American Journal of Epidemiology and Infectious Disease, 2020, Vol. 8, No. 2, 63-77
Available online at http://pubs.sciepub.com/ajeid/8/2/3
Published by Science and Education Publishing
DOI:10.12691/ajeid-8-2-3

Microbiological Profile, Sensitivity and Drug Resistance of Germs Responsible for Lower Respiratory Tract Infections in Yaounde, Cameroon

Laure Ngando[1,2,*], Leopold Mbous Nguimbus[3,4], Claris Killa[3,4], Thérèse Nkoa[1], Dieudonné Adiogo[5]

[1]Department of Microbiology, Faculty of Medecine and Biomedical Sciences, University of Yaounde I, Yaounde, Cameroon
[2]Laboratory of Bacteriology/Mycology, Centre Pasteur of Cameroon, Yaounde, Cameroon
[3]Department of Biochemistry, Faculty of Sciences, University of Yaounde I, Yaounde, Cameroon
[4]Catholic University of Central Africa, School of Health Science, Yaounde, Cameroon
[5]Department of Biological Sciences, Faculty of Medicine and Pharmaceutical Sciences, University of Douala, Douala, Cameroon
*Corresponding author: laurengando2013@gmail.com

Received July 20, 2020; Revised August 22, 2020; Accepted August 31, 2020

Abstract **Background:** Lower respiratory tract infections (LRTIs) remains a serious public health problem in worldwide despite advances of medicine. The objectives of this study were to present the profile of germs responsible for LRTIs in Yaounde between 2010 to 2019, analyse the association between these germs with the gender and age groups of the study participants and present sensitivity and resistance profiles to the drugs used in this research during the same period. **Methods:** This retrospective and observational study was carried out from January 04, 2010 to December 24, 2019 in Yaounde, capital of the Center region, at Centre Pasteur of Cameroon. The laboratory analyses focused on the macroscopic study, the isolation and identification of bacterial and fungal species and the realization of an antimicrobial susceptibility testing by the method of diffusion. The automated method using the Vitek 2-compact automaton has also been used in the context of the search for profiles of sensitivity and resistance to antibiotics and antifungals. **Results:** A total of 1795 samples were analyzed during the study period with a prevalence of LRTIs of 47.8% (858 positive samples). Men were more represented with 449 (48.0%) samples compared to 377 (48.3%) samples for women. This difference in sample distribution by sex was significant ($p = 0.01224$). The age of the infected participants ranged from 7-90 years for a mean age of 51.2 years ± 15.4 SD. The age distribution in groups showed that LRTIs are common among adults aged 41-60 years with 372 (49.4%) samples. The difference in distribution was significant across age groups ($p<0.0001$). The bacterial and fungal species most represented in the study were: *Pseudomonas aeruginosa* (7.24%), *Klebsiella pneumoniae* (6.13%), *Haemophilus influenzae* (4.40%), *Candida albicans* (4.07%), *Streptococcus pneumoniae* (2.01%), *Streptococcus sp.* (1.78%), *Serratia marcescens* (1.56%), *Acinetobacter baumannii* (1.50%), *Enterobacter cloacae* (1.28%), *Pseudomonas fluorescens* (1.23%), *Straphylococcus aureus* (1.23%), *Haemophilus sp.* (1.00%), *Pseudomonas sp.* (0.95%), *Candida sp.* (0.95%), *Escherichia coli* (0.89%), *Stenotrophomonas maltophilia* (0.84%), *Chryseomonas sp.* (0.78%), *Pseudomonas putida* (0.78%), *Streptococcus oralis* (0.78%), *Burkholderia cepacia* (0.72%), *Proteus mirabilis* (0.67%), *Chryseomonas luteola* (0.61%), *Haemophilus parainfluenzae* (0.61%), *Acinetobacter calcoace* (0.50%), *Trichosporon spp.* (0.39%). A statistically significant associations of age groups ($p<0.0001$) and sex ($p = 0.01224$) with the identified germs were obtained in this study. Most of the germs were resistant to bacterial envelope inhibitors with higher resistance to ticarcillin (100% for *Klebsiella pneumoniae* and 75.4% for *Pseudomonas aeruginosa*). For inhibitors of protein synthesis, higher sensitivities were observed for the same germs (92.7% and 83.8% respectively to amikacin, 83.5% to chloramphenicol for *Haemophilus influenzae*). For folic acid synthesis inhibitors, the highest resistance was also found for *Haemophilus influenzae* (87.3%) and *Klebsiella pneumoniae* (71.8%) to cotrimoxazole. The isolated fungi were mostly susceptible to the antifungal agents tested. **Conclusion:** In the light of this work, it is necessary to extend the surveillance of antibiotic resistance strains throughout the country in order to define therapeutic strategies adapted to the local epidemiological data.

Keywords: *lower respiratory tract infections, sensitivity, resistance, antimicrobial susceptibility testing, Vitek 2-compact*

Cite This Article: Laure Ngando, Leopold Mbous Nguimbus, Claris Killa, Thérèse Nkoa, and Dieudonné Adiogo, "Microbiological Profile, Sensitivity and Drug Resistance of Germs Responsible for Lower Respiratory Tract Infections in Yaounde, Cameroon." *American Journal of Epidemiology and Infectious Disease*, vol. 8, no. 2 (2020): 63-77. doi: 10.12691/ajeid-8-2-3.

1. Introduction

Lower Respiratory Tract Infections (LRTIs) are the leading cause of morbidity and mortality in humans with approximately 4 million deaths at all ages worldwide [1,2,3,4]. These LRTIs can lead to severe non-pneumonic forms in young adults, pneumonia or exacerbated life threatening forms in patients with severe obstructive pulmonary disease. The incidence of these infections with pneumonia is encountered quite frequently in developing countries, 2-4% in developed countries compared to 20-30% in underdeveloped countries [1]. Moreover, in the world, these LRTIs are the third leading cause of death and the first cause of mortality in countries where the socio-economic level is low [5]. Pneumonia, an infection of the lungs, is a global health problem [6] especially for patients in intensive care units (ICU) [2,7,8]. Data from the Center for Disease Control and Prevention showed that in the United States in the year 2000, more than 120,000 deaths were recorded in chronic lower respiratory diseases and more than 65,000 deaths in pneumonia [3]. According to reports from the World Health Organization (WHO), pneumonia kills more children worldwide than any other disease, even more than acquired immunodeficiency syndrome (AIDS), malaria and measles combined [4]. In adults, the impact of community-acquired pneumonia (CAP) or nosocomial pneumonia including hospital-acquired pneumonia (HAP) and ventilator-acquired pneumonia (VAP) is also of great concern and remarkably associated with high mortality and morbidity rates [4,9].

The incidence and prevalence of LRTIs can be influenced by many factors including age, gender, occupation, environment, seasons, characteristics of the population at risk, availability of health care services, immunosuppressive drugs, inappropriate antibiotic therapy, distribution of causative pathogens, and the prevalence of antimicrobial resistance [1,2]. The majority of germs encountered in these infections are viral [1,10], but several bacterial or fungal species are involved, particularly those encountered in intensive care units (ICU) such as: *Pseudomonas sp.*, *Acinetobacter sp.*, *Klebsiella sp.*, *Citrobacter sp*. and *Escherichia coli* [11]. Other information shows that these infections are commonly caused by *Pseudomonas aeruginosa*, which is found mainly in the elderly and frequently in patients with lung and heart diseases associated with a substantial level of mortality (over 40%) [12]. For CAP or nosocomial pneumonia, the species involved are: *Haemophilus influenzae*, *Pseudomonas aeruginosa*, *Staphylococcus aureus* and other pathogens grouped into atypical bacteria (with *Mycoplasma spp.*, *Chlamydia spp.*, and *Legionella spp.*) [4,13]. Fungi are also implicated in these respiratory infections with *Candida* species that are responsible for invasive Candidiasis, which affects more than 250,000 people worldwide each year and causes the death of 50,000 people [14]. In addition, respiratory diseases including allergic bronchopulmonary mycosis characterized by an exaggerated immune system response to fungi are frequently caused by *Aspergillus fumigatus* and other fungal species such as *Candida albicans* [15].

The increase in antibiotic and antifungal resistance is a major public health problem and worldwide, the increase in resistance of bacterial strains is a real challenge in communities and hospitals around the world, especially among children and the elderly [2,16,17]. These resistances are caused by Methicillin-resistant *Staphylococcus aureus* (MRSA), Vancomycin-resistant *Staphylococcus aureus (*VRSA), Vancomycin-resistant *Enterococcus (*VRE), Penicillin-resistant *Streptococcus pneumoniae* (PRSP), Extended-spectrum β-Lactamase (ESBL) *Staphylococcus aureus* produced by *Escherichia coli*, *Klebsiella* species (*Klebsiella spp*.), fluoroquinolone and carbapenem-resistant *Enterobacteriaceae and Pseudomonas aeruginosa* [17,18,19,20]. In contrast to bacterial species whose level of resistance is increasing over the years, fungal species, especially those of the genus *Candida*, remain, according to data from some studies, sensitive to most of the antifungal agents tested, especially those of the azole class [21].

In Africa, south of the Sahara, LRTIs are third after HIV/AIDS and malaria in terms of mortality. Furthermore, as the leading cause of death in nine African countries, data from a systematic analysis revealed that in 2015 LRTIs caused the death of 2.74 million people with 103 million disability-adjusted life years (DALYs) [22]. In Cameroon, the management of LRTIs remains a challenge in the medical services and little data is available on their etiology. Nevertheless, studies carried out in our context have shown that the species most involved are *Streptococcus pneumoniae* and *Haemophilus influenzae* which are the most represented followed by *Klebsiella pneumoniae*, *Staphylococcus aureus* and *Moraxella catarrhalis [23]*. In order to provide information on multidrug resistant germs in our context, the objectives of this study carried out between 2010-2019 at the Centre Pasteur of Cameroon were to present the microbiological profile of germs responsible for LRTIs in our context, to assess whether there is a possible association between these germs and the sex and age of the study participants and to present the sensitivity and resistance profiles of isolated organisms to the drugs tested during the same period.

2. Materials and Methods

2.1. Place and Period of Study

This study was carried out from January 4, 2010 to December 24, 2019 in Yaounde, capital of the Center region at the Centre Pasteur of Cameroon (CPC) which is a technical body of the Ministry of Public Health of Cameroon and member of the International Network of Pasteur Institutes.

2.2. Type of Study and Samples

This was an observational and retrospective study of samples from the lower respiratory tract (samples obtained by bronchial aspiration, brushing, sputum, bronchoalveolar lavage and mini-wash) of patients from several health institutions in the city of Yaounde presenting a clinical picture of a LRTI and who came to the Centre Pasteur of Cameroon to carry out a bacteriological and mycological examination of the lower respiratory tract.

2.3. Sample Collection and Analysis

The various samples were taken from a medical act and carried out by the referring specialists. Biological analyses were carried out in the mycobacteriology laboratory. Once in the laboratory, the macroscopic examination was then carried out in order to assess the colour and turbidity of the different samples taken. The bacteriological analysis of the samples was marked by the phase of isolation of germs on appropriate culture media (fresh blood agar, cooked blood agar, CLED medium, MacConkey etc.) associated with Gram staining [24] for the distinction between Gram positive and Gram negative germs. The identification of bacterial strains or species was based on the study of their morphological, cultural and biochemical characteristics (fermentation of sugars, nitrate reduction, search for enzyme such as oxidase, catalase etc.) by using API 20E [25] galleries and by automated method on the Vitek 2-compact apparatus [26,27]. The antimicrobial susceptibility testing was performed by the method of diffusion of antibiotic discs according to the standards of the Antimicrobial Susceptibility Testing Committee of the French Society of Microbiology on Mueller-Hinton agar (MH Agar) and defibrinated horse blood Mueller-Hinton agar and added β-NAD (MH-F Agar) for the determination of antibiotic sensitivity. The Vitek 2-compact automated system was also used to investigate antibiotic susceptibility and resistance profiles [28].

The mycological analyses were carried out using slide and coverglass microscopy with the 10X objective and then with the 40X objective. The culture was carried out on Sabouraud + Chloramphenicol medium for the detection of yeasts in the different samples. Blast assays, the API-20C gallery and the Vitek 2-compact automaton were used to identify the yeasts and study morphological, cultural, biochemical and other characteristics [26,27,29]. The realization of the Antimicrobial Susceptibility Testing took into account the method by diffusion on Sabouraud medium in order to determine the sensitivity or resistance to antifungals [30].

The Antimicrobial Susceptibility Testing, the control of the performance of the antibiotic and antifungal discs, the measurement of the diameters of the inhibition zones observed and the interpretation of the results were carried out in accordance with the recommendations of the authorities in force (CLSI [31], CA-SFM/EUCAST [32]).

2.4. Data Collection and Statistical Analysis

The data were taken from the CPC GLIMS data management software. The data were collected taking into account the variables days and years of collection, sex, age (divided into groups), origin or type of collection, the germs identified, their classifications, and the three-letter code corresponding to the antibiotics and antifungals used. After extraction of data from the GLIMS system, the database was cleaned with Microsoft Office Excel 2019 and statistical analyses were performed using R language version 3.6.1 (2019-07-05) [33]. The finalfit package of the R software was used to create the various analysis tables [34]. The statistical tests used in this research were: The Pearson Chi-square and Fisher's exact test for comparing differences in proportions between qualitative variables, the Kruskal Wallis test for comparing differences in means between the ages of participants according to gender and age groups, and the logistic regression model for determining *Odds-ratio* (OR) values and confidence intervals between identified germs according to the gender variable. The significance level was set at $p<0.05$.

