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Prevalence and antibiotic resistance of bacterial pathogens in respiratory tract samples of geriatric patients

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The ethics approval was obtained from the Non-Interventional Clinical Research Ethics Committee of Karabuk University; No: 2021/452. All procedures in this study involving human participants were performed in accordance with the 1964 Helsinki Declaration and its later amendments.

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Abstract

Background/Aim: The frequency and severity of respiratory tract infections increase with aging. The aim of this study was to determine the bacterial profile of respiratory tract samples in geriatric patients and evaluate the antibiotic susceptibility patterns of the pathogens.

Methods: In this cross-sectional study, a total of 509 clinical samples which were obtained from 302 geriatric patients over 65 years of age and sent to the microbiology laboratory between June 2019-January 2021 were investigated retrospectively. The identification and antibiotic susceptibilities of strains were evaluated with BD-Phoenix-100 fully automated microbiology system.

Results: Of the 302 geriatric patients, 166 (%55) were males and 136 (%45) were females. The most isolated pathogens were *Klebsiella pneumoniae* (25.3%) *Pseudomonas aeruginosa* (22.5%) and *Acinetobacter baumannii* (10.2%), *Corynebacterium striatum* (7.3%), *Escherichia coli* (6.4%), *Staphylococcus aureus* (6.4%) and coagulase-negative staphylococci (4.2%). The production of ESBL in *Klebsiella pneumoniae* strains (52.3%) was higher than in *Escherichia coli* (41%) strains. All *Corynebacterium striatum* samples were resistant to ciprofloxacin, tetracycline, rifampin, and penicillin. Methicillin resistance among *Staphylococcus aureus* (MRSA) isolates was 22.7% and they were 100% susceptible to vancomycin and teicoplanin. Above 90% of *K. pneumoniae*, *P. aeruginosa* and *A. baumannii* positive patients were hospitalized in intensive care units ($P<0.05$). The tobramycin-resistant *E. coli* and colistin-resistant A. *baumannii* rates were highest between 85-99 years of age ($P<0.05$).

Conclusion: K. *pneumoniae*, *P. aeruginosa* and *A. baumannii* were the most common pathogens in respiratory tract samples in geriatric patients, especially those hospitalized in the intensive care units. The antimicrobial resistance rates were higher in patients aged ≥85 years. Vancomycin and teicoplanin were the most effective antibiotics against MRSA. It is thought that the results will be useful in the preparation of treatment protocols and guiding physicians about the correct use of antibiotics.

Keywords: Antibiotic resistance, Geriatric patients, Respiratory tract samples

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Introduction

The World Health Organization has determined the age of 65 and above as 'old age' and, the United Nations has agreed that 60+ years may be denoted as 'old age' [1]. Elderly people are more susceptible to disease, syndromes, injuries, and sickness than adults. In addition, the atypical symptoms pose a diagnostic challenge in the elderly [2].

Respiratory tract infections are the most common cause of antibiotic use and the main causes of morbidity and mortality worldwide. The frequency and severity of respiratory tract infections increase with aging. Respiratory tract infections and pneumoniae accounted for nearly half of all infection-related hospitalizations in elderly individuals [3]. Many different groups of microorganisms can cause respiratory tract infections. The most common causative bacteria are *Streptococcus pneumoniae*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Haemophilus influenzae*, *Moraxella catarrhalis* and *Streptococcus pyogenes* [4, 5]. Also, extended spectrum beta-lactamase (ESBL) producing and carbapenem-resistant *Enterobacterales*, methicillin-resistant *Staphylococcus aureus* (MRSA), vancomycin-resistant enterococci species and multi-drug-resistant *Acinetobacter baumannii* are associated with both nosocomial and community-acquired infections. Multidrug-resistant *Acinetobacter baumannii*, *Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and *Enterobacter* species have become major concerns at hospital settings worldwide [5, 6].

Determining of the common pathogens that cause such infections and the patterns of resistance to existing antimicrobial drugs is crucial for defining therapeutic strategies. Bacterial pathogens responsible for respiratory tract infections and antibiotic resistance may vary by country, regions of the country, hospital, clinics and even clinic wards. Therefore, local surveillance data are required, which include detailed analysis of etiological factors [7].

