

Distribution characteristics of pathogen spectrum in bronchoalveolar lavage fluid of 1526 children with community-acquired pneumonia in Wuhan in 2023

Zhongjian Wang

Hubei Provincial Women and Children's Hospital

Yi Gan

Hubei Provincial Women and Children's Hospital

Miao Wang

Hubei Provincial Women and Children's Hospital

Yunyang Hu

Hubei Provincial Women and Children's Hospital

Yabin Wu

Hubei Provincial Women and Children's Hospital

Ying Cheng

Hubei Provincial Women and Children's Hospital

Tao Huang

Hubei Provincial Women and Children's Hospital

Danna Tu

Hubei Provincial Women and Children's Hospital

Junhua Shu

Hubei Provincial Women and Children's Hospital

Xiaoqin Zhou

62724838@163.com

Hubei Provincial Women and Children's Hospital

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Abstract

Objective To analyze the distribution characteristics of pathogens in the bronchoalveolar lavage fluid of children with community-acquired pneumonia.

Methods A retrospective analysis was performed on the etiological data of 1526 children who were diagnosed and treated at the Maternal and Child Health Hospital of Hubei Province from January 1, 2023, to December 31, 2023.

Results Among the 1526 children, 1524 (99.9%) were positive for pathogens. The top five detected pathogens were *Mycoplasma pneumoniae*, rhinovirus, Epstein–Barrvirus, *Streptococcus pneumoniae*, and human bocavirus. The mixed infection rate was 62%. EB virus, rhinovirus, *Streptococcus pneumoniae*, human bocavirus and *Haemophilus influenzae* were the most common coinfections of *Mycoplasma pneumoniae*. *Staphylococcus aureus* and *Pneumocystis jirovecii* infections were more common in men than in women. Human bocavirus, parainfluenza virus, respiratory syncytial virus, cytomegalovirus, *Pneumocystis jirovecii* and WU polyomavirus are more common in infants and young children, and Epstein–Barrvirus is more common in preschool-aged and school-aged children. More than half (51.6%) of the *Mycoplasma pneumoniae* infections occurred in autumn. *Mycobacterium tuberculosis* complex, human parainfluenza virus and cytomegalovirus were more common in spring and summer, and influenza B virus and adenovirus were more common in autumn and winter. Respiratory syncytial virus, influenza A virus and *Fusobacterium nucleatum* were more common in winter and spring. Enteroviruses were more common in summer and autumn.

Conclusion The positive rate of pathogen detection in bronchoalveolar lavage fluid is extremely high. Most patients had mixed infections. There are sex, age and seasonal differences in the distribution of some pathogens.

1. Introduction

Pneumonia is one of the leading causes of death in children under 5 years of age, and the vast majority of these cases are community-acquired pneumonia (CAP)^[1]. According to statistics, lower respiratory tract infections caused 652 572 deaths in children under 5 years of age worldwide in 2016^[2]. Since the outbreak of COVID-19, the number of patients with pneumonia has increased rapidly, causing a considerable disease burden around the world^[3]. During the COVID-19 pandemic, to control the spread of COVID-19, a series of nonpharmaceutical interventions (NPIs) have been implemented worldwide, including maintaining social distancing, closing schools, wearing masks, restricting travel, and improving personal hygiene, which have significantly reduced the infection rate of 2019-nCoV^[4]. While these NPIs are effective in controlling the transmission of 2019-nCoV, they also affect the seasonal transmission patterns of other respiratory viruses, such as influenza virus, respiratory syncytial virus (RSV), human rhinovirus (HRV), human metapneumovirus (HMPV) and adenovirus (ADV)^[5–7].

The change in the pathogen spectrum of respiratory tract infections in children after the outbreak of the 2019 novel coronavirus has attracted much attention. Liu et al. studied 7107 patients with lower respiratory tract infections. Compared with those in 2019, the infection rates of RSV, ADV, HMPV and influenza viruses decreased significantly in 2020, whereas HRV infection rates increased significantly. After September 2020, human parainfluenza virus (HPIV) infection resumed. In addition, there were significantly fewer coinfections in 2020 than in 2019^[6]. Principi et al. suggested that the prevalence of respiratory pathogens after an epidemic is the result of the cross-influence of various factors (including the variation in the pathogen itself, the immunity of the host, and the mutual interference between the pathogens), and each factor can change the traditional epidemiology of a single virus^[7]. Strengthening the surveillance of pathogen prevalence and vaccination is recommended.

Bronchoalveolar lavage fluid (BALF) is directly collected from the lesion site. Compared with blood culture and sputum culture, BALF can more accurately reflect the etiology of lung disease and guide the use of antibiotics more accurately^[8-10]. To more accurately understand the changes in the respiratory pathogen spectrum of children in the postpandemic era, we summarized the distribution of BALF pathogens in children with CAP in the Maternal and Child Health Hospital of Hubei Province in 2023. This study provides a basis for accurate diagnosis and rational drug use for clinicians and a scientific basis for epidemic prevention departments to formulate targeted prevention and control measures.