3. Results

3.1. Characteristics of Study Population

The number of samples tested between 2010-2019 was 1795 with 858 (47.8%) being positive for a LRTI caused by a bacterium or fungus. The distribution of samples by gender showed that males were the most represented with 449 (48.0%) samples compared to 377 (48.3%) samples for females for a sex ratio of 1.19. This difference in sample distribution by gender was statistically significant ($p = 0.01224$) (Table 1). The age of participants positive for LRTI ranged from 7-90 years for a mean age of 51.2 years ± 15.4 SD. Distribution of the age variable into groups showed that LRTI were most frequently found in adult aged 41-60 years with 372 (49.4%) samples, followed by persons aged ≥ 61 years with 233 (48.9%) samples, then 21-40 years with 194 (45.3%) samples. The difference in the distribution of age groups was statistically significant ($p<0.0001$) (Table 1). The method of sampling most represented was bronchial aspiration with 745 (41.5%) samples from this type of sampling, followed by sputum with 66 (3.7%) samples, then bronchoalveolar lavage with 44 (2.5%). As for the mini-wash and brushing, they were practically unused (2 samples and 1 sample respectively). The difference in the distribution of the types of sampling according to age group was statistically significant ($p = 0.02231$) while according to sex this distribution was not significant ($p = 0.2396$). The year 2015 was the most represented in positive samples (175 samples) for non-significant distribution differences by age group and sex ($p = 0.1599$ and $p = 0.2009$ respectively) (Table 1).

3.2. Distribution of Identified Organisms

Two groups of germs were identified during the study period. Bacteria with 751 (41.8%) samples on the one hand and fungi with 107 (6.0%) samples on the other hand. Among bacteria, gram-negative bacilli were the most represented with 627 (34.9%) samples, followed by gram positive Cocci with 121 (6.7%) samples and gram negative Cocci with only 3 (0.2%) samples. Concerning fungi, levuriform fungi were the most represented with 102 (5.7%) samples against 5 (0.3%) samples for filamentous fungi. During the study period, the most represented bacterial and fungal species were: *Pseudomonas aeruginosa* (7.24%), *Klebsiella pneumoniae* (6.13%), *Haemophilus influenzae* (4.40%), *Candida albicans* (4.07%), *Streptococcus pneumoniae* (2.01%), *Streptococcus sp.* (1.78%), *Serratia marcescens* (1.56%), *Acinetobacter baumannii* (1.50%), *Enterobacter cloacae* (1.28%), *Pseudomonas fluorescens* (1.23%), *Straphylococcus aureus* (1.23%), *Haemophilus sp.* (1.00%), *Pseudomonas sp.* (0.95%), *Candida sp.* (0.95%), *Escherichia coli* (0.89%), *Stenotrophomonas maltophilia*

(0.84%), *Chryseomonas sp.* (0.78%), *Pseudomonas putida* (0.78%), *Streptococcus oralis* (0.78%), *Burkholderia cepacia* (0.72%), *Proteus mirabilis* (0.67%), *Chryseomonas luteola* (0.61%), *Haemophilus parainfluenzae* (0.61%), *Acinetobacter calcoace* (0.50%), *Trichosporon spp.* (0.39%). Other species identified are listed in Table 2.

Table 1. Distribution of sociodemographic variables according to age groups and sex

	Age groups (years)						Sex			
Variables	<21 (n=37) No. (%)	21-40 (n=428) No. (%)	41-60 (n=753) No. (%)	≥61 (n=476) No. (%)	Total (n=1795) No. (%)	P-value	Men (n=935) No. (%)	Women (n=780) No. (%)	Total (n=1795) No. (%)	P-value
Age										
Mean (SD)	16.1 (3.8)	33.5 (5.5)	50.0 (5.7)	70.2 (7.3)	51.2 (15.4)	**<0.0001***	53.0 (15.3)	49.1 (15.3)	51.2 (15.4)	**<0.0001***
Origin										
Bronchial aspiration	13 (35.1)	176 (41.1)	336 (44.6)	218 (45.8)	743 (41.4)	**0.02231**	397 (42.5)	348 (44.6)	745 (41.5)	0.2396
Brushing	0 (0.0)	0 (0.0)	0 (0.0)	1 (0.2)	1 (0.1)		1 (0.1)	0 (0.0)	1 (0.1)	
Sputum	2 (5.4)	10 (2.3)	9 (1.2)	3 (0.6)	24 (1.3)		20 (2.1)	14 (1.8)	34 (1.9)	
ABL	0 (0.0)	8 (1.9)	27 (3.6)	9 (1.9)	44 (2.5)		29 (3.1)	15 (1.9)	44 (2.5)	
Mini-wash	0 (0.0)	0 (0.0)	0 (0.0)	2 (0.4)	2 (0.1)		2 (0.2)	0 (0.0)	2 (0.1)	
Years										
2010	0 (0.0)	14 (3.8)	32 (4.2)	15 (3.2)	61 (3.4)	0.1599	40 (4.8)	26 (3.3)	66 (3.7)	0.2009
2011	0 (0.0)	12 (2.8)	21 (2.8)	23 (4.8)	56 (3.1)		34 (3.6)	27 (3.5)	61 (3.4)	
2012	1 (2.7)	2 (0.5)	13 (1.7)	13 (2.7)	29 (1.6)		15 (1.6)	14 (1.8)	29 (1.6)	
2013	0 (0.0)	12 (2.8)	18 (2.4)	12 (2.5)	42 (2.3)		18 (1.9)	24 (3.1)	42 (2.3)	
2014	1 (2.7)	15 (3.5)	21 (2.8)	16 (3.4)	53 (3.0)		32 (3.4)	21 (2.7)	53 (3.0)	
2015	4 (10.8)	45 (10.5)	86 (11.4)	40 (8.4)	175 (9.7)		104 (11.1)	71 (9.1)	175 (9.7)	
2016	2 (5.4)	28 (6.5)	46 (6.1)	42 (8.8)	118 (6.6)		68 (7.3)	52 (6.7)	120 (6.7)	
2017	0 (0.0)	22 (5.1)	53 (7.0)	25 (5.3)	100 (5.6)		56 (6.0)	44 (5.6)	100 (5.6)	
2018	5 (13.5)	26 (6.1)	39 (5.2)	28 (5.9)	98 (5.5)		43 (4.6)	55 (7.1)	98 (5.5)	
2019	2 (5.4)	18 (4.2)	43 (5.7)	19 (4.0)	82 (4.6)		39 (4.2)	43 (5.5)	82 (4.6)	
Overall prevalence	15 (40.5)	194 (45.3)	372 (49.4)	233 (48.9)	858 (47.8)	**<0.0001**	449 (48.0)	377 (48.3)	858 (47.8)	**0.01224**

P-value: p-value of Pearson's Chi-squared test
*: p-value of Kruskal-Wallis rank sum test
ABL: Alveolar broncho-lavage.

Table 2. The 25 most common organisms isolated from CPC during the study period

Ranking	Organisms	No. of isolates	% of total
	Bacteria		
1	*Pseudomonas aeruginosa*	130	7.24
2	*Klebsiella pneumoniae*	110	6.13
3	*Haemophilus influenzae*	79	4.40
4	*Streptococcus pneumoniae*	36	2.01
5	*Streptococcus sp*	32	1.78
6	*Serratia marcescens*	28	1.56
7	*Acinetobacter baumannii*	27	1.50
8	*Enterobacter cloacae*	23	1.28
9	*Pseudomonas fluorescens*	22	1.23
10	*Straphylococcus aureus*	22	1.23
11	*Haemophilus sp*	18	1.00
12	*Pseudomonas sp*	17	0.95
13	*Escherichia coli*	16	0.89
14	*Stenotrophomonas maltophilia*	15	0.84
15	*Chryseomonas sp*	14	0.78
16	*Pseudomonas putida*	14	0.78
17	*Streptococcus oralis*	14	0.78
18	*Burkholderia cepacia*	13	0.72
19	*Proteus mirabilis*	12	0.67
20	*Chryseomonas luteola*	11	0.61
21	*Haemophilus parainfluenzae*	11	0.61
22	*Acinetobacter calcoace*	9	0.50
	Total	673	37.49
	Fungi		
23	*Candida albicans*	73	4.07
24	*Candida sp*	17	0.95
25	*Trichosporon spp.*	7	0.39
	Total	97	5.41
	Other*	88	4.90

*Other organisms included the following (No.): *Enterobacter aerogenes* (7); *Flavimonas oryzihabitans* (5); *Achromobacter xylosoxidans* (4); *Chryseobacterium sp.* (4); *Morganella morganii* (4); *Streptococcus mitis* (4); *Chryseobacterium meningoseptica* (3); *Citrobacter freundii* (3); *Streptococcus group F* (3); *Aspergillus fumigatus* (2); *Citrobacter koserii* (2); *Cryptococcus neoformans* (2); *Enterobacter sakazakii* (2); *Moraxella sp.* (2); *Pseudomonas stutzeri* (2); *Salmonella sp.* (2); *Serratia liquefaciens* (2); *Streptococcus agalactiae* (2); *Streptococcus constellatus* (2); *Achromobacter denitrificans* (1); *Acinetobacter sp.* (1); *Aeromonas hydrophila* (1); *Aspergillus flavus* (1); *Aspergillus nidulans* (1); *Aspergillus niger* (1); *Candida famata* (1); *Candida parapsilosis* (1); *Candida tropicalis* (1); *Citrobacter braakii* (1); *Comamonas testosteroni* (1); *Eikenella corrodens* (1); *Enterobacter gergoviae* (1); *Enterococcus sp.* (1); *Flavimonas sp.* (1); *Haemophilus parahaemolyticus* (1); *Hafnia alvei* (1); *Kluyvera cryocrescens* (1); *Neisseria sp.* (1); *Pantoea agglomerans* (1); *Pantoea sp.* (1); *Providencia rettgeri* (1); *Pseudomonas mendocina* (1); *Salmonella enteritidis* (1); *Serratia fonticola* (1); *Sphingomonas paucimobilis* (1); *Streptococcus anginosus* (1); *Streptococcus dysgalactiae* (1); *Streptococcus parasanguinis* (1); *Streptococcus pyogenes* (1); *Streptococcus sanguis* (1).

Table 3. Distribution of the 25 most common organisms isolated according to sex

Isolated organisms	Sex		Total (n=1795) No. (%)	OR (95%-CI)	P-value
	Men (n=935) No. (%)	Women (n=780) No. (%)			
Bacteria					
Acinetobacter baumannii	13 (1.4)	14 (1.8)	27 (1.5)	1.29 (0.56-3.01)	0.5028
Acinetobacter calcoace	5 (0.5)	3 (0.4)	8 (0.4)	0.70 (0.11-3.63)	0.7318*
Burkholderia cepacia	6 (0.6)	7 (0.9)	13 (0.8)	1.40 (0.40-5.07)	0.5432
Chryseomonas luteola	4 (0.4)	7 (0.9)	11 (0.6)	2.11 (0.53-9.85)	0.2251
Chryseomonas sp	8 (0.9)	3 (0.4)	11 (0.6)	0.45 (0.08-1.87)	0.2237
Enterobacter cloacae	15 (1.6)	6 (0.8)	21 (1.2)	0.46 (0.15-1.30)	0.1174
Escherichia coli	8 (0.9)	5 (0.6)	13 (0.7)	0.74 (0.19-2.60)	0.6099
Haemophilus influenzae	31 (3.3)	45 (5.8)	76 (4.2)	1.78 (1.09-1.95)	**0.01394**
Haemophilus parainfluenzae	8 (0.9)	3 (0.4)	11 (0.6)	0.45 (0.08-1.87)	0.2237
Haemophilus sp	9 (1.0)	9 (1.2)	18 (1.0)	1.20 (0.42-3.43)	0.6987
Klebsiella pneumoniae	56 (6.0)	47 (6.0)	103 (5.7)	1.00 (0.66-1.53)	0.9748
Proteus mirabilis	8 (0.9)	4 (0.5)	12 (0.7)	0.60 (0.13-2.24)	0.3964
Pseudomonas aeruginosa	76 (8.1)	54 (6.9)	130 (7.2)	0.84 (0.57-1.23)	0.3477
Pseudomonas fluorescens	9 (1.0)	13 (1.7)	22 (1.2)	1.74 (0.69-4.65)	0.197
Pseudomonas putida	4 (0.4)	10 (1.3)	14 (0.8)	3.02 (0.87-13.25)	0.05026
Pseudomonas sp	6 (0.6)	11 (1.4)	17 (0.9)	2.21 (0.75-7.33)	0.1096
Serratia marcescens	18 (1.9)	10 (1.3)	28 (1.6)	0.66 (0.27-1.52)	0.2954
Stenotrophomonas maltophilia	7 (0.7)	7 (0.9)	14 (0.8)	1.20 (0.36-4.03)	0.7331
Straphylococcus aureus	11 (1.2)	10 (1.3)	21 (1.2)	1.09 (0.41-2.85)	0.8431
Streptococcus oralis	9 (1.0)	3 (0.4)	12 (0.7)	0.40 (0.07-1.60)	0.1528
Streptococcus pneumoniae	13 (1.4)	22 (2.8)	35 (1.9)	2.05 (0.98-4.48)	**0.037**
Streptococcus sp	18 (1.9)	14 (1.8)	32 (1.8)	0.93 (0.42-2.00)	0.8426
Fungi					
Candida albicans	44 (4.7)	24 (3.1)	68 (3.9)	0.64 (0.37-1.09)	0.08517
Candida sp	6 (0.6)	10 (1.3)	16 (0.9)	2.01 (0.66-6.76)	0.1696
Trichosporon spp.	3 (0.3)	4 (0.5)	7 (0.4)	1.60 (0.27-10.96)	0.5347
Other organisms	54 (5.7)	32 (4.1)	86 (4.8)	0.70 (0.43-1.11)	0.114
Overall prevalence	449 (48.0)	377 (48.3)	858 (47.8)		**0.01224**

P-value: p-value of Pearson's Chi-squared test
*: P-value of Fisher's exact test
OR: Odd ratio
CI: Confidence interval.

