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RESEARCH

Comparison of *Mycoplasma pneumoniae* infection in children admitted with community acquired pneumonia before and during the COVID-19 pandemic: a retrospective study at a tertiary hospital of southwest China

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Abstract

Purpose The COVID-19 pandemic has notably altered the infection dynamics of various pathogens. This study aimed to evaluate the pandemic's impact on the infection spectrum of *Mycoplasma pneumoniae* (*M. pneumoniae*) among children with community acquired pneumonia (CAP).

Methods We enrolled pediatric CAP patients admitted to a tertiary hospital in southwest China to compare the prevalence and characteristics of *M. pneumoniae* infections before (2018–2019) and during (2020–2022) the COVID-19 pandemic. Detection of *M. pneumoniae* IgM antibodies in serum were conducted using either indirect immunofluorescence or passive agglutination methods.

Results The study included 1505 *M. pneumoniae*-positive and 3160 *M. pneumoniae*-negative CAP patients. Notable findings were the higher age and frequency of pneumonia-associated symptoms in *M. pneumoniae*-positive patients, alongside a lower male proportion and fewer respiratory co-infections. The year 2019 saw a notable increase in *M. pneumoniae* infections compared to 2018, followed by a decline from 2020 to 2022. The COVID-19 pandemic period witnessed significant alterations in age distribution, male proportion, and co-infections with specific pathogens in both *M. pneumoniae*-positive and negative patients. The *M. pneumoniae* infections were predominantly seasonal, peaking in autumn and winter during 2018 and 2019. Although there was a sharp drop in February 2020, the infection still peaked in cold months of 2020 and 2021. However, the typical seasonal pattern was nearly absent in 2022.

Conclusions The COVID-19 pandemic has markedly changed the infection landscape of *M. pneumoniae* in pediatric CAP patients, with shifts observed in infection rates, demographic profiles, co-infections, and seasonal patterns.

Keywords COVID-19 · *Mycoplasma pneumoniae* · Epidemiology · Community acquired pneumonia · Pediatrics

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Introduction

While community acquired pneumonia (CAP) may not always be at the forefront of public health concerns, its impact on children's health globally is significant, with considerable mortality and morbidity rates [1]. *Mycoplasma pneumoniae* (*M. pneumoniae*), a notable atypical pathogen, emerges as a primary culprit in pediatric CAP cases. Studies indicate that between 4 and 39% of children hospitalized for CAP test positive for *M. pneumoniae*, either through nucleic acid or serology testing [2]. While infections with *M. pneumoniae* are typically mild and self-resolving, they can nonetheless lead to severe pneumonia and extrapulmonary complications across all age groups [3]. Moreover, there is a concerning prevalence of macrolide-resistant *M. pneumoniae* [4]. Clearly, ongoing monitoring of *M. pneumoniae* epidemiology is crucial for effective disease management.

In recent years, the implementation of non-pharmaceutical interventions (NPIs), like social distancing and mask-wearing, aimed at controlling COVID-19, have not only curtailed the spread of SARS-CoV-2 but also markedly altered the infection dynamics of various other pathogens. Notably, during the COVID-19 pandemic, there has been a significant decrease in the detection rate of *M. pneumoniae* infections [5–7]. These shifts have also influenced the clinical characteristics of patients infected with *M. pneumoniae* [8]. However, existing studies often encompass relatively brief spans of the pandemic and rarely shed light on the specific trends of *M. pneumoniae* infection in pediatric CAP patients in southwest China.

To address this gap, our study was undertaken at a prominent tertiary hospital in southwest China. Our goal was to compare and analyze the patterns of *M. pneumoniae* infection in pediatric CAP patients, focusing on the periods before (2018–2019) and during (2020–2022) the COVID-19 pandemic.

Materials and methods

Study population

This retrospective study was carried out at the Yongchuan Hospital of Chongqing Medical University, spanning from January 2018 to December 2022. Children diagnosed with CAP were meticulously identified by seasoned pediatricians, leveraging a comprehensive approach that combined clinical symptoms, chest imaging, and laboratory results. Additionally, chest imaging was meticulously evaluated by expert radiologists. Our study specifically targeted CAP inpatients aged from 1 month to 18 years. The exclusion criteria were rigorously applied to ensure the integrity and focus of our research, including: (1) Children outside the specified age range. (2) Patients diagnosed with healthcare-associated pneumonia. (3) Patients with incomplete medical records or missing *M. pneumoniae* test results. Individuals falling into any of these categories were systematically excluded from the study. Ethical approval for this study was granted by the ethics committee of Yongchuan Hospital of Chongqing Medical University (Approval No. 2023-KeLunShen-76).

