

Analysis of the Sputum Culture Spectrum of Children with Respiratory Tract Infection in Wuxi Between 2014 and 2021

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Objective: We retrospectively analysed related clinical data to determine the influencing factors to better prevent and treat children's respiratory tract infection.

Methods: The study participants were children with respiratory tract infection who had sputum cultured in our hospital between 2014 and 2021. Sputum samples were extracted using negative suction pressure and sent to the hospital microbiological laboratory for testing. The testing results were analysed.

Results: A total of 4610 sputum samples were collected, and 508 positive samples were detected. The positive rate of pathogenic bacteria was 11.02%. *Escherichia coli* infection was more common in male patients (11.11%), whereas *Haemophilus influenzae* infection was more common in female patients (17.54%); the infection rates of these 2 bacteria are increasing annually. There were 304 (59.84%) strains of gram-negative bacteria, 172 (33.86%) strains of gram-positive bacteria and 32 (6.3%) strains of fungi. In children between 0 and 3 years old, the proportions of gram-negative bacteria were significantly higher than those of gram-positive bacteria in 2016–2017, 2018–2019 and 2020–2021 ($p < 0.01$). In every age group, the constituent ratio of gram-negative bacteria was significantly higher than that of gram-positive bacteria ($p < 0.01$) except for the 3–6-year age group. The proportion of *Staphylococcus aureus* in 2014–2015, 2016–2017, 2018–2019 and 2020–2021 was 25.64%, 25.20%, 22.98% and 16.44%, respectively. The proportion of *H. influenzae* in 2014–2015 was significantly lower than that in other years ($p < 0.01$). *Haemolyticus staphylococcus* and *E. coli* were more common in newborns, accounting for 19.12%.

Conclusion: The pathogens of respiratory tract infection in children change dynamically. There are significant differences in pathogens of respiratory tract infections among different age groups, years and seasons. Clinicians should pay attention to changes in the pathogen spectrum and improve drug resistance monitoring.

Keywords: children, respiratory tract infection, sputum culture, pathogen spectrum

Introduction

The immune resistance of children is lower, making respiratory tract infection one of the more common paediatric diseases.¹ This type of infection seriously affects children's health and has become a global public health concern.² Identifying the type of the pathogenic bacteria is vital to its treatment. Children's susceptibility to respiratory tract infection is mainly caused by the anatomical, physiological and immune characteristics of their respiratory systems, resulting in the reduced specific and non-specific immune function of the respiratory tract, especially in infants. As children age, the growth environment of pathogenic bacteria changes. The pathogenic bacteria of the respiratory tract may vary with age, sex and season, with these factors varying almost every year.³ An analysis of the sputum culture profile in children with respiratory tract infection can accurately display the latest types and trends of pathogenic bacteria in these patients in real time, and the timely and accurate detection of pathogenic bacteria and selection of appropriate antimicrobial agents have key clinical implications for the treatment of childhood bacterial pneumonia.^{4,5}

The aim of this study was to analyse the characteristics, distribution and variation of pathogens isolated from the sputum culture of children with respiratory tract infection in our hospital between 2014 and 2021. We retrospectively analysed these clinical data to determine related influencing factors to better prevent and treat children's respiratory tract infection.

Materials and Methods

General Information

The clinical data of children (aged between 28 days and 15 years) with respiratory tract infection admitted to Affiliated Hospital of Jiangnan University between January 2014 and December 2021 were retrospectively collected. All specimens collected were from patients with lower respiratory tract infections. The inclusion and exclusion criteria were based on the diagnostic criteria for nosocomial infection issued by the Ministry of Health of China ([2001]2). To prevent hospital data breaches, all case data have been transcribed manually with patient consent and have not been copied directly from the computer. We used negative suction pressure to help suction deep throat sputum, and sputum specimens were sent to the hospital microbiology laboratory for testing. Affiliated Hospital of Jiangnan University approved the study after ethical review (IRB number: LS2021088). Informed consent was waived by our institutional review board due to the retrospective nature of our study, and data were anonymized and kept confidential, and the study met the ethical standards of the World Medical Association's Declaration of Helsinki.