3.3. Association of Identified Organisms with Age and Sex

An association between the germs responsible for lower respiratory tract infections and gender was found in this study. Indeed, the proportion of respiratory infection was higher in male patients with 449 (48.0%) samples compared to 377 (48.3%) samples for female patients. This difference in the distribution of identified germs according to sex was statistically significant (p = 0.01224). The species for which the difference in distribution was significant according to sex were *Haemophilus influenzae* (p = 0.01394) and *Streptococcus pneumoniae* (p = 0.037) with women being the most contaminated. In addition, the logistic regression model showed that gender is a risk factor for *Haemophilus influenzae* infection with women being 1.78 times more at risk than men (OR=1.78, CI =1.09-1.95) (Table 3). Differences in distribution between sex and the other species identified were also observed, but these were not statistically significant.

In our study, age was also associated with the germs involved in lower respiratory tract infection with a significant difference in distribution from one age group to another (p<0.0001). The species associated with infection by age group were *Haemophilus influenzae* (p = 0.01425) followed by *Haemophilus sp.* (p = 0.001952) and *Streptococcus oralis* (p = 0.04143). The age group 41-60 years was the most concerned by the infection with *Pseudomonas aeruginosa* and *Klebsiella pneumoniae* germs which were the most represented in the study and which were strongly found in this age group despite a non-statistically significant difference in distribution (p = 0.2656 and p = 0.5888 respectively). The distributions of the other species identified during the course of the study according to age groups are shown in Table 4 with an overall non-significant difference in proportion for most of the organisms listed.

3.4. Drug Susceptibility and Resistance Profiles of Isolated Organisms during the Study

In the course of the study, 60 antibiotics and 7 antifungals were used to test the sensitivity of germs present in lower respiratory tract infections. The classes of antibiotics used in this study were: penicillin antibiotics with penicillin G (PEN), ampicillin (AMP), amoxicillin (AMO), amoxicillin + clavulanic acid (AMC), ampicillin + sulbactan (FAM), ticarcillin (TIC), ticarcillin + clavulanic acid (TCC), piperacillin (PIC), piperacillin + tazobactam (TZP), enterococcal ampicillin (AME), piperacillin + tazobactam (PIT), ampicillin + sulbactan (SAM), oxacillin (OXA); aminoglycosides with gentamicin (GEN), spectinomycin (SPT), kanamycin strong dose (KAN), tobramicin (TOB), amikacin (AKN), netilmicin (NET), kanamycin 1000 (KAH), gentamicin 500 (GEH), gentamicin 250 (GE2); cephalosporins with cefatrizine (CFT), cefuroxime (CXM), cefoxitin (CXT),

cefotaxime (CTX), ceftazidime (CAZ), cefixime (CFM), cefepime (FEP); carbapenems with imipenem (IMI), meropenem (MER), ertapenem (ETP); quinolones with nalidixic acid (NAL), ofloxacin (OFL), pefloxacin (PEF), norfloxacin (NOR), ciprofloxacin (CIP), levofloxacin (LEV), moxifloxacin (MXF); sulfonamides with sulfonamid (SSS), trimethoprim + sulfamethoxazole or cotrimoxazole (SXT/TSU); cyclines with tetracycline (TET), minocycline (MIN), tigecycline (TGC); macrolides and related with erythromycin (ERY), lincomycin (LIN), clindamycin (CLI/CM), telithromycin (TEL), pristinamycin (PRI), quinupristin + dalfopristin (QDA); peptides with colistin (COL), vancomycin (VAN), teicoplanin (TEC); phenicols with chloramphenicol (CMP); monobactams with aztreonam (ATM); nitrofurans with nitrofurantoin (FUR); oxazolidinones with linezolid (LIZ) and various antibiotics with rifampicin (RFA), fusidic acid (FUC), fosfomycin (FOS). For antifungal agents, the classes represented were azoles with miconazole (MIC), econazole (ECO), ketoconazole (KET), fluconazole (FLU), clotrimazole (CLO) and polyenes with amphotericin B (AMB) and nystatin (NYS) (see Table 5).

This research showed that most of the bacteria identified were resistant to penicillin antibiotics with: 90.9% resistance to penicillin G for *Staphylococcus aureus*; 87.0% and 88.2% resistance to amoxicillin for *Enterobacter cloacae*, and *Klebsiella pneumoniae* respectively; 87.0% and 82.1% resistance to amoxicillin + clavulanic acid; 70.4%, 92.3%, 81.8%, 100%, 100%, 83.3%, 75.4%, 81.8%, 92.9%, 76.5% and 73.3% ticarcillin resistance for *Acinetobacter baumannii*, *Burkholderia cepacia*, *Chryseomonas luteola*, *Escherichia coli*, *Klebsiella pneumoniae*, *Proteus mirabilis*, *Pseudomonas aeruginosa*, *Pseudomonas fluorescens*, *Pseudomonas putida*, *Pseudomonas sp.* and *Stenotrophomonas maltophilia* respectively; 86.7%, 70.8%, 85.7%, 92.3% and 81.8% resistance to ticarcillin + clavulanic acid for *Stenotrophomonas maltophilia*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Burkholderia cepacia* and *Chryseomonas luteola* respectively; 75.0% resistance to Piperacillin for *Escherichia coli*. The other antibiotic resistance patterns of the penicillin class of antibiotics are shown in Table 5. Within this same antibiotic family, high percentages of susceptibility were also observed. For example, *Streptococcus oralis* with 71.4% sensitivity to ampicillin; *Streptococcus pneumoniae* with 83.3% sensitivity to amoxicillin; *Serratia marcescens with* 85.7% sensitivity to ticarcillin; *Stenotrophomonas maltophilia* with 80.0% sensitivity to ticarcillin + clavulanic acid; *Burkholderia cepacia* and *Chryseomonas sp.* with respectively 84.6% and 85.7% sensitivity to piperacillin; *Serratia marcescens* and *Chryseomonas sp.* with respectively 75.0% and 71.4% sensitivity to piperacillin + tazobactam. See Table 5 for more information.

Table 4. Distribution of the 25 most common organisms isolated according to age groups

Isolated organisms	Age groups (years) <21 (n=37) No. (%)	21-40 (n=428) No. (%)	41-60 (n=753) No. (%)	≥61 (n=476) No. (%)	Total (n=1795) No. (%)	P-value
Bacteria						
Acinetobacter baumannii	1 (2.7)	4 (0.9)	16 (2.1)	6 (1.3)	27 (1.5)	0.2753*
Acinetobacter calcoace	0 (0.0)	2 (0.5)	3 (0.4)	3 (0.6)	8 (0.4)	0.9155*
Burkholderia cepacia	1 (2.7)	3 (0.7)	6 (0.8)	3 (0.6)	13 (0.8)	0.4773*
Chryseomonas luteola	0 (0.0)	3 (0.7)	5 (0.7)	2 (0.4)	10 (0.6)	0.8788*
Chryseomonas sp	0 (0.0)	5 (1.2)	3 (0.4)	2 (0.4)	10 (0.6)	0.3961*
Enterobacter cloacae	0 (0.0)	3 (0.7)	11 (1.5)	6 (1.3)	20 (1.1)	0.7116*
Escherichia coli	0 (0.0)	1 (0.2)	6 (0.8)	6 (1.3)	13 (0.7)	0.3831*
Haemophilus influenzae	6 (16.2)	21 (4.9)	27 (3.6)	20 (4.2)	74 (4.1)	**0.01425***
Haemophilus parainfluenzae	0 (0.0)	3 (0.7)	2 (0.3)	6 (1.3)	11 (0.6)	0.2003*
Haemophilus sp	0 (0.0)	7 (1.6)	1 (0.1)	10 (2.1)	18 (1.0)	**0.001952***
Klebsiella pneumoniae	1 (2.7)	21 (4.9)	50 (6.6)	31 (6.5)	103 (5.7)	0.5888*
Proteus mirabilis	0 (0.0)	0 (0.0)	7 (0.9)	5 (1.1)	12 (0.7)	0.14*
Pseudomonas aeruginosa	3 (8.1)	30 (7.0)	68 (9.0)	29 (6.1)	130 (7.2)	0.2656*
Pseudomonas fluorescens	0 (0.0)	5 (1.2)	12 (1.6)	5 (1.1)	22 (1.2)	0.8368*
Pseudomonas putida	0 (0.0)	7 (1.6)	4 (0.5)	3 (0.6)	14 (0.8)	0.2393*
Pseudomonas sp	0 (0.0)	3 (0.7)	9 (1.2)	5 (1.1)	17 (0.9)	0.8479*
Serratia marcescens	0 (0.0)	7 (1.6)	18 (2.4)	3 (0.6)	28 (1.6)	0.1128*
Stenotrophomonas maltophilia	0 (0.0)	4 (0.9)	6 (0.8)	4 (0.8)	14 (0.8)	0.9583*
Straphylococcus aureus	0 (0.0)	2 (0.5)	11 (1.5)	8 (1.7)	21 (1.2)	0.3176*
Streptococcus oralis	0 (0.0)	5 (1.2)	1 (0.1)	6 (1.3)	12 (0.7)	**0.04143***
Streptococcus pneumoniae	2 (5.4)	6 (1.4)	15 (2.0)	11 (2.3)	34 (1.9)	0.2907*
Streptococcus sp	0 (0.0)	7 (1.6)	11 (1.5)	13 (2.7)	31 (1.7)	0.4168*
Fungi						
Candida albicans	0 (0.0)	16 (3.7)	25 (3.3)	23 (4.8)	64 (3.7)	0.4239*
Candida sp	0 (0.0)	6 (1.4)	8 (1.1)	2 (0.4)	16 (0.9)	0.4486*
Trichosporon spp.	0 (0.0)	2 (0.5)	5 (0.7)	0 (0.0)	7 (0.4)	0.3473*
Other organisms	1 (2.7)	21 (4.9)	42 (5.6)	21 (4.4)	85 (4.7)	0.8191*
Overall prevalence	15 (40.5)	194 (45.3)	372 (49.4)	233 (48.9)	858 (47.8)	**<0.0001**

*: p-value of Fisher's exact test.

Table 5. Susceptibility and Resistance rates for the 22 most common bacteria isolated from CPC during de study period