The aim of this study was to determine the etiological agents causing respiratory tract infections in geriatric patients and evaluate the antibiotic susceptibility patterns of the pathogens, which would provide information to optimize accurate timely diagnosis, and treatment of the elderly patients.

Materials and methods

In this study, 509 respiratory tract samples obtained from 302 geriatric patients over 65 years of age and sent to the microbiology laboratory from various clinics such as the Intensive Care Unit, Chest Diseases, Internal Medicine, Palliative Care, Cardiology, Medical Oncology, General Surgery, Neurology, etc. in Karabuk University Training and Research Hospital between June 2019-January 2021 were investigated retrospectively. The other clinical samples test results, repeated patient results and the patients <65 years of age were excluded from this study. These results were obtained from the laboratory information system.

Clinical samples, including endotracheal aspirate (ETA), sputum, and bronchoalveolar lavage (BAL) were cultured on 5% sheep blood agar (RTA laboratories, Kocaeli, Turkey), Eosin Methylene Blue agar (EMB) (RTA), and Chocolate Agar (RTA) and incubated aerobically at 37°C for 24-48 hours.

The identification and antibiotic susceptibility of strains were determined with the BD/Phoenix-100 (Becton Dickinson, USA) automated system. Antibiotic susceptibility test results were evaluated as per EUCAST (The European Committee on Antimicrobial Susceptibility Testing) guidelines and the production of the ESBL (extended spectrum beta lactamase) enzyme was determined using the combined disk diffusion method [8]. The *E. coli* ATCC 25922, *S. aureus* ATCC 25923, and *P. aeruginosa* ATCC 27853 were used as quality control strains.

Statistical analysis

Data were analyzed using Statistical Package for the Social Sciences (SPSS for IBM-PC 20.0; SPSS Inc., USA). Descriptive statistics were stated as number (n), percentage (%), and median value. The Kolmogorov–Smirnov test was used to determine whether the variables were normally distributed. For the comparison of continuous variables, the two-sample t-test was used. The Pearson's Chi-squared test or Fisher's Exact test was used for comparison of categorical variables if applicable. A probability (*P*) value of <0.05 was considered statistically significant at 95% confidence interval.

Results

A total of 302 geriatric patients comprising 166 (%55) males and 136 (%45) females were included in the study. All the patients were >65 years of age and the median age of the patients was 79 (65-99) years.

In our study, 302 outpatients and inpatients were investigated, 84.4% (255/302) of which were hospitalized in the Intensive Care Unit, 7.9% (24/302), in Chest Diseases, 2.6% (8/302), in Internal Medicine, 2.3% (7/302), in Palliative Care, and 26 % (8/302) in Cardiology, Medical Oncology, General Surgery, Neurology, etc. A total of 509 clinical samples were examined, including 80% (410/509) endotracheal aspirates (ETA), 11% (53/509) sputum samples, 9% (46/509) bronchoalveolar lavage (BAL).

In 500 (98%) of 509 samples, pathogenic microorganisms were detected. No growth was observed in 9 samples (1.8%). Most isolated pathogens were Gram negative bacteria (68%, n=339), and the rate of Gram-positive bacteria was lower (20%, n=102). In the present study, 35 different pathogenic bacteria were isolated, and more than one microorganism growth was detected in 82 (27.1%) patients. The most isolated pathogens were *Klebsiella pneumoniae* (25.3%) *Pseudomonas aeruginosa* (22.5%) and *Acinetobacter baumannii* (10.2%), *Corynebacterium striatum* (7.3%), *Escherichia coli* (6.4%), *Staphylococcus aureus* (6.4%) and coagulase- negative staphylococci (CNS) (4.2%). The prevalence and distribution of the samples according to the isolated pathogens is shown in Table 1.