Specimens collection for *M. pneumoniae* detection

Upon admission, venous blood samples were obtained from the patients and then centrifuged to separate serum. The presence of *M. pneumoniae* was determined by detecting Immunoglobulin M (IgM) antibodies in the serum, using either an indirect immunofluorescence assay (IFA) or a passive particle agglutination (PPA) kit (Fujirebio, Japan), following the manufacturer's instructions. For the passive agglutination test, an antibody titer of $\geq$1:160 was deemed indicative of a *M. pneumoniae* infection.

Identification of respiratory co-infections

Our research delved into the viral and bacterial co-infections among the pediatric CAP patients. For the detection of viral co-infections, venous blood or nasopharyngeal swab samples were collected from the patients at the time of their admission by skilled medical personnel. The scope of our viral testing encompassed five key respiratory viruses: influenza virus A (IVA), influenza virus B (IVB), parainfluenza virus (PIV), respiratory syncytial virus (RSV), and adenovirus (ADV). Serum IgM antibodies targeting these viruses were quantified using IFA for those samples taken from venous blood. While nasopharyngeal swab samples were subjected to analysis with a multiplex direct immunofluorescence assay kit (Diagnostic Hybrids, Athens, Ohio, USA), adhering to established protocols. The presence of positive findings from either serum or nasopharyngeal swab samples constituted the basis for identifying viral co-infections.

For the investigation of bacterial co-infections, we focused on four key respiratory bacteria: *Streptococcus pneumoniae* (*S. pneumoniae*), *Haemophilus influenzae* (*H. influenzae*), *Moraxella catarrhalis* (*M. catarrhalis*), and *Staphylococcus aureus* (*S. aureus*). Sputum samples from the patients were collected immediately upon their admission for the analysis of bacterial morphology. During the bacterial culture process, the samples were cultured on MacConkey, blood, and chocolate agar plates and then incubated at 37°C in a 5% CO2 atmosphere for 18–24 h. Bacterial identification was subsequently conducted using the Vitek-2 Compact system (BioMérieux, France).

Statistical analysis

The normality of quantitative data was assessed using the Kolmogorov–Smirnov test. Data conforming to normal distribution were expressed as mean ± standard deviation (SD), and inter-group comparisons were made using Student's t-test. Non-normally distributed data were represented as medians and interquartile ranges, with the Mann–Whitney U test employed for group comparisons. The categorical variables were assessed for statistical significance by comparing the actual and theoretical frequencies using two-tailed chi-square test, Fisher's exact test, or Yates' continuity corrected chi-square test as appropriate. The comparison of viral and bacterial co-infections was made after excluding patients who did not have corresponding pathogenic results. All statistical analyses were performed utilizing GraphPad Prism 9.0 Software (San Diego, CA, USA). A *P*-value of less than 0.05 was considered statistically significant.

Results

Overall demographic and clinical characteristics of enrolled patients

Out of 6115 children hospitalized with CAP from January 2018 to December 2022, 4665 collected blood specimens for *M. pneumoniae* detection. Within this cohort, the *M. pneumoniae* test yielded positive results for 1505 children and negative results for 3160 children. Specifically, the infection was detected through IFA in 65 patients and through PPA in 1405 patients. Additionally, 35 patients exhibited positive results via both testing methods. The prevalence of infection was notably higher among males (807 out of 2752, representing 53.62%) compared to females (698 out of 1913, or 46.38%), with this difference being statistically significant ($P < 0.0001$). The distribution and incidence rates of positive cases across various age groups were as follows: 24.63% (739 cases) were children under 3 years, 44.59% (544 cases) were children aged 3 to less than 6 years, 47.08% (145 cases) were children aged 6 to less than 10 years, and 56.2% (77 cases) were children aged 10 years and older.