Antibiotics	Isolated bacteria (No.)							
	Acinetobacter baumannii (n=27)	*Acinetobacter calcoace* (n=9)	*Burkholderia cepacia* (n=13)	*Chryseomonas luteola* (n=11)	*Chryseomonas sp.* (n=14)	*Enterobacter cloacae* (n=23)	*Escherichia coli* (n=16)	*Haemophilus influenzae* (n=79)
	%I/%S/%R							
PEN	NA	NA	NA	NA	NA	NA	NA	0/0/5.1
AMP	NA	NA	NA	NA	NA	0/0/8.7	0/0/31.3	2.5/22.8/43.0
AMO	NA	NA	NA	NA	NA	0/0/87.0	0/0/68.8	0/1.3/0
AMC	NA	NA	NA	NA	NA	4.3/4.3/87.0	18.8/31.3/50.0	1.3/62.0/10.1
FAM	0/3.7/0	0/44.4/11.1	NA	NA	NA	NA	NA	NA
TIC	0/29.6/70.4	0/55.6/44.4	0/7.7/92.3	0/18.2/81.8	0/42.9/50.0	0/34.8/60.9	0/0/100.0	NA
TCC	3.7/33.3/63.0	0/44.4/55.6	0/7.7/92.3	0/18.2/81.8	0/42.9/50.0	0/4.3/17.4	0/18.8/6.3	NA
PIC	0/59.3/40.7	0/66.7/33.3	7.7/84.6/7.7	0/63.6/36.4	0/85.7/0	4.3/39.1/30.4	0/0/75.0	NA
TZP	0/11.1/0	11.1/44.4/0	NA	0/27.8/0	0/14.3/0	8.7/13.0/0	6.3/37.5/6.3	NA
IMI	11.1/55.6/0	0/66.7/0	15.4/15.4/38.5	18.9/0/27.3	0/21.4/42.9	4.3/52.2/0	0/62.5/0	NA
MER	18.5/37.0/0	0/11.1/0	23.1/46.2/7.7	18.2/18.2/0	0/21.4/42.8	NA	NA	NA
CFT	3.7/0/0	NA	NA	NA	NA	0/0/95.7	6.3/18.8/75.0	0/22.8/7.6
CXM	NA	NA	NA	NA	NA	0/0/8.7	0/6.3/12.5	NA
CXT	3.7/0/0	NA	NA	NA	NA	0/4.3/47.8	0/50.0/6.3	NA
CTX	3.7/0/0	NA	NA	NA	NA	0/69.6/26.1	0/68.8/31.3	0/94.9/1.3
CAZ	7.4/85.2/0	22.2/66.7/0	0/100.0/0	18.2/72.7/9.1	42.9/42.9/7.1	0/69.6/21.7	0/62.5/37.5	NA
CFM	NA	NA	NA	NA	NA	0/0/8.7	0/0/12.5	NA
FEP	3.7/37.0/11.1	11.1/22.2/0	0/30.8/7.7	9.1/18.2/18.2	28.6/42.9/0	0/26.1/8.7	0/12.6/6.3	NA
ATM	NA	NA	NA	NA	NA	NA	0/6.3/0	NA
GEN	0/66.7/29.6	0/77.7/22.2	0/53.8/46.2	0/9.1/90.9	0/28.6/57.1	0/82.6/13.0	6.3/50.0/43.8	3.8/41.8/3.8
SPT	NA	NA	NA	NA	NA	NA	NA	NA
KAN	NA	NA	NA	NA	NA	NA	NA	NA
TOB	0/66.7/25.9	0/88.9/11.1	0/61.5/30.8	0/18.2/81.8	0/0/92.9	0/82.6/13.0	6.3/43.8/43.8	NA
AKN	0/88.9/3.7	0/100.0/0	0/61.5/38.5	0/27.3/72.7	28.6/28.6/35.7	0/95.7/0	6.3/75.0/18.8	NA
NET	0/7.4/0	0/55.6/0	NA	0/0/9.1	0/7.1/50.0	0/8.7/8.7	0/18.8/6.3	NA
KAH	NA	NA	NA	NA	NA	NA	NA	NA
GEH	NA	NA	NA	NA	NA	NA	NA	NA
GE2	NA	NA	NA	NA	NA	NA	NA	NA
CMP	0/0/3.7	NA	NA	NA	NA	NA	NA	1.3/83.5/10.1
TET	0/3.7/0	NA	NA	NA	NA	0/0/8.7	0/6.3/25.0	6.3/70.9/16.5
MIN	0/3.7/0	NA	NA	NA	NA	NA	NA	NA
ERY	NA	NA	NA	NA	NA	NA	NA	2.5/2.5/10.1
LIN	NA	NA	NA	NA	NA	NA	NA	NA
CLI/CM	NA	NA	NA	NA	NA	NA	NA	NA
PRI	NA	NA	NA	NA	NA	NA	NA	NA
COL	0/66.7/14.8	0/55.6/11.1	0/15.4/76.9	0/9.1/81.8	0/0/78.6	0/0/0	0/0/0	0/0/0
SSS	NA	NA	NA	NA	NA	NA	NA	NA
FUR	NA	NA	NA	NA	NA	NA	NA	NA
NAL	NA	NA	NA	NA	NA	0/56.5/30.4	0/25.0/43.8	0/21.5/1.3
OFL	3.7/7.4/0	0/44.4/11.1	0/0/7.7	0/0/18.1	0/35.7/28.6	4.3/60.9/30.4	0/31.3/62.5	NA
PEF	3.7/0/0	NA	NA	NA	NA	NA	NA	NA
NOR	NA	NA	NA	NA	NA	NA	NA	NA
CIP	11.1/63.0/14.8	0/100.0/0	15.4/30.8/53.8	18.2/18.2/45.5	0/50.0/28.6	8.7/69.6/17.4	0/62.5/37.5	0/46.8/3.8
RFA	25.9/33.3/3.7	22.2/44.4/33.3	53.8/15.4/0	45.5/0/9.1	0/28.6/28.6	NA	NA	NA
FUC	NA	NA	NA	NA	NA	NA	NA	NA
FOS	0/14.8/33.3	0/0/66.7	0/7.7/84.6	0/0/54.5	0/0/57.1	0/34.8/39.1	0/87.5/0	NA
VAN	NA	NA	NA	NA	NA	NA	NA	NA
TEC	NA	NA	NA	NA	NA	NA	NA	NA
SXT/TSU	0/22.2/55.6	0/55.6/44.4	0/61.5/15.4	0/36.4/18.2	0/57.1/28.6	0/47.8/43.5	0/0/93.8	1.3/3.8/87.3
AME	NA	NA	NA	NA	NA	NA	NA	NA
LEV	NA	NA	NA	NA	NA	NA	NA	0/10.1/0
LIZ	NA	NA	NA	NA	NA	NA	NA	NA
MXF	NA	NA	NA	NA	NA	NA	NA	0/1.3/0
PIT	3.7/51.9/14.8	0/33.3/11.1	7.7/61.5/7.7	0/45.5/27.3	7.1/71.4/0	0/47.8/21.7	12.5/31.3/0	NA
QDA	NA	NA	NA	NA	NA	NA	NA	NA
SAM	NA	NA	NA	NA	0/7.1/0	NA	NA	NA
TEL	NA	NA	NA	NA	NA	NA	NA	NA
OXA	NA	NA	NA	NA	NA	NA	NA	NA
ETP	NA	NA	NA	NA	NA	0/8.7/0	0/6.3/0	NA
TGC	NA	NA	NA	NA	NA	NA	NA	NA

PEN: Penicillin G; AMP: Ampicillin; AMO: Amoxicillin; AMC: Amoxicillin + clavulanic acid; FAM: Ampicillin + Sulbactan; TIC: Ticarcillin; TCC: Ticarcillin + clavulanic acid; PIC: Piperacillin; TZP: Piperacillin + Tazobactam; IMI: Imipenem; MER: Meropenem; CFT: Cefatrizine; CXM: Cefuroxime; CXT: Cefoxitin; CTX: Cefotaxime; CAZ: Ceftazidime; CFM: Cephixime; FEP: Cefepime; ATM: Aztreonam; GEN: Gentamicin; SPT: Spectinomycin; KAN: Kanamycin strong dose; TOB: Tobramicin; AKN: Amikacin; NET: Netilmicin; KAH: Kanamycin 1000; GEH: Gentamicin 500; GE2: Gentamicin 250; CMP: Chloramphenicol; TET: Tetracycline; MIN: Minocycline; ERY: Erythromycin; LIN: Lincomycin; CLI/CM: Clindamycin; PRI: Pristinamycin; COL: Colistin; SSS: Sulfonamid; SXT/TSU: Trimethoprim/sulfamethoxazole (Cotrimoxazole); FUR: Nitrofurantoïn; NAL: Nalidixic acid; OFL: Ofloxacin; PEF: Pefloxacin; NOR: Norfloxacin; CIP: Ciprofloxacin; RFA: Rifampicin; FUC: Fusidic acid; FOS: Fosfomycin; VAN: Vancomycin; TEC: Teicoplanin; AME: Ampicillin Enterocoque; LEV: Levofloxacine; LIZ: Linezolid; MXF: Moxifloxacin; PIT: Piperacillin + Tazobactam; QDA: Quinupristin + Dalfopristin; SAM: Ampicillin + Sulbactan; TEL: Telithromycin; OXA: Oxacillin; ETP: Ertapenem; TGC: Tigecyclin; I: Intermediate; S: Susceptibility; R: Resistance; NA: not available.

Table 5. Susceptibility and Resistance rates for the 22 most common bacteria isolated from CPC during de study period (Continued)

Antibiotics	Isolated bacteria (No.)							
	Haemophilus parainfluenzae (n=11)	*Haemophilus sp.* (n=18)	*Klebsiella pneumoniae* (n=110)	*Proteus mirabilis* (n=12)	*Pseudomonas aeruginosa* (n=130)	*Pseudomonas fluorescens* (n=22)	*Pseudomonas putida* (n=14)	*Pseudomonas sp.* (n=17)
	%I/%S/%R							
PEN	0/0/1.3	0/0/5.6	NA	NA	NA	NA	NA	NA
AMP	0/36.4/45.5	5.6/44.4/50.0	0/0/11.8	0/0/16.7	NA	NA	NA	NA
AMO	NA	NA	0/0/88.2	0/16.7/66.7	NA	NA	NA	NA
AMC	0/90.9/0	0/88.9/11.1	6.4/49.1/44.5	8.3/66.7/25.0	NA	NA	NA	NA
FAM	NA	NA	NA	NA	NA	NA	NA	NA
TIC	NA	NA	0/0/100.0	0/16.7/83.3	1.5/21.5/75.4	0/13.6/81.8	0/7.1/92.9	0/11.8/76.5
TCC	NA	NA	0/9.1/12.7	0/8.3/0	0.8/25.4/70.8	0/18.2/68.2	0/7.1/85.7	0/17.6/70.6
PIC	NA	NA	0.9/10.9/57.3	0/8.3/25.0	20.0/63.1/12.3	0/81.8/9.1	0/42.9/57.1	0/70.6/11.8
TZP	NA	NA	5.5/24.5/0	0/16.7/0	1.5/0.8/0	NA	NA	NA
IMI	NA	NA	0.9/64.5/0.9	16.7/41.7/0	6.9/50.0/11.5	9.1/72.7/18.2	7.1/71.4/0	41.2/11.8/11.8
MER	NA	NA	0/3.6/0	NA	9.3/43.8/13.1	59.1/9.1/18.2	28.6/35.7/0	29.4/17.6/23.5
CFT	NA	NA	0.9/41.8/54.5	0/66.7/25.0	NA	NA	NA	NA
CXM	NA	NA	0/4.5/4.5	NA	NA	NA	NA	NA
CXT	NA	NA	0.9/45.5/12.7	0/50.0/0	NA	NA	NA	NA
CTX	0/81.8/0	0/94.4/5.6	3.6/46.7/47.3	0/91.7/8.3	NA	NA	NA	NA
CAZ	NA	NA	11.8/47.3/40.0	9.1/91.7/0	2.3/91.5/6.2	9.1/86.4/4.5	7.1/71.4/21.4	5.9/76.5/5.9
CFM	NA	NA	0/3.6/5.5	NA	NA	NA	NA	NA
FEP	NA	NA	7.3/7.3/3.6	0/8.3/0	10.8/53.8/6.2	4.5/77.3/9.1	7.1/64.3/0	0/52.9/11.8
ATM	NA	NA	NA	NA	0.8/0/0.8	NA	NA	NA
GEN	0/36.4/0	11.1/33.3/0	0.9/49.1/49.1	0/91.7/8.3	0/65.4/33.8	0/77.3/22.7	0/50.0/50.0	0/58.8/29.4
SPT	NA	NA	NA	NA	NA	NA	NA	NA
KAN	NA	NA	NA	NA	NA	NA	NA	NA
TOB	NA	NA	0/51.8/44.5	0/91.7/8.3	0.8/76.2/19.2	0/77.3/18.2	0/64.3/35.7	0/52.9/23.5
AKN	NA	NA	5.5/92.7/1.8	0/100.0/0	6.2/83.8/9.2	9.1/77.3/13.6	0/92.9/7.1	0/58.8/29.4
NET	NA	NA	0.9/10.9/7.3	0/8.3/0	0/0.8/0	NA	NA	0/0/5.9
KAH	NA	NA	NA	NA	NA	NA	NA	NA
GEH	0/9.1/0	NA	NA	NA	NA	NA	NA	NA
GE2	NA	0/11.1/0	NA	NA	NA	NA	NA	NA
CMP	0/72.7/9.1	5.6/83.3/5.6	0/1.8/0	NA	NA	NA	NA	NA
TET	0/54.5/18.2	5.6/72.2/22.2	0/3.6/10.0	0/0/8.3	NA	NA	NA	NA
MIN	NA	NA	NA	NA	NA	NA	NA	NA
ERY	NA	NA	NA	NA	NA	NA	NA	NA
LIN	NA	NA	NA	NA	NA	NA	NA	NA
CLI/CM	NA	NA	NA	NA	NA	NA	NA	NA
PRI	NA	NA	NA	NA	NA	NA	NA	NA
COL	0/0/0	0/0/0	0/0/0	0/0/0	0/75.4/8.5	0/68.2/22.7	0/92.9/7.1	0/29.4/41.2
SSS	NA	NA	NA	NA	NA	NA	NA	NA
FUR	NA	NA	NA	NA	NA	NA	NA	NA
NAL	0/18.2/0	0/11.1/5.6	1.8/48.2/36.4	0/75.0/16.7	NA	NA	NA	NA
OFL	NA	NA	4.5/56.4/34.5	0/83.3/16.7	0.8/7.7/3.8	0/9.1/0	0/0/21.4	0/0/5.9
PEF	NA	NA	0/0.9/0	NA	NA	NA	NA	NA
NOR	NA	NA	NA	NA	NA	NA	NA	NA
CIP	0/36.4/0	0/44.4/11.1	10.0/69.1/20.9	0/100.0/0	5.4/79.2/11.5	0/90.9/4.5	7.1/50.0/42.9	17.6/52.9/17.6
RFA	NA	0/5.6/0	NA	NA	15.4/3.1/33.8	13.6/4.5/4.5	21.4/0/14.3	35.3/29.4/5.9
FUC	NA	NA	NA	NA	NA	NA	NA	NA
FOS	NA	NA	0/60.0/5.5	0/25.0/16.7	0/6.9/55.4	0/0/27.3	0/7.1/35.7	0/5.9/58.8
VAN	NA	NA	NA	NA	NA	NA	NA	NA
TEC	NA	NA	NA	NA	NA	NA	NA	NA
SXT/TSU	0/9.1/72.7	0/5.6/94.4	0/28.2/71.8	0/16.7/75.0	0/4.6/47.7	0/13.6/27.3	0/7.1/35.7	0/23.5/41.2
AME	NA	NA	NA	NA	NA	NA	NA	NA
LEV	NA	0/5.6/0	NA	NA	0/0.8/0.8	0/4.5/0	NA	0/5.9/0
LIZ	NA	NA	NA	NA	NA	NA	NA	NA
MXF	NA	0/11.1/0	NA	NA	NA	NA	NA	NA
PIT	NA	NA	12.7/12.7/12.7	0/75.0/0	20.0/56.2/4.6	0/31.8/9.1	7.1/21.4/42.9	0/70.6/11.8
QDA	NA	NA	NA	NA	NA	NA	NA	NA
SAM	NA	NA	NA	NA	0/0.8/0	NA	0/0/7.1	NA
TEL	NA	NA	NA	NA	NA	NA	NA	NA
OXA	NA	NA	NA	NA	NA	NA	NA	NA
ETP	NA	NA	0/5.5/0.9	0/16.7/0	NA	NA	NA	NA
TGC	NA	NA	NA	NA	NA	NA	NA	NA