K. pneumoniae, *P. aeruginosa* and *A. baumannii* positivity were 93.4%, 92.9% and 90%, respectively, among patients hospitalized in the Intensive Care Units. The distribution of *K. pneumoniae*, *P. aeruginosa* and *A. baumannii* positivity was examined according to clinics, which revealed that above

90% of positive patients were hospitalized in the intensive care units (P<0.05).

Table 1: The distribution of the samples according to the isolated pathogens

Pathogens	ETA		Sputum		BAL		TOTAL	
	n	%	n	%	n	%	n	%
Klebsiella pneumoniae	116	91.5	6	4.4	5	4.1	127	25.3
Pseudomonas aeruginosa	94	84	9	7.7	9	8.3	112	22.5
Acinetobacter baumannii	41	79.7	3	6.8	7	13.4	51	10.2
Corynebacterium striatum	34	94.1	1	1.3	2	4.6	37	7.3
Escherichia coli	21	67.1	8	24.9	3	8	32	6.4
Staphyloccocus aureus	30	92.4	-	-	2	7.6	32	6.4
*CNS**	14	66.6	4	16.9	3	16.5	21	4.2
Entorobacter cloacae	7	51.5	2	16.4	5	32.2	14	2.9
Klebsiella oxytoca	7	63.6	-	-	4	36.4	11	2.3
Serratia marcescens	6	85.7	1	14.3	-	-	7	1.4
Stenotophomonas maltophilia	5	83.3	1	14.3	1	14.3	7	1.4
Burkhoderia cepacia	6	85.7	1	14.3	-	-	7	1.4
Enterobacter aerogenes	6	85.7	1	14.3	-	-	7	1.4
Citrobacter spp.	5	83.3	-	-	1	16.7	6	1.3
Enterococcus faecalis	2	66.6	1	33.3	-	-	3	0.6
Candida albicans	1	33.3	1	33.3	1	33.3	3	0.6
Other *Corynebacterium spp.*	2	66.6	1	33.3	-	-	3	0.6
Chryseobacterium indologenes	2	100	-	-	-	-	2	0.4
Achromobacter spp.	2	100	-	-	-	-	2	0.4
Gamella haemolysans	-	-	2	100	-	-	2	0.4
Leuconostoc spp.	2	100	-	-	-	-	2	0.4
Other *Candida spp.*	1	50	1	50	-	-	2	0.4
Streptococcus acidominimus	-	-	2	100	-	-	2	0.4
Sphingomonas paucimobilis	-	-	-	-	2	100	2	0.4
Providencia stuartii	1	100	-	-	-	-	1	0.2
Entorobacter gergoviae	1	100	-	-	-	-	1	0.2
Streptococcus agalactiae	1	100	-	-	-	-	1	0.2
Delfia acidovorans	1	100	-	-	-	-	1	0.2
Enterococcus faecium	-	-	1	100	-	-	1	0.2
Moraxella catarrhalis	1	100	-	-	-	-	1	0.2
TOTAL	409	81.8	46	9.2	45	9	500	100

CNS*: coagulase-negative staphylococci, ETA: endotracheal aspirate, BAL: bronchoalveolar lavage

Antibiotic susceptibility test was performed on all the samples with pathogenic microorganism growth, and antibiotic resistance was detected in 50.4% (252/500). The pathogen with the highest antibiotic resistance was *K. pneumonia,* and it was mostly resistant to ciprofloxacin (95%) and amikacin (93.4%) (P<0.05). The second highest antibiotic resistance was found in *P. aeruginosa* against Levofloxacin (43%) and Cefepime (38%) (P>0.05). The third highest antibiotic resistance was against Ertapenem (100%), Tobramycin (100%) and Levofloxacin (95%), found in *A. baumannii* (P<0.05). Colistin resistance of *K. pneumoniae* and *A. baumanni* isolates were 24% and 5.1%, respectively. The antibiotic resistance profiles of the most isolated pathogens are shown in Table 2.

All *C. striatum* samples were resistant to ciprofloxacin (100%), tetracycline (100%), rifampin (100%), penicillin (98.2%) and clindamycin (82%), but susceptible to vancomycin and linezolid (P<0.05) (Table 2).