As shown in Table 1, the patients with *M. pneumoniae*-positive CAP displayed a significantly higher age but lower proportion of males compared to *M. pneumoniae*-negative patients ($P < 0.05$). The rate of admission to the pediatric intensive care unit (PICU) was similar between the two groups. Cough emerged as the most prevalent symptom of pediatric CAP, succeeded by fever and wheezing. Notably, the incidences of cough and fever were significantly higher in *M. pneumoniae*-positive patients ($P < 0.05$). In contrast to the marked increases in co-infections with PIV, RSV, and *S. aureus* observed in *M. pneumoniae*-negative patients ($P < 0.05$), the prevalence of co-infections with other respiratory pathogens did not significantly differ between the two groups.

Table 1 Comparison of demographic and clinical characteristics between *M. pneumoniae*-positive and -negative pediatric CAP patients

Variables	Positive patients	Negative patients	P value
Number of patients	1505	3160	
Age (months)	36 (18–53)	15 (7–39)	< 0.0001
Male patients [No. (%)]	807 (53.62)	1945 (61.55)	< 0.0001
PICU admission [No. (%)]	7 (0.47)	30 (0.95)	> 0.05
Symptoms [No. (%)]			
Cough	1455 (96.68)	2995 (94.78)	< 0.01
Fever	629 (41.79)	1196 (37.85)	< 0.05
Wheezing	394 (26.18)	861 (27.25)	> 0.05
Respiratory co-infections [No. (%)]			
IVA	16 (1.10)	35 (1.14)	> 0.05
IVB	14 (0.97)	15 (0.49)	> 0.05
PIV	35 (2.44)	136 (4.52)	< 0.001
RSV	136 (9.33)	359 (11.68)	< 0.05
ADV	10 (0.69)	10 (0.33)	> 0.05
S. pneumoniae	287 (19.62)	569 (18.45)	> 0.05
H. influenzae	251 (17.16)	553 (17.93)	> 0.05
M. catarrhalis	247 (16.88)	566 (18.35)	> 0.05
S. aureus	39 (2.67)	164 (5.32)	< 0.0001

Quantitative data were presented as medians (25th to 75th percentiles)

Comparison of *M. pneumoniae*-positives, demographic characteristics, and co-infections in CAP patients before and during the COVID-19 pandemic

In comparison to 2018, *M. pneumoniae* infections saw a significant increase in 2019 ($P < 0.05$). However, from 2020 to 2022, there was a noted decrease, although the differences weren't statistically significant. Nevertheless, the positive rates in 2021 and 2022 were significantly lower than those in 2019 ($P < 0.05$). In *M. pneumoniae*-positive patients, the median age decreased in 2020 compared to 2018, but showed an increase in the years of 2019, 2021, and 2022 ($P < 0.05$). The proportion of male patients in 2020 significantly rose in comparison to 2019 ($P < 0.05$). The gender distribution in 2021 and 2022, however, was similar to that in 2018 and 2019. During the pandemic, there was a noticeable decline in IVA co-infections in 2021 and 2022 compared to 2019. Conversely, RSV co-infections saw an uptick in 2020 relative to 2018 and 2019. *H. influenzae* co-infections diminished in both 2020 and 2022 when contrasted with 2018 and 2019. Moreover, there was an increase in *M.*

Table 2 Comparison of positivity rates, demographic characteristics, and co-infection patterns in *M. pneumoniae*-positive CAP patients before and during the COVID-19 pandemic