PEN: Penicillin G; AMP: Ampicillin; AMO: Amoxicillin; AMC: Amoxicillin + clavulanic acid; FAM: Ampicillin + Sulbactan; TIC: Ticarcillin; TCC: Ticarcillin + clavulanic acid; PIC: Piperacillin; TZP: Piperacillin + Tazobactam; IMI: Imipenem; MER: Meropenem; CFT: Cefatrizine; CXM: Cefuroxime; CXT: Cefoxitin; CTX: Cefotaxime; CAZ: Ceftazidime; CFM: Cephixime; FEP: Cefepime; ATM: Aztreonam; GEN: Gentamicin; SPT: Spectinomycin; KAN: Kanamycin strong dose; TOB: Tobramicin; AKN: Amikacin; NET: Netilmicin; KAH: Kanamycin 1000; GEH: Gentamicin 500; GE2: Gentamicin 250; CMP: Chloramphenicol; TET: Tetracycline; MIN: Minocycline; ERY: Erythromycin; LIN: Lincomycin; CLI/CM: Clindamycin; PRI: Pristinamycin; COL: Colistin; SSS: Sulfonamid; SXT/TSU: Trimethoprim/sulfamethoxazole (Cotrimoxazole); FUR: Nitrofurantoïn; NAL: Nalidixic acid; OFL: Ofloxacin; PEF: Pefloxacin; NOR: Norfloxacin; CIP: Ciprofloxacin; RFA: Rifampicin; FUC: Fusidic acid; FOS: Fosfomycin; VAN: Vancomycin; TEC: Teicoplanin; AME: Ampicillin Enterocoque; LEV: Levofloxacine; LIZ: Linezolid; MXF: Moxifloxacin; PIT: Piperacillin + Tazobactam; QDA: Quinupristin + Dalfopristin; SAM: Ampicillin + Sulbactan; TEL: Telithromycin; OXA: Oxacillin; ETP: Ertapenem; TGC: Tigecyclin; I: Intermediate; S: Susceptibility; R: Resistance; NA: not available.

Table 5. Susceptibility and Resistance rates for the 22 most common bacteria isolated from CPC during de study period (Continued)

Antibiotics	Isolated bacteria (No.)					
	Serratia marcescens (n=28)	*Stenotrophomonas maltophilia* (n=15)	*Staphylococcus aureus* (n=22)	*Streptococcus oralis* (n=14)	*Streptococcus pneumoniae* (n=36)	*Streptococcus sp.* (n=32)
	%I/%S/%R					
PEN	NA	NA	0/4.5/90.9	35.7/50.0/0	13.9/16.7/8.3	18.8/40.6/25.0
AMP	0/0/17.9	NA	NA	7.1/71.4/0	0/2.8/0	3.1/37.5/6.3
AMO	0/14.3/67.9	NA	NA	NA	0/83.3/0	NA
AMC	0/14.3/82.1	NA	NA	NA	0/55.6/0	NA
FAM	NA	0/0/6.7	NA	NA	NA	NA
TIC	3.6/85.7/10.7	0/6.7/73.3	NA	NA	NA	NA
TCC	0/0/3.6	0/80.0/86.7	NA	NA	NA	NA
PIC	0/57.1/10.7	6.7/20.0/46.7	NA	NA	NA	NA
TZP	0/17.9/0	NA	NA	NA	NA	NA
IMI	0/14.3/7.1	0/0/60.0	NA	NA	NA	NA
MER	0/3.6/0	0/6.7/26.7	NA	NA	NA	NA
CFT	3.6/0/96.4	NA	NA	NA	NA	NA
CXM	0/0/3.6	NA	NA	NA	NA	NA
CXT	3.6/7.1/10.7	NA	NA	NA	NA	NA
CTX	0/100.0/0	NA	NA	0/71.4/0	0/38.9/0	3.1/56.3/12.5
CAZ	0/100.0/0	20.0/40.0/26.7	NA	NA	NA	NA
CFM	NA	NA	NA	NA	NA	NA
FEP	0/17.9/0	6.7/6.7/46.7	NA	NA	NA	NA
ATM	NA	NA	NA	NA	NA	NA
GEN	0/71.4/28.6	13.3/13.3/33.3	0/63.6/31.8	NA	NA	NA
SPT	NA	NA	NA	NA	NA	NA
KAN	NA	NA	0/31.8/31.8	NA	NA	NA
TOB	7.1/50.0/39.3	6.7/6.7/26.7	0/36.4/27.3	NA	NA	NA
AKN	10.7/75.0/10.7	13.3/6.7/40.0	NA	NA	NA	NA
NET	NA	0/6.7/6.7	NA	NA	NA	NA
KAH	NA	NA	NA	57.1/14.3/7.1	0/2.8/0	53.1/3.1/18.8
GEH	NA	NA	NA	71.4/14.3/7.1	58.3/8.3/13.9	62.5/6.3/21.9
GE2	NA	NA	NA	NA	NA	NA
CMP	NA	NA	NA	7.1/0/0	2.8/72.2/5.6	0/3.1/0
TET	0/0/17.9	NA	0/36.4/63.6	0/35.7/57.1	0/30.6/63.9	0/31.3/56.3
MIN	NA	0/6.7/0	0/68.2/0	NA	NA	NA
ERY	NA	NA	0/50.0/45.5	0/71.4/28.6	16.7/63.9/13.9	0/50.0/40.6
LIN	NA	NA	4.5/63.6/27.3	NA	0/8.3/0	NA
CLI/CM	NA	NA	0/13.6/13.6	0/7.1/0	8.3/41.7/8.3	0/3.1/0
PRI	NA	NA	0/81.8/0	0/42.9/0	0/83.3/0	0/12.5/3.1
COL	0/0/0	0/20.0/40.0	0/0/0	0/0/0	0/0/0	0/0/0
SSS	NA	NA	NA	NA	NA	NA
FUR	NA	NA	0/63.6/0	0/42.9/0	0/2.8/0	0/68.8/0
NAL	0/78.6/3.6	NA	NA	NA	NA	NA
OFL	3.6/89.3/3.6	0/13.3/6.7	0/13.6/13.6	NA	NA	NA
PEF	NA	NA	0/4.5/0	NA	NA	NA
NOR	NA	NA	0/4.5/0	0/0/7.1	2.8/16.7/16.7	NA
CIP	0/100.0/0	26.7/53.3/13.3	0/4.5/0	0/0/7.1	61.1/11.1/5.6	NA
RFA	NA	20.0/26.7/16.7	22.7/54.5/13.6	0/78.6/0	0/27.8/0	0/53.1/6.3
FUC	NA	NA	0/54.5/0	NA	NA	NA
FOS	0/57.1/7.1	0/0/46.7	0/59.1/0	NA	NA	NA
VAN	NA	NA	0/100.0/0	0/92.9/7.1	0/97.2/0	0/87.5/0
TEC	NA	NA	0/81.8/4.5	0/78.6/0	0/5.6/0	0/81.3/0
SXT/TSU	0/100.0/0	0/80.0/13.3	0/18.2/13.6	0/7.14/64.3	0/2.8/5.6	0/15.6/59.4
AME	NA	NA	NA	0/7.1/0	0/2.8/0	0/0/3.1
LEV	NA	0/13.3/0	0/40.9/18.2	7.1/57.1/28.6	0/83.3/0	3.1/81.3/6.3
LIZ	NA	NA	4.5/59.1/0	7.1/78.6/0	0/8.3/0	0/71.9/0
MXF	NA	NA	0/4.5/0	NA	NA	NA
PIT	0/67.9/0	0/20.0/26.7	NA	NA	NA	NA
QDA	NA	NA	0/95.5/0	0/7.1/0	0/0/2.8	0/12.5/0
SAM	NA	0/0/6.7	NA	NA	NA	NA
TEL	NA	NA	0/31.8/0	0/64.3/0	0/0/2.8	0/68.8/3.1
OXA	NA	NA	0/54.5/45.5	0/0/7.1	2.8/0/2.8	NA
ETP	NA	NA	NA	NA	NA	NA
TGC	NA	NA	0/4.5/0	NA	NA	NA

PEN: Penicillin G; AMP: Ampicillin; AMO: Amoxicillin; AMC: Amoxicillin + clavulanic acid; FAM: Ampicillin + Sulbactan; TIC: Ticarcillin; TCC: Ticarcillin + clavulanic acid; PIC: Piperacillin; TZP: Piperacillin + Tazobactam; IMI: Imipenem; MER: Meropenem; CFT: Cefatrizine; CXM: Cefuroxime; CXT: Cefoxitin; CTX: Cefotaxime; CAZ: Ceftazidime; CFM: Cephixime; FEP: Cefepime; ATM: Aztreonam; GEN: Gentamicin; SPT: Spectinomycin; KAN: Kanamycin strong dose; TOB: Tobramicin; AKN: Amikacin; NET: Netilmicin; KAH: Kanamycin 1000; GEH: Gentamicin 500; GE2: Gentamicin 250; CMP: Chloramphenicol; TET: Tetracycline; MIN: Minocycline; ERY: Erythromycin; LIN: Lincomycin; CLI/CM: Clindamycin; PRI: Pristinamycin; COL: Colistin; SSS: Sulfonamid; SXT/TSU: Trimethoprim/sulfamethoxazole (Cotrimoxazole); FUR: Nitrofurantoïn; NAL: Nalidixic acid; OFL: Ofloxacin; PEF: Pefloxacin; NOR: Norfloxacin; CIP: Ciprofloxacin; RFA: Rifampicin; FUC: Fusidic acid; FOS: Fosfomycin; VAN: Vancomycin; TEC: Teicoplanin; AME: Ampicillin Enterocoque; LEV: Levofloxacine; LIZ: Linezolid; MXF: Moxifloxacin; PIT: Piperacillin + Tazobactam; QDA: Quinupristin + Dalfopristin; SAM: Ampicillin + Sulbactan; TEL: Telithromycin; OXA: Oxacillin; ETP: Ertapenem; TGC: Tigecyclin; I: Intermediate; S: Susceptibility; R: Resistance; NA: not available.

Cephalosporins, inhibitors of bacterial envelope synthesis showed a high sensitivity rate for most of the germs identified with: 100%, 71.4%, 81.8%, 94.4%, 91.7% and 94.9% sensitivity to cefotaxime for *Serratia marcescens, Streptococcus oralis, Haemophilus parainfluenzae, Haemophilus sp., Proteus mirabilis, Haemophilus influenzae* respectively; 85.2%, 100%, 91.7%, 91.5%, 86.4%, 71.4%, 76.5%, 100% sensitivity to ceftazidime for *Acinetobacter baumannii, Burkholderia cepacia, Proteus mirabilis, Pseudomonas aeruginosa, Pseudomonas fluorescens, Pseudomonas putida, Pseudomonas sp. Serratia marcescens* respectively; 77.3% sensitivity to cefepime for *Pseudomonas fluorescens*. However, the two bacterial species that showed a high percentage of resistance to cephalosporins were *Enterobacter cloacae* and *Escherichia coli* with 95.7% and 75.0% resistance to cefatrizine respectively. Other data are contained in Table 5.

Aminosides that inhibit the biosynthesis of bacterial proteins have shown a high level of sensitivity for most of the germs identified as cephalosporins. The antibiotics most represented in terms of sensitivity were amikacin, tobramicin and gentamicin. For amikacin, the most represented species in terms of sensitivity were: *Acinetobacter baumannii* with 88.9% sensitivity; *Acinetobacter calcoace with* 100.0% sensitivity; *Enterobacter cloacae with* 95.7% sensitivity; *Escherichia coli with* 75% sensitivity, *Klebsiella pneumoniae with* 92.7% sensitivity; *Proteus mirabilis with* 100% sensitivity; *Pseudomonas aeruginosa with* 83.8% sensitivity; *Pseudomonas fluorescens with* 77.3% sensitivity; *Pseudomonas putida with* 92.9% sensitivity and *Serratia marcescens* with 75% sensitivity. For tobramicin, the most sensitive species were: *Proteus mirabilis* (91.7%); *Pseudomonas aeruginosa (*76.2%); *Pseudomonas fluorescens (*77.3%); *Acinetobacter calcoace (*88.9%); *Chryseomonas luteola (*81.8%); *Chryseomonas sp.* (92.9%) and *Enterobacter cloacae (*82.6%). For gentamicin, sensitivity percentages were high for *Acinetobacter calcoace* (77.7%); *Chryseomonas luteola* (90.9%); *Enterobacter cloacae (*82.6%); *Proteus mirabilis* (91.7%); *Pseudomonas fluorescens (*77.3%) and *Serratia marcescens (*71.4%). Resistance levels were also observed for the aminoglycoside antibiotics with 90.9% resistance to gentamicin for *Chryseomonas luteola*; 81.8% and 92.9% resistance to tobramicin for *Chryseomonas luteola* and *Chryseomonas sp.* respectively and 72.7% resistance to amikacin for the same species. Table 5 presents in detail the resistance and susceptibility patterns of the other species identified in this study.