Obtaining Clinical Test Parameters

Sputum samples were collected within 24 h of admission, and pathogenic bacteria were isolated. Children under 6 years received a water rinse to clean their mouths. The children were placed in a semi-recumbent position. After local anaesthesia, a sterile closed sputum suction tube was inserted and connected to a negative pressure suction device, which collects secretions from deep in the airway. The tip of the suction tube was cut to collect the culture. After gargling with saline, children over 6 years were given a 3% saline nebulised inhalation to induce expectoration (appropriate local anaesthesia was given when the child was unable to tolerate the procedure). All the samples were sent for examination within 1 h (microscopic observation of sputum samples: white blood cells $>25 \times 10^9/L$, squamous epithelial cells $<10 \times 10^9/L$) and monitored continuously for 2 to 3 days. Each pathogen was cultured twice.

Inducing sputum is a more non-invasive method but can cause infection if the equipment is not thoroughly cleaned; negative pressure sputum provides better specimens but can damage the trachea, leading to injury and inflammation in patients. The degree of patient cooperation influences which of the 2 sampling methods is chosen. In practice, doctors use the age of 6 years as the dividing line between the 2 methods to unify standards.

Bacterial/Fungi Culture and Identification

The samples were inoculated into a chocolate medium, blood medium, MacConkey medium (Zhengzhou Renfa có Sai Biotechnology, Henan, China) and Sabour's medium for bacterial isolation and culture. The chocolate medium was cultured at 35°C in a 5% carbon dioxide incubator for 18–24 h, and the blood, MacConkey and Sabour mediums were cultured at 35°C for 18–24 h in the incubator. According to the basic technical standards of an NHC clinical microbiological examination in China, if fungal colonies are found, mycelia or spores must be identified under a microscope before fungal growth is confirmed. The dominant and absolute dominant bacteria were selected for pure culture. Microbial identification testing using a VITEK®2 Compact automatic microbiology analyser (Meyrié Diagnostic Products, Shanghai, China) continued for approximately 18–24 h.

Statistical Methods

The statistical software SPSS 26.0 was used in this study, and statistical data were expressed as a rate. The difference between ages, sexes, seasons and years was tested using the chi-square test. Fisher's exact test was used for analysis. When $p < 0.05$, the difference was considered statistically significant.

Results

Distribution of Pathogens

A total of 4610 sputum specimens were obtained, and 508 strains of pathogenic bacteria were detected by eliminating the duplicate strains through the practice of retaining the first strain of the same bacteria from the same patient. Of the 4610 sputum specimens, 508 (11.02%) were positive. Among the positive samples, 40.2% (204/508) were gram-positive and 59.8% (304/508) were gram-negative. The gram-negative bacteria were composed of *Haemophilus* (18.3%, $n = 55$), *Enterobacteriaceae* (58.6%, $n = 178$) and non-fermenting gram-negative bacteria (23.3%, $n = 71$). The positive rate of neonatal specimens was 27.75% (136/490), which is significantly higher than that of paediatric internal medicine [9.03% (372/4120) ($\chi^2 = 156.61$, $p < 0.01$)]. Of the 508 positive specimens, there were 112 strains of *Staphylococcus aureus*, 59 of *Klebsiella pneumoniae*, 59 of *Escherichia coli*, 55 of *Haemophilus influenzae* (Among them, 13 BLPAR and 10 BLNAR strains were detected), 41 of *Acinetobacter baumannii*, 26 of *Staphylococcus haemolyticus*, 22 of *Streptococcus pneumoniae*, 22 of *Enterobacter cloacae subspecies* and 17 of *Pseudomonas aeruginosa*.