Variables	2018	2019	2020	2021	2022
M. pneumoniae-positives [No. (%)]	334 (29.79)	497 (36.41) [a]	238 (33.81)	232 (28.36) [b]	204 (31.05) [b]
Age (months)	32 (17–49)	36 (20–54) [a]	16 (6-42.25) [a, b]	40 (25–51) [a]	51.5 (29–81) [a, b]
Male patients [No. (%)]	177 (52.99)	262 (52.72)	144 (60.50) [b]	105 (45.26)	119 (58.33)
Respiratory co-infections [No. (%)]					
IVA	2 (0.61)	13 (2.66) [a]	1 (0.46)	0 (0.00) [b]	0 (0.00) [b]
IVB	2 (0.61)	7 (1.43)	4 (1.83)	1 (0.43)	0 (0.00)
PIV	6 (1.82)	16 (3.27)	10 (4.57)	2 (0.87)	1 (0.61)
RSV	26 (7.9)	29 (5.93)	51 (23.29) [a, b]	20 (8.66)	10 (5.26)
ADV	2 (0.61)	5 (1.02)	0 (0.00)	0 (0.00)	3 (1.60)
S. pneumoniae	62 (18.79)	99 (20.71)	47 (20.43)	47 (20.61)	32 (16.24)
H. influenzae	61 (18.48)	93 (19.46)	26 (11.3) [a, b]	49 (21.49)	22 (11.17) [a, b]
M. catarrhalis	52 (15.76)	69 (14.44)	45 (19.57)	56 (24.56) [a, b]	25 (12.69)
S. aureus	8 (2.42)	16 (3.35)	6 (2.61)	4 (1.75)	5 (2.54)

Continuous variable was presented as the median (25-75th percentiles); a: $P < 0.05$ Versus 2018; b: $P < 0.05$ Versus 2019

Table 3 Comparison of demographic characteristics and co-infection patterns in *M. pneumoniae*-negative CAP patients before and during the COVID-19 pandemic

Variables	2018	2019	2020	2021	2022
Age (months)	12 (6–26)	13 (6–33)	16.5 (6–41) [a]	20 (9–43) [a, b]	30 (11–52) [a, b]
Male patients [No. (%)]	505 (64.17)	538 (61.98)	259 (55.58) [a, b]	366 (62.46)	277 (61.18)
Respiratory co-infections [No. (%)]					
IVA	12 (1.55)	19 (2.22)	2 (0.45) [b]	0 (0.00) [a, b]	2 (0.50) [b]
IVB	5 (0.65)	7 (0.82)	2 (0.45)	1 (0.17)	0 (0.00)
PIV	30 (3.87)	47 (5.48)	29 (6.47)	14 (2.41) [b]	16 (4.58)
RSV	104 (13.42)	87 (10.15) [a]	84 (18.75) [a, b]	69 (11.88)	15 (3.63) [a, b]
ADV	1 (0.13)	6 (0.70)	1 (0.22)	0 (0.00)	2 (0.50)
S. pneumoniae	148 (19.12)	137 (16.10)	85 (18.85)	119 (21.06) [b]	80 (18.06)
H. influenzae	125 (16.15)	184 (21.62) [a]	46 (10.20) [a, b]	111 (19.65)	87 (19.64)
M. catarrhalis	102 (13.18)	150 (17.63) [a]	116 (25.72) [a, b]	121 (21.42) [a]	77 (17.38)
S. aureus	39 (5.04)	57 (6.70)	24 (5.32)	29 (5.13)	15 (3.39) [b]

Continuous variable was presented as the median (25-75th percentiles); a: $P < 0.05$ Versus 2018; b: $P < 0.05$ Versus 2019

catarrhalis co-infections in 2021 versus 2018 and 2019, with these changes all being statistically significant ($P < 0.05$). However, the occurrence of IVB, PIV, ADV, *S. pneumoniae* and *S. aureus* co-infections among *M. pneumoniae*-positive patients remained consistent across the examined periods, as detailed in Table 2.

In the subset of *M. pneumoniae*-negative CAP patients, significant increases in the median age were observed from 2020 to 2022 compared to the years 2018 and 2019 ($P < 0.05$). Unlike their *M. pneumoniae*-positive counterparts, the proportion of males among this group showed a significant decrease in 2020 ($P < 0.05$), followed by an increase in the subsequent two years. Contrasting with IVB and ADV, the prevalence of other respiratory pathogen infections experienced significant shifts during the COVID-19 pandemic ($P < 0.05$). These changes included reductions in IVA, PIV, *H. influenzae*, and *S. aureus* infections, but increases in *S. pneumoniae* and *M. catarrhalis* infections. The RSV infection increased in 2020 but decreased in the following two years, as detailed in Table 3.

