (53.1)	14 (2.2)	39 (83)

Where: TOB-Tobramycin, CN-Gentamycin, CAZ-Ceftazidime, FEP-Cefepime, CAF-chloramphenicol, AMC-Amoxicillin-clavulanate, CRO-Ceftriaxone, CIP - Ciprofloxacin, MRP– Meropenem, AMP-Ampicillin, SXT-Trimethoprim-us, Doxy-Doxycycline, NT- not tested, spp: species, R-Resistant.

Table 3. Gram-positive bacterial isolates' antibiotic resistance patterns from hospitalized patients with community acquired pneumonia in Jimma University Medical Center, Southwest Ethiopia, 2019.

List of Isolates	Pattern	Antibiotics resistance pattern %									
		CN	CAF	TE	SXT	CIP	OXA	P	FOX	CLD	ERY
S. aureus (9)	R	3 (33.3)	6 (66.7)	7 (77.8)	8 (88.9)	2 (22.2)	NT	9 (100)	8 (88.9)	4 (44.4)	5 (55.6)
S. pneumoniae (7)	R	NT	5 (71.4)	4 (57.1)	6 (85.7)	NT	6 (85.7)	NT	NT	2 (28.6)	3 (42.8)
Total (16)	R	3 (33.3)	11 (68.8)	11 (68.8)	14 (87.5)	2 (22.2)	6 (85.7)	9 (100)	8 (88.9)	6 (37.5)	8 (50)

Where: CN-Gentamycin, CAF-Chloramphenicol, TE-Tetracycline, SXT-Trimethoprim-sulfamethoxazole, CIP-Ciprofloxacin, FOX-Cefoxitin, P-Penicillin, CLD-Clindamycin, and ERY- Erythromycin, OXA-Oxacillin, NT-not tested, spp. species, R-Resistant.

Table 4. Prevalence of multidrug-resistant bacterial isolates from hospitalized patients with community acquired pneumonia in JUMC, Southwest, Ethiopia, 2019.

Bacterial isolates	Level of resistance (number (%))									Total MDR isolates
	R0	R1	R2	R3	R4	R5	R6	R7	≥R8	≥R3 (%)
Klebsiella spp. (19)		1	7	1		4	3	1	1	10 (52.6)
E. coli (6)			2			1		1		4 (66.7)
Citrobacter spp. (4)			1	1		1	1			4 (100)
Proteus spp.						1			1	2 (100)
Enterobacter spp. (4)				1		1		2		4 (100)
Serratia spp.								1		1 (100)
P. aeruginosa (17)					3	3	4	2	3	15 (88.2)
Acinetobacter spp. (7)				1	2		1	1	2	7 (100)
B. cepacia									2	2 (100)
H. influenzae			1		1					1 (50)
S. aureus (9)					1	2	3	3		9 (100)
S. pneumoniae (7)		1	3	1	2					3 (42.9)
Total (80)										62 (77.5)

Where: R0: susceptible to all antibiotics, R1–R8: resistance to 1, 2, 3, 4, 5, 6, 7, and 8 classes of antibiotics, respectively, ≥R3: resistance to 3 or more classes of antibiotics, MDR: multidrug resistance

Table 5. Frequency of ESBL and Carbapenemase producing enterobacteriacae isolates from hospitalized patients with community acquired pneumonia in Jimma Medical Center, Southwest Ethiopia, 2019.

Isolates	ESBL+	AmpC+	ESBL & AmpC+	ESBL+ & ESBL & AmpC+	Carbapenemase producer
Klebsiella spp. (n = 19)	2 (10.5%)	0	4 (21.1%)	6 (31.6%)	3 (15.8%)
E. coli (n = 6)	2 (33.3%)	0	1 (16.7%)	3 (50%)	1 (16.7%)
Enterobacter spp. (n = 4)	2 (50%)	1 (25%)	0	2 (50%)	0
Proteus spp. (n = 2)	1 (50%)	0	1 (50%)	2 (100%)	0
Citrobacter spp. (n = 4)	1 (25%)	0	1 (25%)	2 (100%)	0
Serratia spp. (n = 1)	0	0	0	0	0
Total (n = 36)	8 (22.2%)	1 (2.7%)	7 (19.4%)	15 (41.7%)	4 (11.1%)

Where: ESBL+: Extended beta-lactamase positive Spp.: species.

Table 6. Sputum culture positivity among hospitalized patients with community-acquired pneumonia in JUMC, southwest, Ethiopia, 2019: a bivariate and multivariable analysis of the variables.