Distribution of Bacteria by Sex

The distribution of pathogens between sexes is detailed in Tables 1 and 2; 36.7% (109/297) were gram-positive bacteria and 57.58% (171/297) were gram-negative bacteria. The most common pathogens were *S. aureus* (24.92%), *E. coli* (11.11%) and *K. pneumoniae* (10.44%). Among girls, gram-positive bacteria accounted for 29.86% (63/211) and gram-negative bacteria 63.03% (133/211), and the most common pathogens were *S. aureus* (18.01%), *H. influenzae* (17.54%) and *K. pneumoniae* (13.27%). The constituent ratio of gram-negative bacteria in children was significantly higher than that of gram-positive cocci ($p < 0.01$). The constituent ratio of *H. influenzae* bacteria in girls was significantly higher than that in boys; the difference was significant ($p < 0.01$).

Table 1 Distribution and Constituent Ratio (N, %) of the Main Pathogens in Sputum Culture of the Respiratory 2021 by Sex and Age Rom 2014 to 2021

Species	Number of Strains	Sex		Age			
		Boy	Girl	<1 Month	1 Month~3Years	3~6 Years	>6 Years
<i>Staphylococcus aureus</i>	112 (22.05)	74 (24.92)	38 (18.01)	15 (11.03)	77 (27.21)	16 (25.81)	4 (14.81)
<i>Klebsiella pneumoniae</i>	59 (11.61)	31 (10.44)	28 (13.27)	22 (16.18)	29 (10.25)	5(8.06)	3(11.11)
<i>Escherichia coli.</i>	59 (11.61)	33 (11.11)	26 (12.32)	26 (19.12)	31 (12.33)	1(1.61)	1(3.7)
<i>Haemophilus influenzae.</i>	55 (10.83)	18 (6.0)	37 (17.54)	2(1.47)	35 (13.70)	12 (19.35)	6(22.22)
<i>Acinetobacter baumannii.</i>	41 (8.07)	26 (8.75)	15 (7.1)	13 (9.56)	16 (5.65)	6(9.67)	6(22.22)
<i>Staphylococcus hemolyticus.</i>	26 (5.12)	14 (4.71)	12 (5.69)	26 (19.12)	0 (0)	0 (0)	0 (0)
<i>Streptococcus pneumoniae.</i>	22 (4.33)	11 (3.7)	11 (5.21)	0 (0)	13 (4.59)	9 (14.52)	0 (0)
<i>Enterobacter cloacae subsp.</i>	22 (4.33)	11 (3.7)	11 (5.21)	6 (4.41)	13 (4.59)	2 (3.23)	1 (3.7)
<i>Pseudomonas aeruginosa.</i>	17 (3.35)	12 (4.04)	5 (2.37)	5 (3.68)	9 (3.18)	2 (3.23)	1 (3.7)
Total.	413 (81.3)	230 (77.44)	183 (86.73)	115 (84.56)	223 (78.80)	53 (85.48)	22 (81.48)

Table 2 Distribution and Composition Ratio of Gram-Positive Bacteria, Gram-Negative Bacteria and Fungi in Sputum Culture of Children with Respiratory Tract Infections by Gender and Age from 2014 to 2021 (n, %)

Strain	Number of Strains	Sex		Years			
		Boy	Girl	<1 Month	1 Month~3Years	3~6 Years	>6 Years
Gram-positive bacteria.	172 (33.86)	109 (36.70)	63 (29.86)	48 (35.29)	95 (33.57)	25 (40.32)	4 (14.81)
Gram-negative bacteria.	304 (59.84)	171 (57.58)	133 (63.03)	86 (63.24)	166 (58.66)	30 (48.39)	22 (81.48)
Fungus.	32 (6.3)	17 (5.72)	15 (7.11)	2 (1.47)	22 (7.77)	7 (11.29)	1 (3.70)
Total.	508 (100)	297 (100)	211 (100)	136 (100)	283 (100)	62 (100)	27 (100)