Seasonal variation of *M. pneumoniae* infections before and during the COVID-19 pandemic

The number of *M. pneumoniae* cases displayed a seasonal trend, with higher incidences in autumn and winter for 2018 and 2019. In 2018, despite a sudden spike in June, the infection cases remained low during the warmer months. In 2019, month-to-month variations were observed from January to November, with a significant increase in December. The numbers between April and November, although lower than other months in 2019, were higher than those in the corresponding period of 2018. Even though infections still peaked during colder months in 2020 and 2021, the number of cases was lower than that in 2019. The COVID-19 outbreak caused a sharp decline in infections in February 2020. The infections briefly rebounded during some spring and

summer months in 2020 and 2021. In 2022, the infection cases remained low, lacking a typical seasonal pattern. During the latter part of 2022, coinciding with a local COVID-19 outbreak, there wasn't a notable resurgence in infections. The seasonal trends in *M. pneumoniae* positive rates were atypical throughout the five-year period, both before and during the COVID-19 pandemic, and the trends in positive rates did not always align with the number of positive cases (Fig. 1).

Discussion

This research comprehensively evaluates the variations in *M. pneumoniae* infection among pediatric CAP patients, contrasting the periods before and during the COVID-19 pandemic. The overall positivity rate for *M. pneumoniae* was 32.26%, with a higher prevalence in male patients. When comparing *M. pneumoniae*-positive patients to those who were *M. pneumoniae*-negative, the former group exhibited significantly higher age and frequency of pneumonia-associated symptoms, but lower proportion of male patients and fewer respiratory co-infections. Notably, there was a significant increase in the rate of *M. pneumoniae* infection in 2019 compared to 2018, which was then followed by a decrease from 2020 to 2022. During the COVID-19 pandemic, significant shifts were observed in the age, male proportion, and incidence of respiratory co-infections among pediatric CAP patients, irrespective of *M. pneumoniae* infection status. The number of *M. pneumoniae* infections in colder months in 2020 and 2021 followed a similar trend to that of 2018 and 2019, but the typical seasonal pattern vanished in 2022. The seasonal trends of positivity rate were irregular over these five years.

M. pneumoniae, spread via respiratory droplets in close contact, is a prominent pathogen in pediatric CAP globally [9]. Our study found that 32.26% of pediatric CAP patients tested positive for *M. pneumoniae*, aligning with data from other regions in China [10]. Consistent with existing literature [11], our study observed an increase in infection rate with age. However, in contrast to some previous studies [12], *M. pneumoniae* infection was more prevalent in male patients in our research. The main mechanisms of respiratory symptoms caused by *M. pneumoniae* include adhesion and direct damage, nutrient predation, invasion, toxin production, cytokine-induced inflammation, and immune evasion effects [13]. While generally mild and self-limiting, *M. pneumoniae* can cause severe CAP or extrapulmonary complications in patients of all ages. In our study, the rate of admission to the PICU was comparable between patients testing positive for *M. pneumoniae* and those who were negative. Nonetheless, *M. pneumoniae*-positive patients exhibited a higher prevalence of symptoms such as cough and fever, which may suggest a more severe illness in this group.

The absence of a cell wall makes *M. pneumoniae* inherently resistant to β-lactam antibiotics [14]. Macrolides, tetracyclines, and fluoroquinolones are effective against *M. pneumoniae*, but the widespread use of macrolides has led to significant resistance rates, particularly in Eastern Asian countries [15]. Beyond drug resistance, the complexity of treatment for *M. pneumoniae* infection can be further exacerbated by co-infections with other respiratory pathogens [16]. In our study, RSV and *S. pneumoniae* emerged as the most prevalent viral and bacterial co-infections, respectively. Contrary to previous reports that highlighted a higher rate of viral co-infections [17], our findings indicate that bacterial co-infections were more common, possibly due to the lower sensitivity of the viral detection methods employed. Moreover, compared to *M. pneumoniae*-negative CAP patients, the incidence of PIV, RSV, and *S. aureus* co-infections significantly reduced in *M. pneumoniae*-infected patients, illustrating distinct co-infection patterns. Future research focusing on the severity, outcomes, and antibiotic