2. Materials and Methods

2.1 Patients

The clinical data of 1526 children with CAP who underwent bronchoscopy and bronchoalveolar lavage at Maternal and Child Health Hospital of Hubei Province from January 1, 2023, to December 31, 2023, were retrospectively analyzed. The inclusion criteria were as follows: (1) had a clinical diagnosis of pediatric CAP; (2) were aged 28 days to 15 years; (3) had undergone bronchoscopy and bronchoalveolar lavage with the consent of their guardians; and (4) had complete clinical data. The exclusion criteria were as follows: (1) patients with contraindications to bronchoscopy; (2) patients with contraindications to anesthesia; (3) patients with serious underlying diseases; (4) patients whose guardians refused bronchoscopy; (5) patients with hospital-acquired pneumonia; and (6) patients whose clinical data were incomplete. The indications for bronchoscopy in this study included the following: (1) recurrent or persistent wheezing; (2) unexplained chronic cough; and (3) recurrent respiratory tract infection. (4) Abnormal chest imaging: (1) dysplasia and/or malformation of the trachea, bronchus and lung; (2) atelectasis; (3) consolidation of the lung; (4) pulmonary mass lesions; (5) diffuse lung disease; and (6) etiological diagnosis and treatment of pulmonary infectious diseases. This study was approved by the hospital medical ethics committee(No. 2024-107-01). All methods were performed in accordance with the relevant guidelines and regulations.

2.2 Methods

The clinical information of the patients, including name, sex, age, imaging examination, etiological results, bronchoscopic manifestations, diagnosis, treatment, and complications, was collected through the hospital electronic medical record system. The contraindications for bronchoscopy included the following: (1) severe cardiopulmonary dysfunction; (2) severe arrhythmia; (3) persistent high fever; (4) active hemoptysis, severe hemorrhagic diseases, coagulopathy, or severe pulmonary hypertension; and (5) severe malnutrition in patients who could not tolerate surgery.

Reagents and instruments: Respiratory pathogenic microorganism multiple joint detection kit (Jinqi Rui Company, product number KS608-100HXD96), next generation sequencer (Jinqi Rui Company, product number MiniSeqDx-CN), etc.

Targeted high-throughput next-generation sequencing (tNGS): All patients underwent bronchoscopy, and BALF samples were collected. The collected samples were sent to Golden Med Medical Center for tNGS detection (multiplex PCR combined with next-generation sequencing technology). After the BALF samples were thoroughly mixed, 1 300µl was centrifuged at 12 000 r/min for 5 min. After centrifugation, the supernatant was removed, 500 µL of sample was retained, and the mixture was blown. A 500 µL sample was put into the bead mill tube of the extraction kit, and 50 µL of SDS was added to the wall breaking instrument. After the wall breaking treatment, the samples were centrifuged at 12000 rpm for 5 min, and 400 µL of the supernatant was used for nucleic acid extraction. Ultramultiplex PCR was used to amplify and enrich the target sequence to form short fragments of nucleic acid without interruption. After purification, the products were added to the adapter, and a second round of PCR amplification was performed to construct the library. The library quality was controlled by an ultramicro spectrophotometer, and the libraries were sequenced. After the sequencing was completed, the data were analyzed to form the final report.

The detection range of tNGS in this study included 198 pathogens of the respiratory tract, including 80 bacteria, 79 viruses, 32 fungi and 7 other pathogens (including *Mycoplasma pneumoniae* and *Chlamydia pneumoniae*).

2.3 Statistical analysis

SPSS 29 software was used, the count data are expressed as n (%), and the chi-square test or Fisher's exact probability test was used for comparisons between groups. $P < 0.05$ was considered statistically significant.

3. Results

3.1 Overall distribution of pathogens

Pathogens were detected in 1524 (99.9%) of the 1526 patients. The number of patients infected with the 20 most common pathogens is shown in Figure 1. The five most common pathogens were *Mycoplasma pneumoniae* (MP, 93.0%, 1419/1526), HRV (15.5%,237/1526), Epstein–Barr virus (EBV, 14.5%,221/1526),

Streptococcus pneumoniae (SP, 14.4%, 219/1526), and human bocavirus (HBoV, 9.8%, 149/1526). SP, *Haemophilus influenzae* (HI), *Bordetella pertussis* (BP), *Trophomonas whipplei* (TW) and *Staphylococcus aureus* (SA) were the five most common bacteria. The five most common viruses were HRV, EBV, HBoV, HPIV and RSV. Among all the patients, 575 (38%) had only one pathogen, 456 (30%) had two pathogens, 252 (16%) had three pathogens, and 241 (16%) had four or more pathogens (Figure 1). Mixed infection was found in 62% of the patients. The most common coinfections were MP with EBV (13.6%, 208/1526), MP with HRV (13.5%, 206/1526), MP with SP (12.5%, 191/1526), MP with HBoV (8.9%, 136/1526), and MP with HI (7.4%, 113/1526).