Almost all bacterial species identified in this study were sensitive to quinolones. The sensitivity profiles presented in Table 5 showed that only the species *Serratia marcescens* was more sensitive to nalidixic acid with a percentage sensitivity of 78.6%. *Serratia marcescens* and *Proteus mirabilis* were more sensitive to ofloxacin with sensitivity rates of 89.3% and 83.3% respectively. ciprofloxacin, systemic fluoroquinolone had the highest sensitivity rates with *Acinetobacter calcoace* (100.0%), *Proteus mirabilis* (100.0%), *Pseudomonas aeruginosa* (79.2%), *Pseudomonas fluorescens* (90.9%) and *Serratia marcescens* (100%). High levels of sensitivity were also observed for levofloxacin with 83.3% sensitivity for *Streptococcus pneumoniae* and 81.3% sensitivity for *Streptococcus sp*.

Other antibiotics involved in inhibiting protein synthesis, notably macrolides and related compounds, have shown significant levels of sensitivity for the identified germs. These are the true macrolides with erythromycin which showed 71.4% sensitivity for *Streptococcus oralis.* The ketolides with notably telithromycin which showed 64.3% and 68.8% sensitivity for Streptococcus *oralis* and *Streptococcus sp.* species respectively. Concerning synergistins or streptogramins, the *Staphylococcus aureus* species had a 95.5% sensitivity to quinupristin + dalfopristin and the *Staphylococcus aureus* and *Streptococcus pneumoniae* species showed percentages of sensitivity of 81.8% and 83.3% respectively for pristinamycin.

Sulfonamides, inhibitors of folic acid synthesis, showed high levels of resistance for the germs isolated in this study. *Staphylococcus aureus* was the bacterial species with a high level of resistance to trimethoprim + sulfamethoxazole, i.e. 50%. Cotrimoxazole (sulfamethoxazole + trimethoprim) also showed significant levels of resistance for the following species: 93.8% resistance for *Escherichia coli*; 87.3% resistance for *Haemophilus influenzae*; 72.7% resistance to *Haemophilus parainfluenzae*; 94.4% resistance to *Haemophilus sp.*; 71.8% resistance to *Klebsiella pneumoniae;* 75.0% resistance to *Proteus mirabilis* and 47.7% resistance to *Pseudomonas aeruginosa*. Concerning susceptibility, only *Serratia marcescens* and *Stenotrophomonas maltophilia* species showed significant levels of susceptibility to cotrimoxazole with 100.0% and 80.0% sensitivity respectively. See Table 5 for further information.

Among the inhibitors of bacterial envelope synthesis, three antibiotics of the carbapenem class were also used during the study period. These included imipenem, meropenem and ertapenem. The species with a higher level of sensitivity to imipenem were *Pseudomonas fluorescens with* 72.7% sensitivity, followed by *Klebsiella pneumoniae with* 64.5% sensitivity and *Pseudomonas aeruginosa* with 50.0% sensitivity. For meropenem, the highest sensitivity levels were observed for *Pseudomonas aeruginosa* (43.8%) and *Burkholderia cepacia* (46.2%). Only *Chryseomonas sp.* was the most represented in terms of resistance (42.8% resistance to meropenem). No germs were represented in terms of resistance and susceptibility to ertapenem (see Table 5).

Table 6. Susceptibility and Resistance rates for the 3 most common fungi isolated from CPC during de study period

Isolated organisms (No.)	%I/%S/%R						
	MIC	ECO	KET	FLU	AMB	NYS	CLO
Candida albicans (73)	2.7/89.0/0	1.4/87.7/0	1.3/79.5/1.3	0/5.5/0	1.4/82.2/9.6	0/82.2/6.8	4.1/83.6/1.4
Candida sp. (17)	0/58.8/0	0/70.6/0	5.9/64.6/0	0/5.9/0	0/52.9/17.6	0/47.1/17.6	17.6/52.9/0
Trichosporon spp. (7)	0/57.1/0	0/57.1/0	0/57.1/0	NA	0/42.9/14.3	0/57.1/0	14.3/42.9/0

MIC: Miconazole; ECO: Econazole; KET: Ketoconazole; FLU: Fluconazole; AMB: Amphotericin B; NYS: Nystatin; CLO: Clotrimazole; NA: not available; I: Intermediate; S: Susceptibility; R: Resistance.

Cyclin class antibiotics were also represented in terms of sensitivity in this study. The bacterial species most concerned were *Haemophilus sp.* with 72.2% sensitivity to tetracycline followed by *Haemophilus influenzae* which had 70.9% sensitivity to the same antibiotic. For minocycline, only the *Staphylococcus aureus* species was strongly involved in sensitivity with a rate of 68.2%.

Peptide class antibiotics have also been used to test the sensitivity and resistance of isolated germs in LRTIs. These are colistin, vancomycin and teicoplanin. Colistin, a polypeptide antibiotic, showed high levels of resistance for *Burkholderia cepacia* (76.9%), *Chryseomonas luteola* (81.8%) and *Chryseomonas sp.* (78.6%). Depending on the sensitivity, the following species were most concerned: *Pseudomonas aeruginosa* (75.4%); *Pseudomonas fluorescens* (68.2%); *Pseudomonas putida* (92.9%). Most of the germs isolated were susceptible to vancomycin with *Staphylococcus aureus*, *Streptococcus oralis*, *Streptococcus pneumoniae* and *Streptococcus sp*. for which sensitivity was particularly high (100.0%, 92.9%, 97.2% and 87.5% respectively). The same species (*Staphylococcus aureus*, *Streptococcus oralis* and *Streptococcus sp*.) were also particularly sensitive to teicoplanin with sensitivity percentages of 81.8%, 78.6% and 81.3% respectively.

Other classes of antibiotics less represented than the previous ones were also used in this study. This is the class of chloramphenicol for which the most sensitive germs were *Haemophilus influenzae* (83.5%), *Haemophilus sp.* (83.3%) and *Streptococcus pneumoniae* (72.2%). The class of nitrofurans whose mechanisms of action are complex or unknown with nitrofurantoin for which the most sensitive organisms were *Staphylococcus aureus* (63.6%) and *Streptococcus sp.* (68.8%). In the case of various antibiotics such as rifampicin used as an antituberculosis drug, the most sensitive species were *Staphylococcus aureus*, *Streptococcus oralis* and *Streptococcus sp.* with sensitivity percentages of 54.5%, 78.6% and 53.1% respectively. The same previous species were also the most represented in terms of sensitivities for oxazolidinones with sensitivities of 59.1%, 78.6% and 71.9% to linezolid. Fosfomycin which is an inhibitor of bacterial envelope synthesis was also represented in terms of sensitivity and resistance. The isolated germs most resistant to this antibiotic were: *Acinetobacter calcoace* (66.7%); *Burkholderia cepacia* (84.6%); *Chryseomonas luteola* (54.5%); *Chryseomonas sp.* (57.1%); *Pseudomonas aeruginosa* (55.4%) and *Pseudomonas sp.* (58.8%). For sensitivity to this antibiotic, the most represented were: *Escherichia coli* (87.5%); *Klebsiella pneumoniae* (60%); *Serratia marcescens (*57.1%) and *Staphylococcus aureus* (59.1%). For fusidic acid, only *Staphylococcus aureus* was the most represented in terms of sensitivity (54.5%).

In mycology, the fungi most represented in LRTIs were *Candida albicans*, *Candida sp.* and *Trichosporon spp.* Table 6 shows the sensitivity and resistance profiles to the antifungal agents used in this research. The two classes represented here are azoles and polyenes. For azoles, sensitivity levels were high for *Candida albicans* to miconazole (89.0%), econazole (87.7%), ketoconazole (79.5%) and clotrimazole (83.6%). Other *Candida* strains (*Candida sp.*) were also susceptible to azoles with econazole having the highest level of sensitivity (70.6%). *Trichosporon spp.* showed similar sensitivity levels to miconazole, econazole and ketoconazole (57.1% for these three antifungal agents). Clotrimazole had a lower sensitivity level (42.9%). For the polyene class of antifungal agents, *Candida albicans* was equally sensitive to amphotericin B and nystatin with a sensitivity level of 82.2% for these two antifungal agents. For the other strains of Candida (*Candida sp.*) the sensitivity to amphotericin B was 52.9% while that of nystatin was 47.1%. Finally, the percentage sensitivity of *Trichosporon spp.* to nystatin was 57.1% and 42.9% for amphotericin B.

4. Discussion

The results of this study revealed that the prevalence of LRTIs was 47.8% (858 positive samples). This prevalence of LRTIs is below that found by Zhanel *et al.* [18] in 2010 in Canada, where the prevalence of infection was 53.7%, or that found by Bajpai *et al.* [2] in 2013, who obtained 86.08% positive cultures on respiratory samples. In the research conducted by Ahmed *et al.* [35], the prevalence of positive respiratory samples for a gram-negative bacillus was 17.03%, which is lower than that obtained in the present study. In the study conducted in Cameroon by Tchatchouang *et al.* [23] published in 2019, the prevalence of LRTIs (46.8%) was close to that obtained in the present study. These observed differences in prevalence could be explained by the environment, the seasons, the characteristics of the population at risk, the availability of health care services as specified by Vijay and Dalela [1] or Bajpai *et al.* [2]. In this study, men were the most represented with 449 (48.0%) samples compared to 377 (48.3%) samples for women for a sex ratio of 1.2. This difference in gender distribution was statistically significant ($p = 0.01224$). The age of participants positive for LRTI ranged from 7-90 years for a mean age of 51.2 years ± 15.4 SD. The distribution of this age variable into groups showed that adults (41-60 years and ≥ 61 years) were the most affected in our context. Similar results were obtained in the study by Ahmed *et al.* [35] where there were 227 (76.17%) male samples versus 71 (23.83%) female samples with patients between 61-80 years of age being most affected. In the study by Samad *et al.* [36] published in 2017 the prevalence of respiratory infections was 57.56% with men who were the most contaminated (54.93%) compared to women (45.07%). The study carried out in Cameroon at the Pneumology Department of Jamot Hospital by Tchatchouang *et al.* [23] also showed that men (64%) are more affected by respiratory infections than women (36%) as in the present study. Another study carried out by Kengne *et al.* [37] between May and October 2014 at the Military Hospital in Yaounde showed that women were more affected by LRTIs with *Streptococcus pneumoniae* than men with a significant difference in distribution compared to sex ($\chi^2 = 18.95$, $p = 0.008$) with in particular adults who were the most infected (30-44 years old). In the study by Vijay and Dalela [1], men (56.5%) were also at greater risk of infection than women (20.5%) as in the present study. The fact that men are the most concerned by the infection in our context could be explained by the characteristics of the male population of the study, particularly professional

activity which exposes them more to the infection than women.

Two families of germs were identified in this study with on the one hand bacteria with 751 (41.8%) samples and on the other hand fungi with 107 (6.0%) samples. Among the bacteria, Gram-negative bacilli were the most represented (34.9%), followed by Gram-positive Cocci (6.7%) and Gram-negative Cocci (0.2%). These results are consistent with those obtained in other studies [1,2,35,38,39,10,41,42,43,] where most of the germs encountered in LRTIs were Gram-negative bacteria with a predominance of bacilli over Cocci. Concerning fungi, they were less represented with *Candida albicans which was* the most abundant species. This result is close to that of Golas *et al.* [21] where *Candida albicans* was the second most represented yeast after *Candida glabrata* in the lower respiratory tract samples, or those of the study by Gileles-Hillel *et al.* [44] where *Candida albicans* was the predominant species among the fungi followed by *Aspergillus fumigatus*, *Candida glabrata* and *Candida parapsilosis*. Approximately 80 bacterial and fungal species were isolated during the study period and the most represented (those with a prevalence greater than or equal to 0.50%) in the context of LRTIs were: *Pseudomonas aeruginosa* (7.24%), *Klebsiella pneumoniae* (6.13%), *Haemophilus influenzae* (4.40%), *Candida albicans* (4.07%), *Streptococcus pneumoniae* (2.01%), *Streptococcus sp.* (1.78%), *Serratia marcescens* (1.56%), *Acinetobacter baumannii* (1.50%), *Enterobacter cloacae* (1.28%), *Pseudomonas fluorescens* (1.23%), *Straphylococcus aureus* (1.23%), *Haemophilus sp.* (1.00%), *Pseudomonas sp.* (0.95%), *Candida sp.* (0.95%), *Escherichia coli* (0.89%), *Stenotrophomonas maltophilia* (0.84%), *Chryseomonas sp.* (0.78%), *Pseudomonas putida* (0.78%), *Streptococcus oralis* (0.78%), *Burkholderia cepacia* (0.72%), *Proteus mirabilis* (0.67%), *Chryseomonas luteola* (0.61%), *Haemophilus parainfluenzae* (0.61%), *Acinetobacter calcoace* (0.50%). These results are close to those obtained in other studies [9,12,13,17,18,38,45-51] where most of the germs encountered in LRTIs are: *Pseudomonas aeruginosa*, *Haemophilus influenzae*, *Klebsiella pneumoniae*, *Streptococcus pneumoniae* with precisely that of Zhao *et al.* [52] where *Candida albicans* was strongly represented in the lower respiratory tract as is the case in the present study.