Strain Changes by Year

The changes in strains in different years are shown in Tables 3 and 4. In 2014, 172 (33.86) strains of gram-positive bacteria were detected. In 2021, the constituent ratio showed a downward trend. A total of 304 (59.84) strains of gram-negative bacteria were detected, increasing annually. In the past 8 years, the proportion of *S. aureus* has peaked, but this proportion has been declining annually. In 2014–2015, *S. haemolyticus* occupied second place, and its constituent ratio was significantly higher than that of the other 3 groups ($X^2 = 18.22, 19.87$ and $25.21, p < 0.01$). The constituent ratio of *H. influenzae* in 2014–2015 was significantly lower than that in the other 3 groups ($X^2 = 7.38, 12.93$ and $11.73, p < 0.01$). In 2016–2017, 2018–2019 and 2020–2021, the proportion of gram-negative bacteria was significantly higher than that of gram-positive bacteria (2021: $X^2 = 16.68, 32.63$ and $34.30, p < 0.01$). The constituent ratio of gram-negative bacteria in 2014–2015 was significantly lower than that in the other 3 groups ($X^2 = 4.241, 4.62$ and $7.49, p < 0.05$), and the proportion of gram-negative bacteria increased annually.

Distribution of Bacteria by Age

The distribution of bacteria in different age groups is shown in Tables 1 and 2. The most common pathogens in children less than 1 month old were *S. haemolyticus* (19.12%, 26/136), *E. coli* (19.12%, 26/136) and *K. pneumoniae* (16.18%, 22/136). The most common pathogens in children between the ages of 1 month and 3 years were *S. aureus* (27.21%, 77/283), *H. influenzae* (13.70%, 35/283) and *E. coli* (12.33%, 31/283). Among children aged 3–6, the main pathogens were *S. aureus* (25.81%, 16/62), *H. influenzae* (19.35%, 12/62) and *A. baumannii* (9.68%, 6/62).

Among children over 6 years old, the main pathogens were *H. influenzae* (22.2%, 6/27), *A. baumannii* (22.2%, 6/27) and *S. aureus* (14.8%, 4/27). Gram-positive bacteria accounted for 40.32% (25/62) in children aged 3 to 6, whereas gram-negative bacteria accounted for 81.48% (22/27) in children older than 6. Except for the age group of 3–6 years old, the detected Gram negative bacteria were significantly higher than Gram positive bacteria ($X^2 = 21.24, 35.84$ and 24.03 ,

Table 3 Distribution and Composition Ratio of Main Pathogenic Bacteria in Sputum Culture of Children with Respiratory Tract Infections in Different Seasons and Years from 2014 to 2021 (n, %)

Strain.	Number of Strains	Seasons		Years			
		Spring and Summer	Autumn And Winter	2014–2015	2016–2017	2018–2019	2020–2021
<i>Staphylococcus aureus</i> .	112 (22.05)	33 (16.5)	79 (25.65)	20 (25.64)	31 (25.20)	37 (22.98)	24 (16.44)
<i>Klebsiella pneumoniae</i>	59 (11.61)	26 (13.0)	33 (10.71)	11 (14.1)	18 (14.63)	16 (9.94)	14 (9.59)
<i>Escherichia coli</i> .	59 (11.61)	26 (13.0)	33 (10.71)	7 (8.97)	14 (11.38)	20 (12.42)	18 (12.33)
<i>Haemophilus influenzae</i> .	55 (10.83)	25 (12.5)	30 (9.74)	0 (0)	11 (8.94)	24 (14.9)	20 (13.70)
<i>Acinetobacter baumannii</i> .	41 (8.07)	22 (11.0)	19 (6.17)	5 (6.41)	9 (7.32)	13 (8.07)	14 (9.59)
<i>Staphylococcus hemolyticus</i> .	26 (5.12)	13 (6.5)	13 (4.22)	16 (20.51)	3 (2.44)	5 (3.11)	2 (1.37)
<i>Streptococcus pneumoniae</i> .	22 (4.33)	5 (2.5)	17 (5.52)	0 (0)	3 (2.44)	3 (1.86)	16 (10.96)
<i>Enterobacter cloacae subsp</i> .	22 (4.33)	11 (5.5)	11 (3.57)	1 (1.28)	6 (4.88)	11 (6.83)	4 (2.74)
<i>Pseudomonas aeruginosa</i> .	17 (3.35)	8 (4.0)	9 (2.92)	1 (1.28)	6 (4.88)	4 (2.48)	6 (4.11)
Total	413 (81.3)	169 (84.5)	244 (79.22)	61 (78.2)	101 (82.11)	133 (82.61)	118 (80.82)