Variables		Culture result		COR (95% CI)	AOR (95% CI)	P-value
		Negative (%)	Positive (%)			
Age, year	18-35	35 (46.7)	20 (26.7)	1		
	36-49	24 (32)	22 (29.3)	1.60 (0.72-3.56)	0.89 (0.34-2.32)	0.804
	50-64	12 (16)	15	2.19 (0.86- 5.58)	1.12 (0.34-3.65)	0.850
	>65	4 (5.3)	18 (24)	7.87 (2.44-26.54)	4.11 (1.04-16.27)	0.044*
Sex	Female	41 (54.7)	38 (50.7)	1		
	Male	34 (45.3)	37 (49.3)	1.17 (0.62-2.23)		
Residence	Urban	33 (44)	31 (41.3)	1		
	Rural	42 (56)	44 (58.7)	1.12 (0.58-2.13)		
Tobacco smoking status						
	No	73 (97.3)	57 (76)	1		
	Yes	2 (2.7)	18 (24)	11.53 (2.57-51.73)	7.00 (1.36-36.18)	0.020*
Alcohol consumption						
	No	69 (92.0)	64 (85.3)	1		
	Yes	6 (8.0)	11 (14.7)	1.98 (0.69-5.65)		
Previous history of pneumonia						
	No	70 (93.3)	46 (61.3)	1		
	Yes	5 (6.7)	29 (38.7)	8.83 (3.19-24.46)	6.58 (2.11-20.54)	0.001*
History of Antibiotic use						
	No	28 (37.3)	12 (16)	1	1	
	Yes	47 (62.7)	63 (84)	3.13 (1.44-6.77)	2.47 (0.95-6.44)	0.063
Renal disease						
	No	62 (82.7)	57 (76)	1		
	Yes	13 (17.3)	18 (24)	1.51 (0.68-3.45)		
Chronic heart disease						
	No	66 (86)	52 (69.3)	1		
	Yes	9 (14)	23 (30.7)	3.24 (1.38-7.64)	3.01 (1.34-7.97)	0.026*
Chronic respiratory disease						
	No	67 (89.3)	52 (69.3)	1	4.04 (1.40-11.61)	0.010*
	Yes	8 (10.7)	23 (30.7)	3.70 (1.53-8.95)		
HIV/AIDS						
	NO	61 (81.3)	62 (82.7)	1		
	Yes	14 (18.7)	13 (17.3)	0.91 (0.39-0.21)		
Diabetes						
	NO	63 (84)	65 (86.7)	1		
	Yes	12 (16)	10 (13.3)	0.81 (0.34-2.00)		

Where: COR: Crude odds ratio, AOR: Adjusted odds ratio, CI: Confidence interval, Chronic respiratory disease: COPD + Asthma + Bronchiectasis, *: statically significant

patients had a 50% prevalence of culture-confirmed community-acquired bacterial pneumonia, which is comparable to the 50.4% study finding from Egypt (23) and lower than study finding reported in Nigeria at 81.5% (24). But this finding was higher than studies reported in Sri Lanka 29.4% (25) and Philippines 40.0% (26). This study found was also higher than previous studies' findings published on bacterial etiology of community-acquired pneumonia among adult outpatients in Ethiopia, ranging from 32.1% -45.0% (13-16). The variation in study population, geographic area, sample size and type, differences

in specific methodologies and diagnostic methods, mean duration of hospital exposure, and prior antibiotic use may all contribute to the difference in the prevalence of aetiology of community acquired pneumonia in various studies.

In this study, 80% of the isolates were Gram-negative bacilli. The most frequently isolated bacteria were *Klebsiella* spp. (22.3%) and *P. aeruginosa* (21.4%) (Fig. 1), which was comparable to other studies reported from China, the most common pathogen was *Acinetobacter baumannii, Klebsiella* spp, *P. aeuruginosa* (27), whereas the most isolated organism in Nigeria were *Streptococcus pneumoniae* followed by *Klebsiella pneumoniae* and *Staphylococcus aureus* (24). On the other hand, the commonly prevalent bacterial isolates in other studies conducted in different geographical regions of Ethiopia and elsewhere in the world were *S. pneumoniae, Klebsiella* spp., *S. aureus* and *Pseudomonas* species (13-16, 28). These high rates of gram-negative bacterial etiologies of community acquired pneumonia in current study might be explained by previous use of antibiotics and its consequent selective pressure, patient type (many of study participants had chronic disease), and diagnostic methods.

In this study, a high antibiotic resistance rate was observed with most groups of tested antibiotic with a multidrug resistance rate of 77.5% of isolates (Tables 2, 3, and 4). Frequently isolated *Klebsiella* spp. showed resistance ranging from 68.4% to 47.4% to third and fourth-generation cephalosporins, and 73.9% to doxycycline. The ceftriaxone resistance rate in this study (84.4%) was higher than in previous studies reported in Ethiopia, ranging from 13.2-19.4%. We also noticed that 88.9% of isolated *S. aureus* were MRSA. This MRSA rate was also higher than previous studies in Ethiopia (13-15, 24). This high resistance might be due to the regular use of these antibiotics that have been prescribed frequently, which contributes to the development of drug resistance through time. In addition, the difference between the different studies could be the fact that our study subjects were hospitalized patients and commonly with underlying diseases. But the MDR resistance rate was lower than the rate of antibiotic resistance patterns of bacterial isolates among patients with lower respiratory tract infection reported in the same study setting by Mussema et al. 93.8% of the isolates were MDR and the resistance rates of gram-negative bacterial isolates were ranged from 88% to 80% to third and fourth-generation cephalosporin's (18). This might be as a result of exposure to beta lactam medications repeatedly during recurrent exacerbations.