The rates of antibiotic resistance of *E. coli* to ciprofloxacin, TMP-SMX, gentamicin, and piperacillin-tazobactam were 92%, 62%, 22%, and 14%, respectively. The production of ESBL in *E. coli* strains was 41%. The production of ESBL in *K. pneumoniae* strains (52.3%) was a bit higher than that in E. coli (41%) strains (P>0.05).

Among *Staphylococcus aureus* isolates, 22.7% were methicillin-resistant (MRSA). MRSA isolates were 100% sensitive to vancomycin and teicoplanin (P<0.05).

The antimicrobial resistance results of the predominant organisms were investigated by age groups. Tobramycin-resistant *E. coli* and Colistin-resistant *A. baumannii* rates were highest between 85-99 years of age (P<0.05). Antimicrobial resistance results for the predominant organisms by age group are shown in Table 3.

Table 2: The antibiotic resistance profiles of the most isolated six pathogens

%	*Klebsiella pneumoniae* (n:127)	*Pseudomonas aeruginosa* (n:112)	*Acinetobacter baumannii* (n:51)	*Corynebacterium striatum* (n:37)	*Escherichia coli* (n:32)	*Staphylococcus aureus* (n:32)	*P*-value
AK	77.1*	6	79	0	4	4	0.03
AX	-	-	-	-	74	-	NA
AMC	93.4	-	-	0	-	-	NA
AM	100	-	-	0	92.5	-	0.73
SAM	97	-	-	-	65.3	-	0.46
FEP	92.3	36.2	-	-	65.3	-	0.54
CAZ	92.3	36	-	-	63	-	0.67
CRO	93.4	-	--	-	78	-	0.63
CXM	93.4	-		-	85	-	0.60
CIP	95*	34.2	95	100*	92.5	4	0.02
DA	-	-	-	74.5	-	19.2	0.57
CT	23	5.3	5.1	-	0	-	0.42
DAP	-	-	-	14.2	-	-	NA
E	-	-	-	25	-	23	0.73
ETP	77	-	100*	-	0	-	0.01
FF	-	-	-	0	0	0	0.01
FA	-	-	-	0	-	11.5	0.34
CN	80.4	16	89.3	82.2*	22.2	8	0.04
IPM	61.1	43	90.4	-	-	-	0.62
LEV	91.3	43.2	95*	14.2	92.5	4	0.02
LNZ	-	-	-	0	-	-	NA
MEM	64	34.5	91	-	0	-	0.65
MXF	-	-	-	0	-	4	0.31
OX	-	-	-	0	-	31	0.52
P	-	-	-	98.2*	-	85	0.03
TPZ	87	35.3	-	-	15	-	0.72
RA	-	-	-	100*	-	5.2	0.03
TE	55	-	-	100*	-	27	0.04
TOB	-	-	100*	-	-	-	0.02
SXT	83	-	77.3	33.3	63	11.5	0.47
TGC	-	-	7.1	-	-	-	NA
VA	-	-	-	0	-	-	NA

AK: Amikacin, AX: Amoxicillin, AMC: Amoxicillin/ Clavulanic acid, AM: Ampicillin, SAM: Ampicillin/Sulbactam, FEP: Cefepime, CAZ: Ceftazidime, CRO: Ceftriaxone, CXM: Cefuroxime, CIP: Ciprofloxacin, DA: Clindamycin, CT: Colistin, DAP: Daptomycin, E: Erythromycin, ETP: Ertapenem, FF: Fosfomycin, FA: Fusidic acid, CN: Gentamicin, IPM: İmipenem, LEV: Levofloxacin, LNZ: Linezolid, MEM: Meropenem, MXF: Moxifloxacin, OX: Oxacillin, P: Penicillin, TPZ: Piperacillin +Tazobactam, RA: Rifampin, TE: Tetracycline, TOB: Tobramycin, SXT: Trimethoprim + Sulfamethoxazole, TGC: Tigecycline, VA: Vancomycin; *P<0.05, NA: Not applicable

Table 3: Antimicrobial resistance results for the predominant organisms by age group