Table 4 Distribution and Composition Ratio of Gram-Positive Bacteria, Gram-Negative Bacteria and Fungi in Sputum Culture of Children with Respiratory Tract Infections in Different Seasons and Years from 2014 to 2021 (n, %)

Strain	Number of Strains	Seasons		Years			
		Spring and Summer	Autumn And Winter	2014–2015	2016–2017	2018–2019	2020–2021
Gram-positive bacteria.	172 (33.86)	59 (29.5)	113 (36.69)	37 (47.44)	43 (34.96)	47 (29.19)	45 (30.82)
Gram-negative bacteria.	304 (59.84)	135 (67.5)	169 (54.87)	36 (46.15)	75 (60.97)	98 (60.87)	95 (65.07)
Fungus.	32 (6.3)	6 (3.0)	26 (8.44)	5 (6.41)	5 (4.07)	16 (9.94)	6 (4.11)
Total.	508 (100)	200 (100)	308 (100)	78 (100)	123 (100)	161 (100)	146 (100)

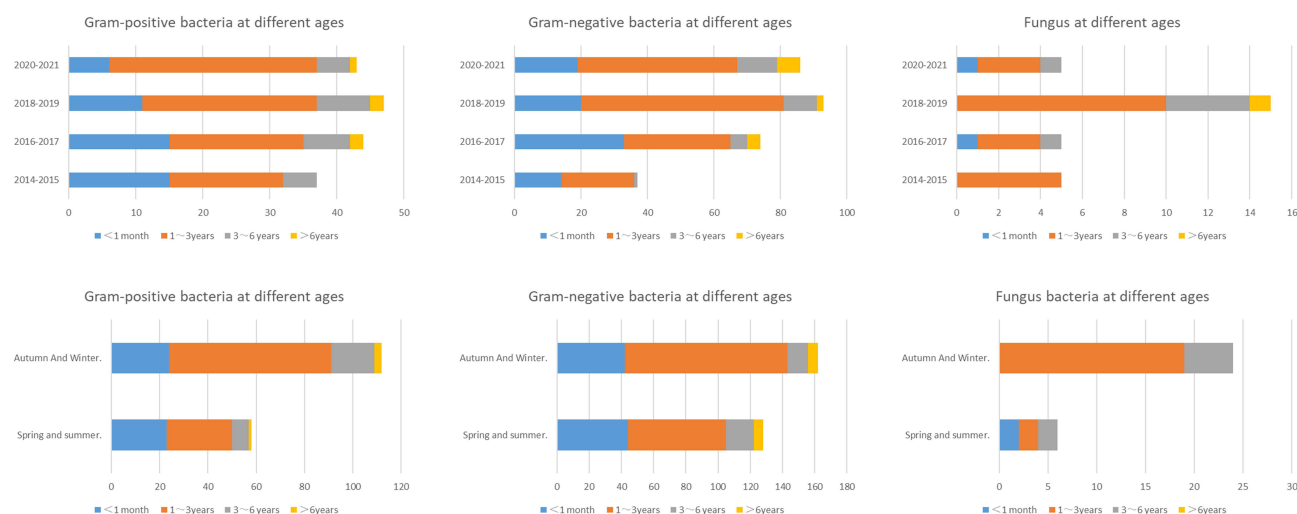


Figure 1 Distribution of bacteria and fungi in children of different ages in different years and seasons (stacked bar chart).