3.2 Distribution of pathogens by sex

There were 745 males and 781 females. Table 1 shows the comparison of the distributions of some pathogens in different sexes. SA and *Pneumocystis jirovecii* (PJ) infections were more common in males than in females ($P < 0.05$). There was no significant difference in the distribution of other pathogens between the sexes.

3.3 Distribution of pathogens by age

All patients were divided into four age groups, including 56 infants (28d-1y, 3.7%), 239 toddlers (1-3y, 15.7%), 564 preschool children (4-6y, 37%), and 667 school-aged children (7-15y, 43.7%). The distribution of the top 20 common pathogens in different age groups is shown in Figure 2. Table 2 shows the comparison of the distributions of some pathogens in different age groups. HBoV, HPIV, RSV, cytomegalovirus (CMV), PJ and WU polyomavirus were more common in infants and young children ($P < 0.05$). EBV infection was more common in preschool-aged and school-aged children ($P < 0.05$).

3.4 Distribution of pathogens by season

All patients were divided into four groups according to season: the spring group (March--May), 121 cases (7.9%); the summer group (June--August), 435 cases (28.5%); the autumn group (September--November), 732 cases (48%); and the winter group (December--February), 238 cases (15.6%). The distributions of the top 20 common pathogens in different seasons are shown in Figure 3. A comparison of the distributions of some pathogens in different seasons is shown in Table 3 and Table 4. More than half (51.6%) of the MP infections occurred in autumn. *Mycobacterium tuberculosis* complex, HPIV and CMV infections were more common in spring and summer ($P < 0.05$). Influenza B virus (Flu-B) and ADV infections were more common in autumn and winter ($P < 0.05$). RSV, influenza A virus (Flu-A) and *Fusobacterium nucleatum* infections were more common in winter and spring ($P < 0.05$). Enterovirus infection was more common in summer and autumn ($P < 0.05$).

4. Discussion

Pediatric CAP causes many deaths every year, and identifying the pathogens causing pediatric CAP as soon as possible and providing accurate and reasonable anti-infective treatment are very

important^[2]. Alveolar biopsy tissue and bronchoalveolar lavage fluid (BALF) are the most accurate samples for CAP pathogen detection^[11-12]. In 2023, multiple pathogens were detected after the COVID-19 epidemic. This study summarizes the distribution characteristics of the BALF pathogen spectrum in children with CAP in 2023.

In this study, the detection rate of pathogens in the BALF of children with CAP was 99.9%. Lv et al. reported that among 4804 children with respiratory tract infections, the total positive rate was 77.87%^[13]. Wu et al. reported that 7046 out of 10435 children with acute respiratory tract infections were positive for at least one pathogen, with a total positive rate of 67.5%^[14]. There are great differences in the positive detection rates of pathogenic microorganisms among different studies, which may be related to differences in region, climate, patient immunity after the epidemic and test samples. The five most common pathogens identified in this study were MP (93.0%), HRV, EBV, SP and HBoV. Wu et al. reported that MP was the most common pathogen detected in 10435 children with acute respiratory tract infection, with a positive rate of 56.9%^[14]. Wang et al. reported that the pathogens most commonly detected in BALF samples from 573 children were ADV (21.82%), MP (20.24%), HRV (13.96%), SP (8.90%) and HI (8.90%)^[15]. The detection rate of MP significantly increased in this study, which was considered to be related to the selection of research subjects. Most of the children in this study had atelectasis, pulmonary consolidation, or severe pneumonia. In addition, the increased detection rate of MP was related to intermittent outbreaks of MP after NPI. A number of studies have confirmed that the infection rate of MP increased significantly in 2023 and that there was a multiregional epidemic^[16-18]. The two most common bacteria infecting children with CAP in this study were SP and HI, which is consistent with the results of other studies^{[2][15]}. The two most common viruses were HRV and EBV, which is different from the findings of other studies. Hao et al. reported that RSV and ADV were the two most common viruses in a study of 1500 CAP patients in 2015^[1]. Shi et al. reported that HRV and RSV were the two most common viruses in a study of 10396 children with acute respiratory tract infection from 2021-2022^[19]. Wang et al. reported that the two most common viruses infecting 573 children were ADV and HRV^[15]. The higher EBV infection rate in this study was considered to be related to immune abnormalities after the COVID-19 pandemic.