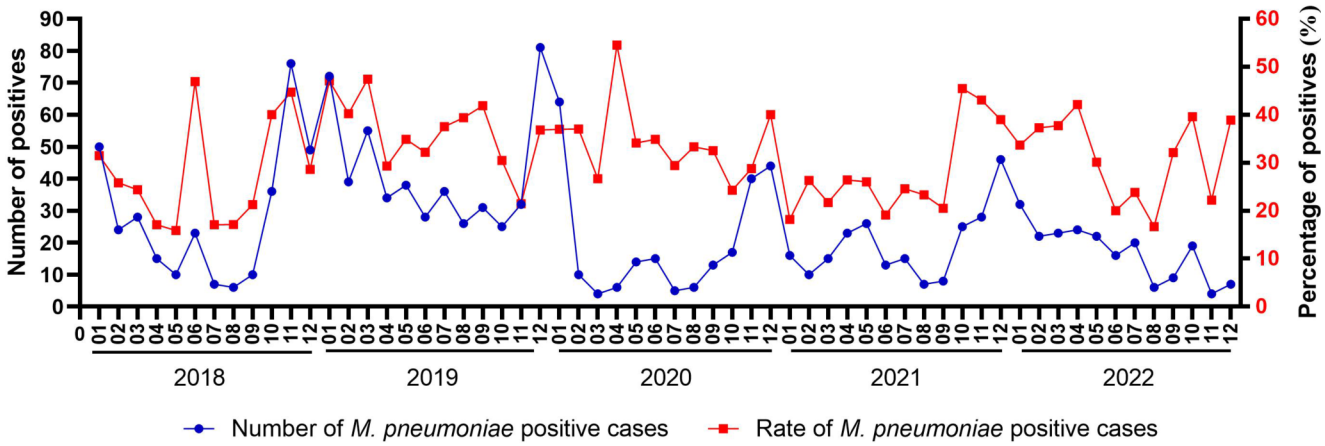

Fig. 1 Seasonal patterns of *M. pneumoniae* infection from 2018 to 2022

resistance of infections could offer deeper insights into the patterns of *M. pneumoniae* infections in community settings, thereby enhancing our understanding and management of this disease.

The COVID-19 pandemic has markedly influenced the infection landscape of various pathogens in recent years. In our study, the *M. pneumoniae* positivity rate in pediatric CAP patients increased significantly in 2019, but then decreased from 2020 to 2022, reaching levels similar to 2018. The rates in 2021 and 2022 were significantly lower than in 2019. This pattern mirrors several studies reporting increases in *M. pneumoniae* infections in 2019 and decreases during the COVID-19 pandemic [12, 18–20]. Epidemiologically, *M. pneumoniae* infections are perennial, with epidemics every few years across diverse climates [21]. For instance, Europe and Israel typically experience *M. pneumoniae* epidemics at intervals of 1 to 3 years [21]. A recent simultaneous epidemic in multiple countries, primarily in Europe and Asia, occurred in late 2019–early 2020 [22]. The introduction of NPIs against COVID-19 abruptly ended these epidemics and significantly reduced *M. pneumoniae* detection globally. Even when other respiratory pathogens resurged, *M. pneumoniae* infection remained suppressed in the second year of the pandemic [23]. Similar phenomenon was observed in our study. This delayed resurgence is noteworthy as it might be unique to *M. pneumoniae*, possibly due to its slow generation time, long incubation period, and relatively low transmission rate, which might necessitate a longer interval for the re-establishment of infections within a population [24]. These insights highlight the crucial need for continuous monitoring of *M. pneumoniae* epidemiology.

Beyond the positive rate, significant shifts in the demographic characteristics of pediatric CAP patients were evident during the COVID-19 pandemic. In our research, the median age of *M. pneumoniae*-infected children increased in 2019, followed by a decrease in 2020, and subsequent increases in 2021 and 2022. Several studies have noted shifts in age distribution of positive cases during the pandemic [12, 25, 26]. Unlike previous findings [12, 27], our study observed a higher proportion of male patients in 2020 compared to 2019. However, the gender distribution in 2021 and 2022 mirrored that of 2018 and 2019. In a distinct trend from *M. pneumoniae*-positive CAP patients, those without *M. pneumoniae* infection witnessed significant age increases from 2020 to 2022, alongside a notable decrease in the male proportion in 2020. These findings underscore divergent demographic trends between the two patient groups throughout the pandemic period.