$p < 0.01$). Gram-negative bacteria accounted for 81.48% in children over 6 years. Over time, fewer gram-positive bacteria existed in children under 1 month old. Between 1 month and 3 years, the number of gram-positive bacteria increased over time; gram-negative bacteria also increased over time in this age group (Figure 1). *S. haemolyticus* was only identified in the neonatal period of less than 1 month; its proportion was the highest and was not found in any age group older than 1 month. The proportions of *H. influenzae* in the 1-month, 1-month–3-years, 3–6-years and >6-years age groups were 1.47%, 13.7%, 19.35% and 22.22%, respectively. The composition ratio of *E. coli* in the <1-month and 1-month–3-years age groups was significantly higher than that of the 3–6-years age group, and the difference was statistically significant ($\chi^2 = 11.08, 5.274, p < 0.05$).

Distribution of Pathogens by Season

The distribution of pathogens by season is shown in Tables 3 and 4. In spring and summer, gram-positive bacteria accounted for 29.5% (59/200) and gram-negative bacteria for 67.5% (135/200). The top 3 pathogens were *S. aureus* at 16.5% (33/200), *E. coli* at 13% (26/200) and *K. pneumoniae* at 13% (26/200). In autumn and winter, gram-positive bacteria accounted for 36.69% (113/308) and gram-negative bacteria for 54.87% (169/308), with the top 3 being *S. aureus* at 25.65% (79/308), *E. coli* at 10.71% (33/308) and *K. pneumoniae* at 10.71% (33/308). The composition ratio of gram-negative bacteria was significantly higher than that of gram-positive bacteria in both spring and summer and autumn and winter, and the difference was statistically significant ($p < 0.01$, Figure 1); the composition ratio of gram-negative bacteria in spring and summer was significantly higher than that in autumn and winter, and the difference was statistically significant ($p < 0.01$). The gram-negative bacteria were composed of *Haemophilus* (7.4%, $n = 10$), *Enterobacteriaceae* (74.1%, $n = 100$) and non-fermenting gram-negative bacteria (18.5%, $n = 25$) in spring and summer; the gram-negative bacteria were composed of *Haemophilus* (26.6%, $n = 45$), *Enterobacteriaceae* (46.2%, $n = 78$) and non-fermenting gram-negative bacteria (27.2%, $n = 46$) in autumn and winter. The composition of *S. aureus* in autumn and winter was significantly higher than that in spring and summer, and the difference was statistically significant ($p < 0.05$).

Discussion

In this study, the detection rate of pathogens in the sputum culture of children with respiratory tract infection was consistent with that of previous reports, but the proportion of pathogenic bacteria was different.^{6–8} In total, 508 strains of pathogenic bacteria were detected in 4610 sputum samples from children with respiratory tract infection. The positive rate was 11.01%, and the proportion of children under 3 years was 82.48%, which is consistent with the 76.05% reported by Wang.⁹ The top 5 strains were *S. aureus*, *K. pneumoniae*, *E. coli*, *H. influenzae* and *A. baumannii*, of which 59.84% were gram-negative; gram-positive bacteria accounted for 33.86%. Gram-negative bacteria therefore dominated.