	Antimicrobial susceptibility by age group[a]								
	65-74 years old			75-84 years old			85-99 years old		
Pathogen organisms (EUCAST criteria)	n	R (%)	S (%)	n	R (%)	S (%)	n	R (%)	S (%)
Klebsiella pneumoniae	38			48			41		
AK		71.4	28.6		74.3	25.7		86.2	13.8
AMC		96.4	3.6		91.4	8.6		93.1	6.9
AM		100	-		100	-		100	-
SAM		100	-		91.4	8.6		100	-
FEP		96.4	3.6		85.7	14.3		96.6	3.4
CAZ		96.4	3.6		88.6	11.4		93.1	3.4
CRO		96.4	3.6		88.6	11.4		96.6	3.4
CXM		96.4	3.6		88.6	11.4		96.6	3.4
CIP		96.4	3.6		91.4	8.6		96.6	3.4
CT		33.3	-		13.8	-		25.9	3.7
9.8ETP		78.7	14.9		77.8	15.9		74.5	13.8
CN		75	25		80	20		86.2	24
IPM		65.2	13		63.9	27.9		54	3.4
LEV		92.9	3.6		88.6	8.6		93.1	3.4
MEM		69.6	21.7		67.2	24.1		54	24
TPZ		89.3	7.1		80	17.2		93.1	6.9
TE		82.1	17.9		77.1	22.9		89.7	6.9
SXT		52.9	11.8		66.7	8.3		43.5	4.3
Pseudomonas aeruginosa	28			38			46		
AK		10.8	89.2		8	88		11.3	82.3
FEP		50	50		22	78		45.2	54.8
CAZ		52.6	47.4		24	76		35.5	64.5
CIP		29.7	67.6		30	70		40.3	59.7
CT		6.5	-		2.3	6.8		7.3	-
CN		18.4	81.6		10.6	89.4		17.7	80.6
IPM		56.4	40		40.5	59.5		36.4	56.8
LEV		50	50		42	58		40.3	59.7
MEM		55.6	38.9		30.7	49.3		25.3	51.6
TPZ		52.6	47.4		20	80		37.1	62.9
Acinetobacter baumannii	11			16			24		
AK		88.9	11.1		100	-		80	20
CIP		100	-		100	-		100	-
CT		-	-		-	10		6.7*	6.7
ETP		-	-		100	-		100	-
CN		77.8	22.2		85.7	14.3		95	5
IPM		81.3	6.3		95.8	-		94.9	-
LEV		100	-		100	-		100	-
MEM		81.3	6.3		100	-		94.6	-
TOB		-	-		100	-		-	-
SXT		100	-		78.6	7.1		85	15
Corynebacterium striatum	11			15			11		
CIP		100	-		100	-		100	-
DA		76.5	23.5		76.2	23.8		70.6	23.5
DAP		50	-		-	-		-	-
CN		89.5	5.3		75	25		84.2	10.5
LNZ		-	100		-	100		-	94.4
P		100	-		100	-		94.4	5.6
RA		100	-		100	-		100	-
TE		100	-		100	-		100	-
SXT		-	-		50	50		-	-
VA		-	100		-	100		-	100
Escherichia coli	13			6			13		
AK		9.1	90.9		-	100		-	100
AX		81.8	18.1		80	20		63.6	27.4
AM		90.9	9.1		80	20		100	-
SAM		72.7	27.3		80	20		50	50
FEP		54.5	45.5		40	40		90	10
CAZ		63.6	27.3		40	60		72.7	9.1
CRO		63.6	36.4		60	40		100	-
CXM		81.8	18.1		60	40		100	-
CIP		81.8	9.1		100	-		100	-
CT		-	20		-	33.3		-	11.1
ETP		-	92.9		-	100		-	100
FF		-	-		-	-		-	100
CN		27.3	72.7		20	80		18.1	81.8
IMP		-	92.9		-	100		-	100
LEV		81.8	9.1		100	-		100	-
MEM		-	92.3		-	100		-	100
TPZ		18.1	63.6		20	40		9.1	72.7
TOB		-	-		-	-		100*	-
SXT		63.6	36.4		80	20		54.5	45.5
TGC		-	50		-	-		-	-
Staphylococcus aureus	5			16			11		
AK		-	100		7.7	92.3		-	100
CIP		-	100		7.7	92.3		-	100
DA		25	75		23.1	76.9		11.1	88.9
DAP		-	100		-	100		-	100
E		50	50		23.1	76.9		11.1	88.9
FF		-	100		-	100		-	100
FA		-	100		15.4	84.6		11.1	88.9
CN		-	100		15.4	84.6		-	100
LEV		-	100		7.7	92.3		-	100
LNZ		-	100		-	100		-	100
MXF		-	100		7.7	92.3		-	100
OX		25	75		30.8	69.2		33.3	66.7
P		50	50		84.6	15.14		100	-
RA		-	66.6		10	-		-	-
TEL		-	100		-	100		-	100
TE		25	75		30.8	69.2		22.2	77.8
SXT		-	100		7.7	92.3		22.2	77.8
VA		-	100		-	100		-	100