The results of our study showed that a statistically significant association between isolated germs by gender and age groups exists in our context ($p = 0.01224$ and $p<0.0001$ respectively). The species for which the difference in distribution was significant by gender were *Haemophilus influenzae* ($p = 0.01394$) and *Streptococcus pneumoniae* ($p = 0.037$) with the females who were more infected than the males. For the other isolated germs, men were the most concerned by the infection however, the differences in distribution were not significant ($p>0.05$). The logistic regression model showed that sex is a risk factor for *Haemophilus influenzae* infection with women being 1.78 times more at risk than men (OR = 1.78, CI = 1.09-1.95, $p = 0.01394$). The species associated with infection by age group were *Haemophilus influenzae* ($p = 0.01425$) followed by *Haemophilus sp.* ($p = 0.001952$) and *Streptococcus oralis* ($p = 0.04143$). The 41-60 year age group was most affected by infection with *Pseudomonas aeruginosa*, and *Klebsiella pneumoniae*, which were the most represented germs in the study and were strongly found in this age group despite a non-statistically significant difference in distribution ($p = 0.2656$ and $p = 0.5888$ respectively). The studies by Kengne et *al.* [37], Ahmed *et al.* [35] and Vijay and Dalela [1] also showed that the sex and age of patients with LRTIs were risk factors for infection, with men overall being the most contaminated and adults (>30 years).

In this work, several classes or families of antibiotics were used to highlight the sensitivity and resistance profiles of isolated organisms. The most represented families were penicillins, cephalosporins, aminosides, quinolones, macrolides and related, glycopeptides, penems, sulfonamides, cyclines and other various antibiotics. With regard to antifungals, the only classes represented were those of the azoles and polyenes. The present study showed that the most resistant predominant species were: *Pseudomonas aeruginosa, Klebsiella pneumoniae, Haemophilus influenzae, Streptococcus pneumoniae* and the yeast *Candida albicans. Pseudomonas aeruginosa*, the Gram-negative bacillus most represented in our study was multi-resistant (MDR) to most of the classes of antibiotics represented in this research. Levels of resistance were first observed to ticarcillin (75.4%) and then to ticarcillin + clavulanic acid (70.8%). *Pseudomonas aeruginosa* was also highly resistant to cefotaxime of the cephalosporin class with 91.5% resistance to this antibiotic. Aminosides were found to be effective against *Pseudomonas aeruginosa* in the present study with 83.8% sensitivity to amikacin and 76.2% sensitivity to tobramycin. ciprofloxacin, a systemic quinolone, was also very effective against *Pseudomonas aeruginosa* with a 79.2% sensitivity rate. Among the sulfonamides, only cotrimoxazole (sulfamethoxazole + trimethoprim) showed a high level of resistance to *Pseudomonas aeruginosa* (47.7%). In the class of penems, *Pseudomonas aeruginosa* showed 50% sensitivity to imipenem and 43.8% sensitivity to meropenem. For the antibiotics of the peptide class, colistin showed a sensitivity of 75.4%. Fosfomycin, which is an inhibitor of bacterial envelope synthesis, showed a resistance percentage of 55.4%. These results are close to those of Farooq *et al.* [53], where *Pseudomonas aeruginosa* was MDR to most of the antibiotics used: 81.6% resistance to imipenem, 80.4% resistance to ciprofloxacin, 78% resistance to ceftazidime, 74.2% resistance to gentamicin, 66% resistance to amikacin, 62% resistance to piperacillin + tazobactam and 40% resistance to ceftolozane + tazobactam. Research by Samad *et al. [36]* also revealed multidrug resistance of *Pseudomonas aeruginosa* and *Pseudomonas aeruginosa* MDR. Antibiotics for which resistance to *Pseudomonas aeruginosa was* observed were: cefoperazone + sulbactam (83.10%) and piperacillin + tazobactam (66.20%). As for MDR *Pseudomonas aeruginosa*, it had a resistance level of 96.43% to piperacillin + tazobactam and 100% resistance to cefoperazone + sulbactam. In the same research, high levels of sensitivity were observed for amikacin (82.14%) and meropenem (78.54%).

The second most represented species, *Klebsiella pneumoniae* was also like the previous one involved in multiple levels of resistance to the antibiotics used in this study: 88.2% resistance to amoxicillin, 100% resistance

to ticarcillin and 71.8% resistance to cotrimoxazole (sulfamethoxazole + trimethoprim). With regard to susceptibility, high levels were observed for amikacin (92.7%), imipenem (64.5%), and fosfomycin (60%). These results are similar to the study of Vijay and Dalela [1] where *Klebsiella pneumoniae* was the most represented in LRTIs. In their study, the highest resistance was found for augmentin (74.64%), ceftriaxone (49.29%), ciprofloxacin (77.46%), chloramphenicol (74.64%), erythromycin (67.6%), gentamycin (59.15%) and ofloxacin (81.69%). In the study by Ahmed *et al* [35], *Klebsiella pneumoniae* was also highly represented in LRTIs as in the present study with higher resistance levels (> 80%) for cefepime (80.9%), cefuroxime (83.3%), ceftazidime (84.1%) and aztreonam (88.9%). Imipenem and amikacin produced different resistance results compared to the present study, i.e. 7.8% resistance to imipenem versus 0.9% obtained in this study and 34.3% resistance to amikacin versus 1.8% obtained in our study. In the study by Rammaert *et al.* in contrast [54], Extended Spectrum β-Lactamase-producing *Klebsiella pneumoniae* (ESBL-producing *KP)* was associated with 50% resistance to gentamicin, 87.5% sensitivity to ciprofloxacin and 100% sensitivity to fosfomycin. For non-ESBL-producing *KP*, high sensitivities were observed for amoxicillin/clavulanic acid (94.7%), cefotaxime (97.4%), cefepime (96.7%), ceftazidime (97.4%), ticarcillin (2.5%), imipenem (97.4%), nalidixic acid (83.3%), ciprofloxacin (92.3%), gentamicin (89.7%), amikacin (97.4%), and cotrimoxazole (61.3%).

Haemophilus influenzae and *Streptococcus pneumoniae* were the most Gram-negative bacilli in this study after *Pseudomonas aeruginosa* and *Klebsiella pneumoniae*. *Haemophilus influenzae* was more sensitive to cefotaxime (94.9%), tetracyclin (70.9%) and chloramphenicol (83.5%). Only cotrimoxazole (87.3%) was ineffective against *Haemophilus influenzae*. As for *Streptococcus pneumoniae*, our study revealed that it was more sensitive to the antibiotics levofloxacin (83.3%), pristinamycin (83.3%), vancomycin (97.2%) and chloramphenicol (72.2%). These results are different from those of Feshchenko *et al.* [46], where *Streptococcus pneumoniae* was 87.3% sensitive to penicillin according to CLSI (oral) breakpoints and 99.3% according to CLSI iv breakpoints. Sensitivity to amoxicillin + clavulanic acid, ceftriaxone and levofloxacin was 100% according to the CLSI breakpoints and the pharmacokinetic/pharmacodynamic (PK/PD). Sensitivities to cephalosporins and macrolides were 95.5% and 88.1% respectively. In the same study, all strains of *Haemophilus influenzae* isolated were sensitive to amoxicillin + clavulanic acid, ceftriaxone, ciprofloxacin, cefixime and levofloxacin for all breakpoints (EUCAST, CLSI and PK/PD). The sensitivity of cefuroxime was 100% according to the CLSI breakpoints and 73.1% according to the EUCAST and PK/PD breakpoints. Another monitoring study of antibiotic resistance carried out in Pakistan by Zafar *et al.* [48] between 2002-2015 showed that the resistance of *Streptococcus pneumoniae* strains to erythromycin and clarithromycin was evolving around 2004 until 2007 with an increase in the reduction of penicillin sensitivity. The same study also showed that *Haemophilus influenzae* was 100% sensitive to amoxicillin + clavulanic acid and 97.4% sensitive to ampicillin between 2014 and 2015. In Vietnam, Van *et al.* [47], obtained results close to those obtained in the present study with complete sensitivity of *Streptococcus pneumoniae* to vancomycin. In their study, *Streptococcus pneumoniae* in children was less sensitive to most antibiotics than in the elderly. *Haemophilus influenzae* was more sensitive to amoxicillin + clavulanic acid (97.4%) and also to ceftriaxone according to CLSI and PK/PD breakpoints and not those of the EUCAST. In Russia [49], lower sensitivities to penicillin, macrolides and cotrimoxazole were obtained compared to the present study for *Streptococcus pneumoniae*. However, isolates were highly sensitive (≥92.8%) to fluoroquinolones with *Haemophilus influenzae* which showed reduced sensitivity to ampicillin, cefaclor, clarithromycin and cotrimoxazole. In Greece, Torumkuney *et al.* [50] showed that resistance of *Streptococcus pneumoniae* was increased for macrolides and that the activity of clarithromycin against *Haemophilus influenzae* decreased during the study period.

Our study showed that *Candida albicans* was highly sensitive to antifungals of the azole class with 89% sensitivity to miconazole, 87.7% sensitivity to econazole, 79.5% sensitivity to ketoconazole and 83.6% sensitivity to clotrimazole. Sensitivity levels to polyenes were also very high with 82.2% sensitivity to amphotericin B and nystatin. These results are close to those of Golas *et al.* [21] where *Candida albicans* was sensitive for all the antifungal agents used: 100% sensitivity to amphotericin B, 100% sensitivity to fluconazole, 97% sensitivity to itraconazole and 100% sensitivity to voriconazole, posaconazole and caspofungin. In the research of Zeng *et al.* [14], *Candida albicans* was the most represented in LRTIs followed by *Candida glabrata*, Candida *tropicalis*, Candida *krusei*, *Candida parapsilosis* and other *Candida* species with different results in terms of antifungal activity compared to the present study. In their study, isolated yeasts were resistant to fluconazole, itraconazole and voriconazole with percentages of 18.6%, 23.1% and 18.5% respectively.

In view of the results of this study, in particular the high levels of resistance to antibiotics, it would be necessary for certain classes of drugs not to be used in the context of monotherapy. In addition, a mapping of the resistance genes of organisms isolated from the respiratory tract must be done by molecular biology analyzes in order to improve antibiotic therapy in our context. Finally, the actors of the Ministry of Public Health as well as the hospital staff must promote the implementation of large scale awareness campaigns in order to reduce the large scale consumption of antibiotics, self-medication or any risky behavior that may favor the increase in antibiotic resistant strains.

5. Conclusion

Lower respiratory tract infections have until now been a public health problem throughout the world in general and in developing countries in particular. Moreover, despite the many advances that have been made in both diagnosis and treatment, the increase in the rates of antibiotic resistance of germs is complicating the management of patients. This retrospective observational study, which took place in Yaounde between 2010 and 2019, showed

that lower respiratory tract infections due to bacterial and fungal species were high in the cameroonian context. This study also showed that the risk of infection was also associated with age and sex with men being the most infected on the one hand and adult being the most concerned by the contamination on the other hand. The alarming finding of antibiotic resistance observed in this study should lead practitioners to prescribe these drugs rationally, preferably based on the data of an antibiotic susceptibility test. Thus, it is more than necessary to establish a regular surveillance of antibiotic resistance which must be generalized at the level of all health care centers in order to define therapeutic and prophylactic strategies adapted to the local epidemiology. The judicious application of preventive measures can only be conceived as part of a prevention programme involving all hospital departments.

List of Abbreviations

CAP	Community-acquired Pneumonia
CA-SFM	Comité de l'antibiogramme de la Société Française de Microbiologie
CLSI	Clinical and Laboratory Standard Institute
CPC	Centre Pasteur of Cameroon
DALYs	Disability-Adjusted Life Years
ESBL	Extended Spectrum β-Lactamase
EUCAST	European committee on antimicrobial susceptibility testing
HAP	Hospital-acquired Pneumonia
HIV/AIDs	Human Immunodeficiency Virus/Acquired Immunodeficiency syndrome
ICU	Intensive care unit
LRTIs	Lower respiratory tract infections
MDR	Multidrug-resistant
MRSA	Methicillin-resistant *Staphylococcus aureus*
PK/PD	Pharmacokinetic/Pharmacodynamic
PRSP	Penicillin-resistant *Streptococcus pneumoniae*
VAP	Ventilator-acquired *Pneumonia*
VRE	Vancomycin-resistant *Enterococcus*
VRSA	Vancomycin-resistant *Staphylococcus aureus*
WHO	World Health Organization

Acknowledgements

Thanks are due to all the individuals who participated in this study.

Conflicts of Interest

The authors declare that there are no conflicts of interest regarding the publication of this paper.

References

[1] Vijay S, Dalela G. Prevalence of LRTI in Patients Presenting with Productive Cough and Their Antibiotic Resistance Pattern. J Clin Diagn Res. 2016; 10(1): DC09-12.

[2] Bajpai T, Shrivastava G, Bhatambare GS, Deshmukh AB, Chitnis V. Microbiological profile of lower respiratory tract infections in neurological intensive care unit of a tertiary care center from Central India. J Basic Clin Pharm. 2013; 4(3): 51-5.

[3] Appelbaum PC, Gillespie SH, Burley CJ, Tillotson GS. Antimicrobial selection for community-acquired lower respiratory tract infections in the 21st century: a review of gemifloxacin. Int J Antimicrob Agents. 2004; 23(6): 533-46.

[4] Domenech M, Sempere J, de Miguel S, Yuste J. Combination of Antibodies and Antibiotics as a Promising Strategy Against Multidrug-Resistant Pathogens of the Respiratory Tract. Front Immunol. 2018; 9: 2700.