During the COVID-19 pandemic, the landscape of viral and bacterial co-infections alongside *M. pneumoniae* witnessed dramatic shifts [5, 28]. Our research identified several significant changes: a decrease in IVA infections in 2021 and 2022, an uptick in RSV in 2020, a reduction in *H. influenzae* in 2020 and 2022, and an increase in *M. catarrhalis* infections in 2021. For patients without *M. pneumoniae* infection in our study, the pattern of infections with other pathogens varied distinctly. In this group, the incidences of IVA, PIV, *H. influenzae*, and *S. aureus* significantly declined during the pandemic period, whereas infections with *S. pneumoniae* and *M. catarrhalis* saw notable increases. RSV infections, in particular, surged in 2020 but then plummeted to their lowest levels in 2022—a trend rarely reported elsewhere. Concerning seasonal trends, *M. pneumoniae* typically peaks in autumn and winter [29], but the pandemic has altered these patterns, as reported in various studies [12, 25, 30]. Our study found similar seasonal trends in 2018, 2019, 2020, and 2021, with more cases during colder months, though the pattern was not consistent in warmer months. Remarkably, in 2022, the decline in autumn and winter cases led to the disappearance of the typical seasonal pattern. These findings further highlight the pandemic's impact on *M. pneumoniae* infection trends. The absence of a peak at the end of 2022 suggests the possibility of a delayed peak into 2023, underscoring the critical need for ongoing surveillance of *M. pneumoniae* infections and their co-infections to better understand and manage these evolving dynamics.

This study, while providing valuable insights, acknowledges several limitations. Firstly, the resistance rate of *M. pneumoniae* varies with genotypes [31], and increased resistance to antibiotics like macrolides complicates its management [32]. Regrettably, our research did not include data to evaluate changes in genotypes and antibiotic resistance of *M. pneumoniae* during the pandemic. Secondly, the diagnostic accuracy for *M. pneumoniae* infection is not absolute with single test. The IFA and PPA used in our study, while useful, do not match the sensitivity, specificity, and diagnostic performance of polymerase chain reaction (PCR) and chemiluminescence immunoassay (CLIA), leaving room for potential undetected infections [2, 33]. Thirdly, our study did not incorporate novel molecular diagnostic tools that could definitively detect other common respiratory pathogens such as rhinovirus, enterovirus, human parechovirus, and *Pneumocystis jirovecii* [34–38], hence we cannot discount the possibility of co-infections with these pathogens in our patient cohort. Fourthly, the absence of detailed clinical data concerning treatment approaches, antibiotic susceptibility, and patient responses to treatment limited our ability to perform an in-depth analysis of disease dynamics. Fifthly, conducting the research in a large tertiary hospital introduces the possibility of survivorship bias, which might not accurately reflect the broader community epidemiology. Additionally, the retrospective, single-center design of our

study suggests that our findings may not be entirely representative of other geographical areas.

Conclusions

In conclusion, our study delineates the evolution of *M. pneumoniae* infection in pediatric CAP patients on the periods before (2018–2019) and during (2020–2022) the COVID-19 pandemic. We noted substantial differences in age, male proportion, pneumonia-associated symptoms, and co-infections with other respiratory pathogens between *M. pneumoniae*-positive and -negative CAP patients. Notably, there was a significant surge in the positivity rate for *M. pneumoniae* in 2019, which declined to relatively low levels from 2020 to 2022. Throughout the COVID-19 pandemic, significant shifts were also observed in the median age, male proportion, and prevalence of co-infections with certain other pathogens among both groups of CAP patients. Additionally, the typical seasonal infection patterns disappeared in 2022. With the lifting of NPIs against COVID-19 in China since January 2023, a multicenter study involving more participants is crucial for ongoing surveillance of *M. pneumoniae* infection in the post-COVID-19 era.

Author contributions Ling Ai, Beizhong Liu, Liang Fang, and Chanjuan Zhou: Investigation, Data curation, Writing-Original draft preparation, Conceptualization, Methodology, Software; Fang Gong: Visualization, Writing-Reviewing, Validation, Supervision. All authors read and approved the final manuscript.

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

Declarations

Ethics approval The study protocol was approved by the ethics committee of the Yongchuan Hospital of Chongqing Medical University.

Consent to participate As a retrospective study, the need for informed consent was waived.

Consent for publication As a retrospective study, the need for informed consent was waived.

Competing interests The authors declare no competing interests.

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