In this study, the magnitude of ESBL and carbapenemase producing enterobacteriacae were 41.7% (15/36) and 11.1% (4/36) (Table 5), respectively. The resistance for these β-lactam antibiotics due to the production of β-lactamases is becoming a worldwide problem. These can be developed when bacterial gene mutate continuously in response to overuse or misuse of β-lactam antibiotics (18, 29). In this study, the magnitude of ESBLs production was in agreement with study reported in Jimma Ethiopia 40.4% (30), higher than study reported in Addis Ababa Ethiopia 57.7% (31) and Nigeria 58.0% (32), and higher than study finding reported in Nepal 28.1% (33). Concerning to carbapenemase resistance, this study finding was lower than study reported in Jimma Ethiopia 28% (18) and in India, 85% of LRTI isolates were carbapenem resistant (34). These heterogeneity could be brought about by variations in the study population, specimen type, number of samples collected, level of consumption of antibiotics, and methods for identification. Moreover, variation in resistance to antibiotics might be due to difference in availability and owing to little use of them.

High resistance to these commonly recommended antibiotics might be due to irrational use of antibiotics and self-medication of these drugs in community and hospital settings. Moreover, prior use of antibiotics had significant association with MDR pattern of the bacterial isolates (Table 7). This result also might be highlights a lack of antimicrobial stewardship and effective infection control practices in the study area in particular.

In Ethiopia, there are indications of misuse of antibiotics in and out of hospital settings. These, together with the rapid spread of resistant bacteria and poor surveillance system, contributed to the problem of AMR (35). In addition, a recent systematic review reports on bacterial infection in Ethiopia indicated that most bacterial isolates were resistant to widely used antibiotics (36). Hence, antibiotic resistance is an important clinical concern in our country, which demands tireless efforts to rationalize antibiotic use in and out -of-hospital settings.

In addition, according to this study, finding, aging ≥65 years (AOR: 4.11; 95% CI: 1.04-16.27), tobacco smoking (AOR: 7.00; 95% CI: 1.36-36.18), previous

Table 7. Association between multidrug-resistant bacterial isolation and a history of antibiotics use from a sputum samples among hospitalized patients with community acquired pneumonia in Jimma Medical Center, Ethiopia, 2019.

Variable	Categories	MDR		Odds ratio (95% CI)	P-value
		Yes	No		
Bacterial isolates from patient with a history of antibiotic use	Yes (68)	56	12	4.7 (1.3-16.9)	P = 0.019
	No (12)	6	6	1	

history of pneumonia (AOR: 6.58; 95% CI: 2.11-20.54), chronic heart disease (AOR: 3.01; 95% CI: 1.34-7.97), and Chronic respiratory disease (AOR: 4.04; 95% CI: 1.40-11.67) were significantly associated with sputum culture positivity (Table 6). This finding is consistent with different studies reported in the different part of the world (13-16, 37-39).

There is sufficient data to conclude that advancing age is a significant risk factor that is directly related to aging-related physiological changes and a higher prevalence of chronic diseases. Elderly people are more susceptible to CAP due to changed lung defense systems such as impaired mucociliary clearance, impaired alveolar defense, inefficient coughing, and swallowing difficulties (40, 41).

Impaired left ventricular performance with heart failure may all help to explain the association between chronic heart disease and CAP (42). In addition, persistent mucus production, physiological changes that impair host immunity, the presence of potentially pathogenic bacteria in the airways, infection, and chronic respiratory disease patients may be more likely to develop pneumonia than healthy people (38, 43).

Limitations of the study. The proportion of culture confirmed pneumonia might be under estimated since prior antibiotic therapy affects the recovery of some bacterial etiologies. Contrary, specimen passes through URT where a lot of contaminants are there, so despite we use sputum validity criteria to overcome the problem, still some of the isolates might be a contaminant. Although combinations of different classes of antibiotics were tested, newer beta-lactamase inhibitors and fluoroquinolones, were not tested. Even though this study focused on hospitalized patients, unlike other Ethiopian studies done on outpatients, this study used a limited sample size due to limited resources. In the last, the study was only conducted at JUMC, therefore the data acquired there might not be typical of all Ethiopian adults who were hospitalized for pneumonia.

CONCLUSION

A comparable culture positive rate was reported in this study with predominant bacterial etiologies of *Klebsiella* spp., *P. aeruginosa*, and *S. aureus.* Many of the isolated bacteria were MDR's and ESBL producers. The prior antibiotic exposure were found to be highly associated with the MDR pattern. Thus, proper management of patients with pneumonia in the setting should put these and other identified factors into consideration. Additionally, regular monitoring of pneumonia etiologies and their antibiotic susceptibility pattern is necessary to raise the standard of therapy and to rationalize antibiotic use in and out -of-hospital settings.

ACKNOWLEDGEMENTS

We would like to thank Jimma University for providing the ethical approval necessary to conduct this study. Additionally, we are appreciative of the data collectors and study participants who voluntarily took part in the investigation.

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