Since the COVID-19 pandemic, an increasing number of children with CAP have been infected with multiple pathogens at the same time. In the present study, the mixed infection rate was as high as 62%. The most common coinfections were MP with EBV (13.6%), MP with HRV (13.5%), and MP with SP (12.5%). Wu et al.'s study of 10435 children with respiratory tract infections revealed that the mixed infection rate was 39.6%, and MP combined with Flu-B infection was the most common^[14]. Zhao et al. performed pathogen detection on 4148 CAP children, 38.18% of whom had mixed infections, and the most common combination was MP combined with HRV^[20]. Lv et al. performed pathogen detection on 4804 children with upper respiratory tract infections; the mixed infection rate was 43.40%, and SP combined with HRV infection was the most common infection^[13]. The mixed infection rate of children in this study was higher than that reported in other studies. The reasons for this are related mainly to the

different samples collected, immune abnormalities after COVID-19 infection, the implementation of NPI, and the periodicity of the pathogen itself.

In the present study, the vast majority of pathogens showed no significant difference in sex distribution; only SA and PJ infections were more common in males than in females. Zhang et al. reported that there was no statistically significant difference in the sex distribution of different pathogens during the COVID-19 epidemic^[21]. Li et al. reported that there was no sex difference in the pathogen detection rate; however, women were more likely to be infected with viruses, whereas men were more likely to be infected with SP^[22]. A study from India revealed that the incidence of acute lower respiratory infections in children under 5 years of age was greater in boys than in girls, and boys had a 2.4-fold higher rate of acute respiratory infection-related hospitalizations^[23]. Zhu et al. reported that there was a sex difference in the number of pathogens isolated from the lower respiratory tract only in the 0–1-year-old infant group, and there was no difference among the other groups^[24]. *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, *Stenotrophomonas maltophilia*, and *Candida albicans* were more common in male infants. HI, *Moraxella catarrhalis* and SP were more common in female infants. There are differences in the distributions of some pathogen infections according to sex.

In addition to sex, pathogen distribution is also associated with age. In this study, infections with HBoV, HPIV, RSV, CMV, PJ and WU polyomavirus were more common in infants. EBV infection was more common in preschool-aged and school-aged children. Li et al. conducted a retrospective analysis of 12,546 children with respiratory tract infections from 2018-2021 and reported that the incidence of bacterial infection was high in infants, the incidence of viral infection was high in preschool children, and atypical pathogens were the most common in children aged 3-5 years^[22]. Zhang et al.'s study of 7668 patients with respiratory tract infections from 2019-2021 revealed that RSV, HRV, MP and HPIV had relatively high detection rates in the infant group (0-6 months) and the young child group (7 months-2 years). The highest positive rates of respiratory pathogens in children (3–6 years) and adolescents (7–18 years) were associated with MP and HRV^[21]. Lv et al.'s study of 4804 children with respiratory tract infections from 2019-2022 revealed that the infection rates of SP, RSV and HPIV in the infant group were higher than those in other groups. The HRV infection rate was higher in young children than in other groups. The infection rates of Flu-A, *Chlamydia pneumoniae*, MP and HI in preschool-aged and school-aged children are higher than those in infants and young children^[13].

The incidence of infection with many pathogens varies in different seasons. In this study, more than half of the MP infections occurred in autumn. *Mycobacterium tuberculosis* complex, HPIV and CMV infections were more common in spring and summer. Flu-B and ADV infections were more common in autumn and winter. RSV, Flu-A and *Fusobacterium nucleatum* infections were more common in winter and spring. Enterovirus infection was more common in summer and autumn. According to the Beijing Respiratory Pathogen Surveillance System, MP, HPIV and HRV were the main pathogens identified in September 2023; MP, HPIV and ADV were the main pathogens identified in October; and MP and RSV were the main pathogens identified in November. One study revealed that MP plays a key role in increasing respiratory

illness in children in autumn and winter of 2023^[25]. Other studies also revealed that MP infection was an important cause of pneumonia in autumn and winter of 2023, with an increase in the MP infection rate^[26-29]. A study conducted by Shi et al. on 10396 children with acute respiratory infections from 2021-2022 revealed that ADV and Chlamydia pneumoniae infections occurred mostly in spring; that coronavirus and Flu-A infections occurred mostly in summer; that HRV, HBoV, MP, and HPIV infections occurred mostly in autumn; and that RSV and Flu-B infections occurred mostly in winter^[19]. The seasonal prevalence of respiratory pathogens may be related to the following three factors: (i) humidity and temperature; (ii) human behavior (including indoor/outdoor activities, number of close contacts, etc.); and (iii) the effects of changing environmental conditions on host defense mechanisms^[30-31].