[5] Pakhale S, Mulpuru S, Verheij TJM, Kochen MM, Rohde GGU, Bjerre LM. Antibiotics for community-acquired pneumonia in adult outpatients. Cochrane Database Syst Rev. 2014; (10): CD002109.

[6] Haddar CH, Joly J, Carricajo A, Verhoeven PO, Grattard F, Mory O, et al. Strategy using a new antigenic test for rapid diagnosis of Streptococcus pneumoniae infection in respiratory samples from children consulting at hospital. BMC Microbiol. 2020; 20(1): 79.

[7] Alp E, Kalin G, Coskun R, Sungur M, Guven M, Doganay M. Economic burden of ventilator-associated pneumonia in a developing country. J Hosp Infect. 2012; 81(2): 128-30.

[8] Pugh R, Grant C, Cooke RPD, Dempsey G. Short-course versus prolonged-course antibiotic therapy for hospital-acquired pneumonia in critically ill adults. Cochrane Database Syst Rev. 2015; (8): CD007577.

[9] Tansarli GS, Mylonakis E. Systematic Review and Meta-analysis of the Efficacy of Short-Course Antibiotic Treatments for Community-Acquired Pneumonia in Adults. Antimicrob Agents Chemother. 2018; 62(9).

[10] Halls A, Van't Hoff C, Little P, Verheij T, Leydon GM. Qualitative interview study of parents' perspectives, concerns and experiences of the management of lower respiratory tract infections in children in primary care. BMJ Open. 2017; 7(9): e015701.

[11] Goel N, Chaudhary U, Aggarwal R, Bala K. Antibiotic sensitivity pattern of gram negative bacilli isolated from the lower respiratory tract of ventilated patients in the Intensive care unit. Indian J Crit Care Med. 2009; 13(3): 148-51.

[12] Gai X-Y, Bo S-N, Shen N, Zhou Q-T, Yin A-Y, Lu W. Pharmacokinetic-pharmacodynamic analysis of ciprofloxacin in elderly Chinese patients with lower respiratory tract infections caused by Gram-negative bacteria. Chin Med J. 2019; 132(6): 638-46.

[13] Godbole G, Gant V. Respiratory tract infections in the immunocompromised. Curr Opin Pulm Med. 2013; 19(3): 244-50.

[14] Zeng Z-R, Tian G, Ding Y-H, Yang K, Liu J-B, Deng J. Surveillance study of the prevalence, species distribution, antifungal susceptibility, risk factors and mortality of invasive candidiasis in a tertiary teaching hospital in Southwest China. BMC Infect Dis. 2019; 19(1): 939.

[15] Wardhana null, Datau EA. A patient with allergic bronchopulmonary mycosis caused by Aspergillus fumigatus and Candida albicans. Acta Med Indones. 2012; 44(4): 317-23.

[16] Kandeel A, Palms DL, Afifi S, Kandeel Y, Etman A, Hicks LA, et al. An educational intervention to promote appropriate antibiotic use for acute respiratory infections in a district in Egypt- pilot study. BMC Public Health. 2019; 19(Suppl 3): 498.

[17] Santerre Henriksen A, Smart JI, Hamed K. Susceptibility to ceftobiprole of respiratory-tract pathogens collected in the United Kingdom and Ireland during 2014-2015. Infect Drug Resist. 2018; 11: 1309-20.

[18] Zhanel GG, DeCorby M, Adam H, Mulvey MR, McCracken M, Lagacé-Wiens P, et al. Prevalence of antimicrobial-resistant pathogens in Canadian hospitals: results of the Canadian Ward Surveillance Study (CANWARD 2008). Antimicrob Agents Chemother. 2010; 54(11): 4684-93.

[19] Mamishi S, Mohammadian M, Pourakbari B, Hosseinpour Sadeghi R, Haghi Ashtiani MT, Abdosalehi MR, et al. Antibiotic Resistance And Genotyping Of Gram-Positive Bacteria Causing Hospital-Acquired Infection In Patients Referring To Children's Medical Center. Infect Drug Resist. 2019; 12: 3719-26.

[20] An S, Chen J, Wang Z, Wang X, Yan X, Li J, et al. Predominant characteristics of CTX-M-producing Klebsiella pneumoniae isolates from patients with lower respiratory tract infection in multiple medical centers in China. FEMS Microbiol Lett. 2012; 332(2): 137-45.

[21] Gołaś M, Netsvyetayeva I, Sikora M, Piskorska K, Sulik-Tyszka B, Swoboda-Kopeć E. Trends in antifungal susceptibility of Candida species--one year observation. Pol J Microbiol. 2014; 63(2): 217-22.

[22] Tchatchouang S, Bigna JJ, Nzouankeu A, Fonkoua M-C, Nansseu JR, Ndangang MS, et al. Prevalence of respiratory bacterial infections in people with lower respiratory tract infections in Africa: the BARIAFRICA systematic review and meta-analysis protocol. BMJ Open. 2018; 8(9): e023592.

[23] Tchatchouang S, Nzouankeu A, Kenmoe S, Ngando L, Penlap V, Fonkoua M-C, et al. Bacterial Aetiologies of Lower Respiratory Tract Infections among Adults in Yaoundé, Cameroon. Biomed Res Int. 2019; 2019: 4834396.

[24] Coico R. Gram staining. Curr Protoc Microbiol. 2005;Appendix 3:Appendix 3C.

[25] Holmes B, Willcox WR, Lapage SP. Identification of Enterobacteriaceae by the API 20E system. J Clin Pathol. 1978; 31(1): 22-30.

[26] Joyanes P, del Carmen Conejo M, Martínez-Martínez L, Perea EJ. Evaluation of the VITEK 2 System for the Identification and Susceptibility Testing of Three Species of Nonfermenting Gram-Negative Rods Frequently Isolated from Clinical Samples. J Clin Microbiol. 2001; 39(9): 3247-53.

[27] Ligozzi M, Bernini C, Bonora MG, de Fatima M, Zuliani J, Fontana R. Evaluation of the VITEK 2 System for Identification and Antimicrobial Susceptibility Testing of Medically Relevant Gram-Positive Cocci. J Clin Microbiol. 2002; 40(5): 1681-6.

[28] Nakasone I, Kinjo T, Yamane N, Kisanuki K, Shiohira CM. Laboratory-based evaluation of the colorimetric VITEK-2 Compact system for species identification and of the Advanced Expert System for detection of antimicrobial resistances: VITEK-2 Compact system identification and antimicrobial susceptibility testing. Diagn Microbiol Infect Dis. 2007; 58(2): 191-8.

[29] Ramani R, Gromadzki S, Pincus DH, Salkin IF, Chaturvedi V. Efficacy of API 20C and ID 32C Systems for Identification of Common and Rare Clinical Yeast Isolates. J Clin Microbiol. 1998; 36(11): 3396-8.

[30] Cuenca-Estrella M, Arendrup MC, Chryssanthou E, Dannaoui E, Lass-Florl C, Sandven P, et al. Multicentre determination of quality control strains and quality control ranges for antifungal susceptibility testing of yeasts and filamentous fungi using the methods of the Antifungal Susceptibility Testing Subcommittee of the European Committee on Antimicrobial Susceptibility Testing (AFST-EUCAST). Clin Microbiol Infect. 2007; 13(10): 1018-22.

[31] Weinstein MP, Clinical and Laboratory Standards Institute. Performance standards for antimicrobial susceptibility testing. 2019.

[32] Détermination de la sensibilité aux antibiotiques. In: CASFM/EUCAST: Société Française de Microbiologie. 2019. p. 6-25.

[33] R. Core Team. R: A Language and Environment for Statistical Computing. R Foundation for Statistical Computing, Vienna, Austria, 2019. https://www.R-project.org/.

[34] Harrison E, Drake T, Ots R, finalfit: Quickly Create Elegant Regression Results Tables and Plots when Modelling, 2019. https://CRAN.R-project.org/package=finalfit.

[35] Ahmed SM, Jakribettu RP, Meletath SK, B A, Vpa S. Lower Respiratory Tract Infections (LTRIs): An Insight into the Prevalence and the Antibiogram of the Gram Negative, Respiratory, Bacterial Agents. J Clin Diagn Res. 2013; 7(2): 253-6.

[36] Samad A, Ahmed T, Rahim A, Khalil A, Ali I. Antimicrobial susceptibility patterns of clinical isolates of Pseudomonas aeruginosa isolated from patients of respiratory tract infections in a Tertiary Care Hospital, Peshawar. Pak J Med Sci. 2017; 33(3): 670-4.

[37] Kengne M, Lebogo MBB, Nwobegahay JM, Ondigui BE. Antibiotics susceptibility pattern of Streptococcus pneumoniae isolated from sputum cultures of human immunodeficiency virus infected patients in Yaoundé, Cameroon. Pan Afr Med J. 2018; 31: 16.

[38] Vishwanath S, Chawla K, Gopinathan A. Multidrug resistant Gram-negative bacilli in lower respiratory tract infections. Iran J Microbiol. 2013; 5(4): 323-7.

[39] Liu Y-X, Cao Q-M, Ma B-C. Pathogens distribution and drug resistance in patients with acute cerebral infarction complicated with diabetes and nosocomial pulmonary infection. BMC Infect Dis. 2019; 19(1): 603.

[40] Sahu MK, Siddharth B, Choudhury A, Vishnubhatla S, Singh SP, Menon R, et al. Incidence, microbiological profile of nosocomial infections, and their antibiotic resistance patterns in a high volume Cardiac Surgical Intensive Care Unit. Ann Card Anaesth. 2016; 19(2): 281-7.

[41] Xiao Q-Z, Su D-H, Jiang J-H, Zhong N-S. [Distribution and drug-resistance of 3 500 gram-negative bacteria in Guangzhou]. Di Yi Jun Yi Da Xue Xue Bao. 2005; 25(2): 132-8.

[42] Dong L, Zhou X-C, Chen X-F, Yang J-H, Lin J, Zhang H-L, et al. [Detection of etiologic agents and antibiotic resistance in children with acute lower respiratory tract infection in Wenzhou City]. Zhongguo Dang Dai Er Ke Za Zhi. 2006; 8(5): 369-72.

[43] Hua C-Z, Yu H-M, Chen Z-M, Li J-P, Shang S-Q. [Pathogenic bacteria of childhood lower respiratory tract infection]. Zhongguo Dang Dai Er Ke Za Zhi. 2006; 8(5): 365-8.

[44] Gileles-Hillel A, Shoseyov D, Polacheck I, Korem M, Kerem E, Cohen-Cymberknoh M. Association of chronic Candida albicans respiratory infection with a more severe lung disease in patients with cystic fibrosis. Pediatr Pulmonol. 2015; 50(11): 1082-9.

[45] Ginsburg AS, Tinkham L, Riley K, Kay NA, Klugman KP, Gill CJ. Antibiotic non-susceptibility among Streptococcus pneumoniae and Haemophilus influenzae isolates identified in African cohorts: a meta-analysis of three decades of published studies. Int J Antimicrob Agents. 2013;42(6): 482-91.

[46] Feshchenko Y, Dzyublik A, Pertseva T, Bratus E, Dzyublik Y, Gladka G, et al. Results from the Survey of Antibiotic Resistance (SOAR) 2011-13 in Ukraine. J Antimicrob Chemother. 2016;71 Suppl 1:i63-69.

[47] Van PH, Binh PT, Minh NHL, Morrissey I, Torumkuney D. Results from the Survey of Antibiotic Resistance (SOAR) 2009-11 in Vietnam. J Antimicrob Chemother. 2016;71 Suppl 1:i93-102.

[48] Zafar A, Hasan R, Nizamuddin S, Mahmood N, Mukhtar S, Ali F, et al. Antibiotic susceptibility in Streptococcus pneumoniae, Haemophilus influenzae and Streptococcus pyogenes in Pakistan: a review of results from the Survey of Antibiotic Resistance (SOAR) 2002-15. J Antimicrob Chemother. 2016;71 Suppl 1: i103-109.

[49] Torumkuney D, Mayanskiy N, Edelstein M, Sidorenko S, Kozhevin R, Morrissey I. Results from the Survey of Antibiotic Resistance (SOAR) 2014-16 in Russia. J Antimicrob Chemother. 2018;73 suppl 5:v14-21.

[50] Torumkuney D, Papaparaskevas J, Morrissey I. Results from the Survey of Antibiotic Resistance (SOAR) 2014-16 in Greece. J Antimicrob Chemother. 2018;73 suppl 5: v36-42.

[51] Abdullah FE, Ahuja KR, Kumar H. Prevalence and emerging resistance of Moraxella catarrhalis in lower respiratory tract infections in Karachi. J Pak Med Assoc. 2013; 63(11): 1342-4.

[52] Zhao X, Wang L, Wei N, Zhang J, Ma W, Zhao H, et al. Epidemiological and clinical characteristics of healthcare-associated infection in elderly patients in a large Chinese tertiary hospital: a 3-year surveillance study. BMC Infect Dis. 2020; 20(1): 121.

[53] Farooq L, Memon Z, Ismail MO, Sadiq S. Frequency and antibiogram of multi-drug resistant pseudomonas aeruginosa in a Tertiary Care Hospital of Pakistan. Pak J Med Sci. 2019; 35(6): 1622-6.

[54] Rammaert B, Goyet S, Beauté J, Hem S, Te V, Try PL, et al. Klebsiella pneumoniae related community-acquired acute lower respiratory infections in Cambodia: clinical characteristics and treatment. BMC Infect Dis. 2012; 12: 3.