S: susceptible, R: resistant, *P<0.05, [a] Antimicrobial resistance was presented as % S and % R

Discussion

Respiratory tract infections are the most common diseases in the elderly and age is a major risk factor for both occurrence and severity of respiratory tract infections. There is insufficient data on the distribution and antimicrobial susceptibility rates of bacterial pathogens that cause respiratory tract infections. Therefore, determining common pathogens and their antimicrobial resistance profiles is crucial. In our study, the most isolated pathogens were Gram-negative bacteria (68%). Premalatha et al. [9] investigated 110 geriatric patients (>65 years) with lower respiratory tract infections and reported 60% Gram-negative bacilli and 9.1% Gram-positive cocci. *K. pneumoniae* (36.8%) was the most frequent pathogen, followed by *P. aeruginosa* (22.3%) and *A. baumannii* (11.8%). In the randomized study by Khattab et al. [10], *K. pneumoniae*, *P. aeroginosa* and *Acinetobacter spp*. were the most common organisms, followed by Methicillin-resistant *Staphylococcus aureus* and *E. coli* in lower respiratory tract infections. In the present study, in line with literature, the most isolated pathogens were *K. pneumoniae, P. aeruginosa, A. baumannii, C. striatum, E. coli* and *S. aureus* in geriatric patients with respiratory tract infections [9-11]. Moreover, above 90% of K. *pneumoniae, P. aeruginosa* and *A. baumannii* positive patients were hospitalized in the intensive care units. The most common nosocomial pathogens in respiratory tract infections are seen among intensive care unit patients and in geriatric hospitals [10-12].

Antibiotic resistance is an important health problem all over the world. It is known that long-term hospitalization and use of antibiotics increase the risk of emergence of multi-resistant microorganisms. Multidrug resistant Gram-negative bacteria studies have focused on *K. pneumoniae, E. coli* (ESBL, carbapenemase), *A. baumannii* and *P. aeruginosa*. In our study, *K. pneumoniae* (52%) was the most common pathogen and a potent ESBL producer and had the highest antibiotic resistance. In many studies, *K. pneumoniae* was the predominant ESBL producing organism, similar to our study [10-12]. Mu et al. [12] reported that 39 strains (31%) out of the total 126 isolates of *K. pneumoniae* were ESBL producers. *K. pneumoniae* and *E. coli* were the second highest ESBL producer strains with 41%. Lin et al. [13] investigated the ESBL producing *Enterobacterales* isolates in geriatric patients in respiratory care wards. They found that the prevalence of ESBL-producing isolates of *K. pneumoniae* and *E. coli*. were 69.7% and 39.5%, respectively. The studies suggest that the prevalence of ESBL worldwide in both *E. coli* and *K. pneumoniae* is markedly increasing and the risk factors for ESBL producing are exposure to antibiotic therapy, age, and length of hospitalization [14-16].