In this study, the infection rates of MP and mixed infection rates of different pathogens were high, the detection rates of common bacteria and viruses also differed from those reported in the past, and the distributions of some pathogens differed according to sex, age and season. In addition to factors such as specimen and region, immune abnormalities after COVID-19 infection are also important. Ryan et al. reported that the peripheral immune system of patients recovering from COVID-19 continues to change for at least 6 months after infection, which may affect the response to subsequent infections with other pathogens and that persistent immune activation may also exacerbate other chronic diseases^[32]. Cohen et al. reported that during the COVID-19 pandemic, due to the implementation of the NPI, the probability of people being exposed to other viruses and bacteria was greatly reduced, and vaccination was also delayed. With the prolonged duration of NPI, due to the long-term lack of immune stimulation, the susceptible population will increase, herd immunity will decline, and eventually, the risk of epidemics will greatly increase^[33].

This study also has certain limitations. First, the subjects in this study were patients who underwent bronchoscopy, and the pathogens of children who did not undergo bronchoscopy were not counted; therefore, the statistics of pathogens may not be comprehensive. In addition, the time span of this study was short, and it was a single-center study involving a limited region. Finally, our etiological analysis did not involve disease severity and cannot discern the severity of pneumonia caused by the pathogen.

In conclusion, by analyzing the composition of the pathogen spectrum in the BALF of CAP patients, this study provides a basis for accurate diagnosis and rational drug use, which is helpful for preventing complications early, shortening the treatment time, improving the prognosis, and reducing pain in children. By analyzing the distribution of pathogens, we can understand the epidemic trends and transmission of clinical pathogens in the region more comprehensively, provide a scientific basis for the development of targeted prevention and control measures, and provide important support for public health prevention and control. In the future, it is necessary to strengthen the rapid detection and extensive multidimensional continuous surveillance of pathogens, improve the vaccination rate, and strengthen health knowledge education and epidemic prevention and control exercises for unknown pathogens.

Declarations

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Authors' contributions

XQZ and JHS contributed equally to the manuscript. XQZ and JHS contributed to the conception and are responsible for the overall content. ZJW, XQZ and JHS designed the study. ZJW, YBW, YC, TH and DNT collected data. ZJW, YG, MW, XQZ and JHS analyzed and interpreted the data. ZJW, YYH, YG and MW contributed to the statistics analysis. ZJW edited the manuscript. XQZ and JHS revised the manuscript. All authors approved the submitted and final versions.

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Data availability

The data underlying this article will be shared on reasonable request to the corresponding author.

Ethics approval

The study was approved by Medical Ethics Review Committee of Maternal and Child Health Hospital of Hubei Province (No. 2024-107-01). Due to the retrospective nature of the study, Medical Ethics Review Committee of Maternal and Child Health Hospital of Hubei Province waived the need of obtaining informed consent.

Consent for publication

All authors agree to the publication of the final manuscript.

Conflict of interest

All the authors declare that they have no conflicts of interest.

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Tables

Table1 Comparison of the distribution of some pathogens in different sexes(n,%)

Groups	MP	HRV	EBV	SP	HBoV	SA	PJ
Male(n=745)	687(92.2)	127(17.0)	109(14.6)	113(15.2)	76(10.2)	33(4.4)	28(3.8)
Female(n=781)	732(93.7)	110(14.1)	112(14.3)	106(13.6)	73(9.3)	15(1.9)	14(1.8)
c ²	1.336	2.551	0.026	0.790	0.316	7.878	5.505
P	0.248	0.110	0.872	0.374	0.574	0.005	0.019

Note:MP, mycoplasma pneumoniae;HRV, human Rhinovirus;EBV, epstein-barr virus;SP, streptococcus pneumoniae;HBoV, human bocavirus;SA, staphylococcus aureus;PJ, pneumocystis jiroveci.

Table2 Comparison of the distribution of some pathogens in different age groups(n,%)

Groups	EBV	HBoV	HPIV	RSV	CMV	PJ	WUPyV
≤3y(n=295)	32(10.8)	66(22.4)	52(17.6)	60(20.3)	24(8.1)	36(12.2)	7(2.4)
4-15y(n=1231)	189(15.4)	83(6.7)	52(4.2)	34(2.8)	10(0.8)	6(0.5)	3(0.2)
c ²	3.901	65.986	67.313	127.19	58.586	122.042	13.462
P	0.048	≤0.001	≤0.001	≤0.001	≤0.001	≤0.001	≤0.001

Note:EBV, epstein-barr virus;HBoV, human bocavirus;HPIV, human parainfluenza virus;RSV, respiratory syncytial virus;CMV, cytomegalovirus;PJ, pneumocystis jiroveci;WUPyV, WU polyomavirus.

Table3 Comparison of the distribution of some pathogens in different seasons(n,%)

Groups	MTBC	HPIV	CMV	Flu-B	ADV
Spring+Summer(n=556)	8(1.4)	71(12.8)	21(3.8)	0(0)	8(1.4)
Autumn+Winter(n=970)	1(0.1)	33(3.4)	13(1.3)	14(1.4)	67(6.9)
c ²	8.598	48.836	9.633	/	22.615
P	0.003	≤0.001	0.002	0.003	≤0.001

Note:MTBC,mycobacterium tuberculosis complex;HPIV, human parainfluenza virus;CMV, cytomegalovirus;Flu-B, influenza B virus;ADV, adenovirus.

Table4 Comparison of the distribution of some pathogens in different seasons(n,%)

Groups	RSV	Flu-A	FN	EV
Spring+Winter(n=359)	50(13.9)	26(7.2)	14(3.9)	3(0.8)
Summer+Autumn(n=1167)	44(3.8)	11(0.9)	8(0.7)	42(3.6)
c ²	49.000	46.054	19.962	6.391
P	≤0.001	≤0.001	≤0.001	0.011

Note:RSV, respiratory syncytial virus;Flu-A, influenza A virus;FN,fusobacterium nucleatum;EV, enterovirus.

Figures

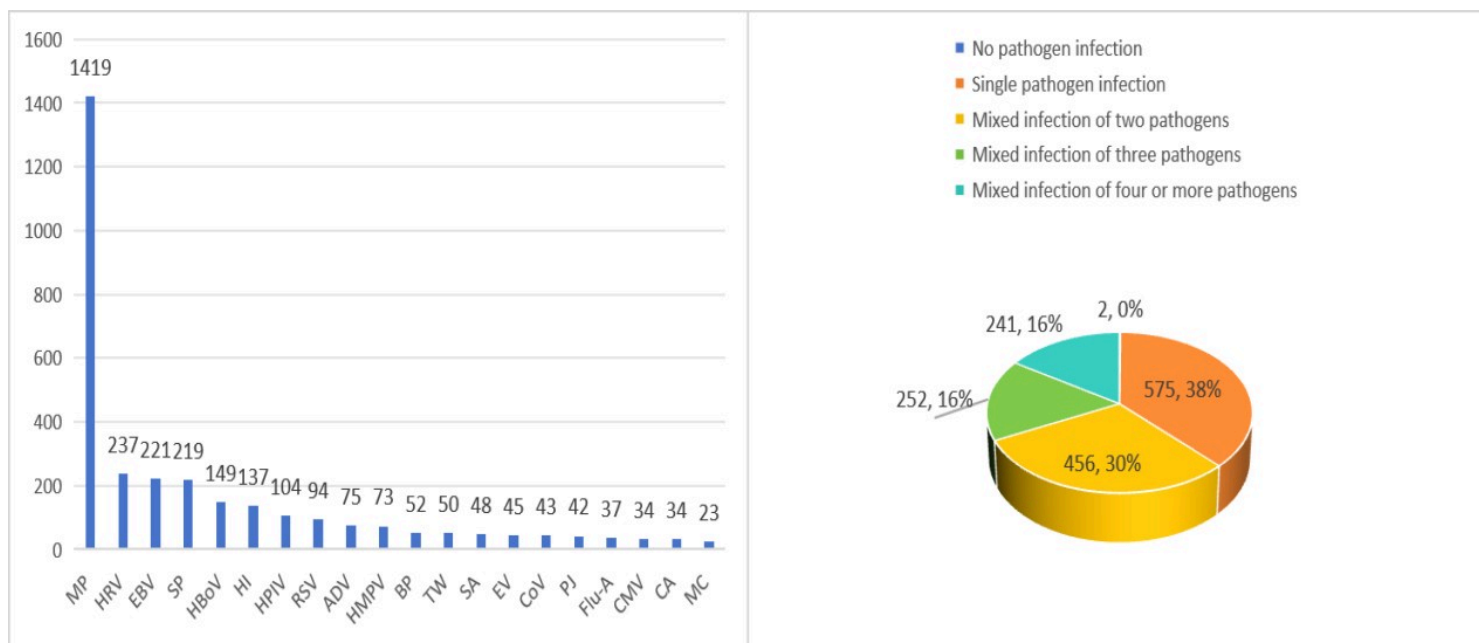


Figure 1

The number of patients infected with the top 20 common pathogens and the mixed infection status of different pathogens

Note: MP, mycoplasma pneumoniae; HRV, human Rhinovirus; EBV, epstein-barr virus; SP, streptococcus pneumoniae; HBoV, human bocavirus; HI, haemophilus influenzae; HPIV, human parainfluenza virus; RSV, respiratory syncytial virus; ADV, adenovirus; HMPV, human metapneumovirus; BP, bordetella pertussis; TW, tropheryma whipplei; SA, staphylococcus aureus; EV, enterovirus; CoV, coronavirus; PJ, pneumocystis jiroveci; Flu-A, influenza A virus; CMV, cytomegalovirus; CA, candida albicans; MC, moraxella catarrhalis.