According to the results of National Antimicrobial Resistance Surveillance 2016 data in Turkey [17], multi-drug resistance was calculated as 83.5% in invasive *Acinetobacter* spp. isolates, and colistin resistance was 6.7%. In our study, carbapenem resistance was around 93% and colistin resistance was lower than the country average (5.1%) among *A. baumannii* isolates. Altay et al. [18] investigated the etiologic agents and their antimicrobial resistances in patients with respiratory tract infections in Turkey and found that the carbapenem resistance was around 40% among *K. pneumoniae* isolates. According to the results of surveillance in 2016 in Turkey [17], multi-drug resistance was 46.1% in invasive *K pneumoniae* isolates, and carbapenem resistance was 40%. Our results were higher compared to those in the literature, with 65% carbapenem resistance in *K. pneumoniae* isolates.

Corynebacterium striatum has been increasingly reported as an infectious agent in patients with long-term hospitalization. Formerly, it was susceptible to many drugs, but it has recently demonstrated high-level resistance to antibiotics such as macrolides, aminoglycosides etc. [19]. The increase in antimicrobial resistance of *C. striatum* is a great concern. Asgin et al. [20] investigated antimicrobial resistance and molecular epidemiology of 81 *C. striatum* strains and they reported that all *C. striatum* strains were resistant to penicillin, cefotaxime, ciprofloxacin, and tetracycline, but susceptible to vancomycin and linezolid. Similarly, in the present study, *C. striatum* showed resistance against most used antibiotics. All *C. striatum* samples were resistant to ciprofloxacin, tetracycline, rifampin, and penicillin, but susceptible to vancomycin and linezolid. Therefore, according to our antibiotic susceptibilities results, linezolid and vancomycin may be selected for the treatment of *C. striatum* infections.

One of the most well-known cases of antimicrobial resistance, Methicillin resistance in *Staphylococcus aureus* (MRSA), has been associated with high mortality rates every year [21]. According to National Antimicrobial Resistance Surveillance System 2016 data, MRSA in *S. aureus* isolates rate was 23.6% in Turkey [17]. EARS-Net 2016 [22] reported that the average rate of MRSA in *S. aureus* isolates is 13.7% in the European Union countries. Akgün and Sayıner [23] investigated 320 coagulase-positive *S. aureus* which were cultured from patients hospitalized in the intensive care unit and reported that the rate of MRSA in *S. aureus* isolates was 20.9% in Turkey. Khattab et al. [10] isolated 8.1% MRSA among the total isolates. They were 100% sensitive to vancomycin and teicoplanin. The present study agrees with the literature: Our rate of MRSA isolates was 22.7% and MRSA isolates were 100% sensitive to vancomycin and teicoplanin [9, 10, 13].

Age was significantly associated with differences in antimicrobial resistance for many pathogenic organisms [25, 26]. Adam et al. [26] investigated the association between age groups (children, adults, and the elderly) and antimicrobial resistance in the most identified pathogens. They reported that resistance rates are often higher among the elderly. In the present study, antimicrobial resistance rates were higher in patients >85 years of age. This may be associated with increased exposure to antimicrobial resistant organisms in long-term care facilities and frequent hospitalizations or high rate of multidrug resistance.

In the coming years, compared to non-resistant bacteria, resistant forms are expected to cause a double risk of developing a severe infections and triple risk of mortality [24].

Limitations

There are some limitations in this study. First, because this is a retrospective single-center study based on laboratory data, the data on the clinical findings and treatments of patients are not available. Second, the reference method for antibiotic susceptibility, the agar dilution test could not be performed.

Conclusion

The most encountered pathogens were *K. pneumoniae*, *P. aeruginosa*, *A. baumannii*, *C. striatum*, *E. coli* and *S. aureus* in respiratory tract samples in geriatric patients. Above 90% of *K. pneumoniae*, *P. aeruginosa* and *A. baumannii* positive geriatric patients were hospitalized in the intensive care units. The antimicrobial resistance rates were higher in patients above 85 years of age. Vancomycin and teicoplanin were the most effective antibiotics against MRSA. It is thought that the results will be useful in the preparation of treatment protocols and in guiding physicians about the correct use of antibiotics. The resistance profiles should be monitored regularly through active surveillance in geriatric patients.

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