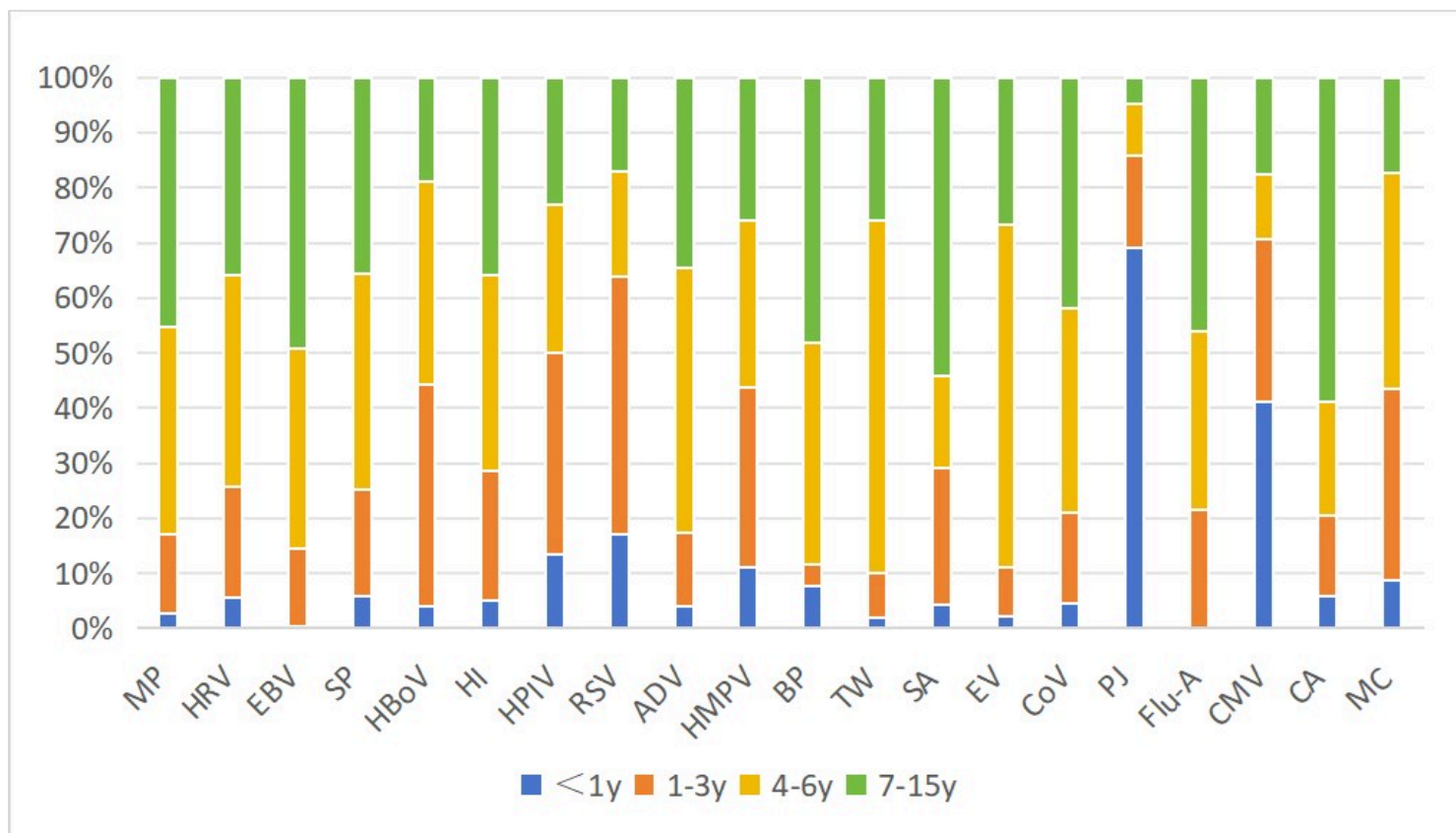


Figure 2

Distribution of the top 20 common pathogens in different age groups

Note: MP, mycoplasma pneumoniae; HRV, human Rhinovirus; EBV, epstein-barr virus; SP, streptococcus pneumoniae; HBoV, human bocavirus; HI, haemophilus influenzae; HPIV, human parainfluenza virus; RSV, respiratory syncytial virus; ADV, adenovirus; HMPV, human metapneumovirus; BP, bordetella pertussis; TW, tropheryma whipplei; SA, staphylococcus aureus; EV, enterovirus; CoV, coronavirus; PJ, pneumocystis jiroveci; Flu-A, influenza A virus; CMV, cytomegalovirus; CA, candida albicans; MC, moraxella catarrhalis.

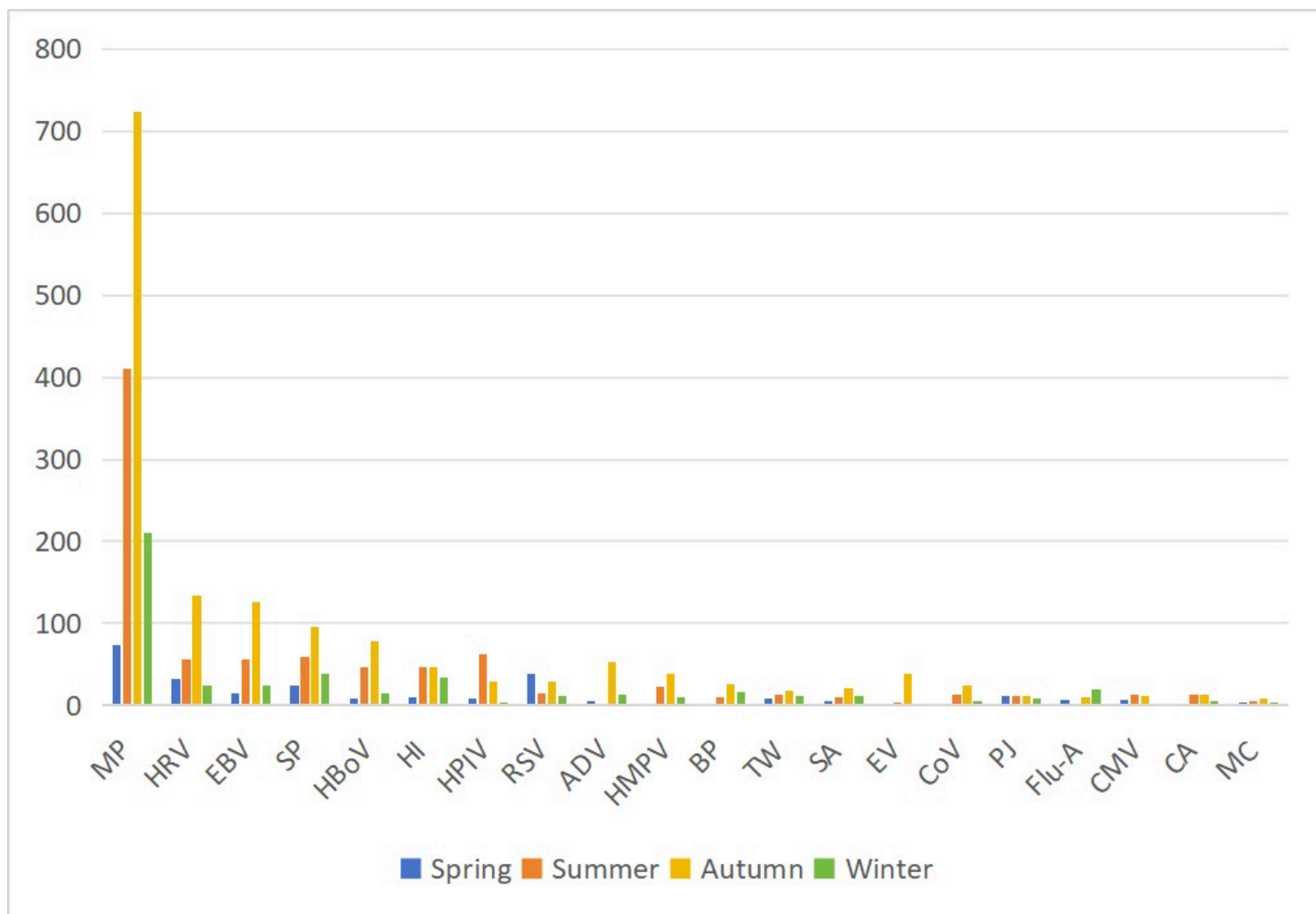


Figure 3

Distribution of the top 20 common pathogens in different seasons

Note: MP, mycoplasma pneumoniae; HRV, human Rhinovirus; EBV, epstein-barr virus; SP, streptococcus pneumoniae; HBoV, human bocavirus; HI, haemophilus influenzae; HPIV, human parainfluenza virus; RSV, respiratory syncytial virus; ADV, adenovirus; HMPV, human metapneumovirus; BP, bordetella pertussis; TW, tropheryma whipplei; SA, staphylococcus aureus; EV, enterovirus; CoV, coronavirus; PJ, pneumocystis jiroveci; Flu-A, influenza A virus; CMV, cytomegalovirus; CA, candida albicans; MC, moraxella catarrhalis.