Understanding the distribution of respiratory tract strains is useful in guiding the clinical medication and treatment of respiratory tract infection in children; it can reduce the abuse of antibiotics and drug resistance of strains, shorten the course of treatment and reduce damage to children and the economic burden on families.¹⁰

However, most studies on the distribution of pathogens in children's respiratory tract infection have lasted for only between 1 and 5 years, with few lasting 8 years or more. The longer the time span, the more accurately research can reflect the changes in pathogenic bacteria in children's respiratory tract infection in a specific area. The results revealed no significant differences between gram-positive bacteria and gram-negative bacteria in 2014–2015, but the proportion of gram-negative bacteria has increased significantly with time, especially in the last 2 years. The data suggest that attention should be paid to gram-negative bacteria infection in children with respiratory tract infection.^{11,12} In the past 2 years, gram-negative bacteria in children's respiratory tract infection have mainly consisted of *H. influenzae* and *E. coli*.⁹ Studies have shown that the aetiology of severe pneumonia in children is also dominated by *H. influenzae* and other gram-negative strains.¹ This study showed that the percentage of respiratory tract infection involving *S. aureus* in children is currently the highest since 2014, which is consistent with the findings of related studies.^{3,13} However, this study also revealed a decreasing trend in the proportion of respiratory tract infection in children, although *S. aureus* remains a key pathogen of necrotising pneumonia in children.¹⁴ These results indicate that we should consider gram-negative bacilli such as *H. influenzae* when encountering severe pneumonia in children and gram-positive bacteria such as *S. aureus* when observing necrotising pneumonia in children. It is particularly important to understand the yearly variations in children's respiratory tract infection to inform the most appropriate choice of drugs for treatment.

The distribution of respiratory tract infection in children has seasonal characteristics; understanding the distribution of pathogenic bacteria is therefore essential. There are differences in the pathogenic bacteria of respiratory tract infection among children during specific seasons.¹⁵ Different seasons have different temperatures and levels of humidity, and viral respiratory infection is more common in winter and spring.¹⁶ Children with congenital heart defects who have community-acquired pneumonia in winter are more susceptible to *S. aureus* and *E. coli* than children with simple community-acquired pneumonia. Our results showed that the constituent ratio of gram-negative bacteria in children with respiratory tract infection was significantly higher than that of gram-positive bacteria in spring, summer, autumn and winter, and gram-negative bacteria were significantly more common in spring and summer than in autumn and winter. The constituent ratio of gram-positive *S. aureus* was higher in autumn and winter than in spring and summer. Gram-positive bacteria did not differ seasonally among children less than 1 month old. In children aged 1 month to 3 years, gram-negative bacteria were significantly more common than gram-positive bacteria. In autumn and winter, when there is a high incidence of respiratory infection in children, clinicians should be on the alert for *S. aureus*.¹⁷

The distribution of pathogenic bacteria in children's respiratory tract infection among different age groups also varied. Newborns were an especially vulnerable group and experienced environmental changes both inside and outside the uterus. The pathogenic bacteria also had age characteristics. The age threshold is one of the criteria used to define the high-risk infection group. The pathogens exhibited a consistent age pattern, with children less than 3 years of age at the highest risk. Reports have shown that *K. pneumoniae*, *E. coli*, *A. baumannii*, *E. cloacae* and *H. influenzae* are the predominant gram-negative bacteria isolated from the lower respiratory tract of newborns.^{18,19} The results of this study were similar to those reported above.

Understanding the distribution of pathogenic bacteria in respiratory tract infection of children of all ages can provide a key basis for treatment. Community-acquired pneumonia in children aged 4 months to 5 years is mainly caused by respiratory viral infections, with a higher proportion of viral infections occurring at younger ages and bacterial infections present at almost all ages.¹³ As in previous reports, *S. aureus* was the most common cause of respiratory tract infection in children aged from 1 month to 3 years as well as in the 3–6 age group. We suggest that the possibility of *S. aureus* infection should be considered when evaluating respiratory tract infections in infants and preschool children. The study also suggested that *H. influenzae* in the <1-month, 1-month–3-years, 3–6-years and >6-years age groups was gradually increasing. We postulate that *H. influenzae* is the main pathogen of respiratory tract infection in school-age children, which is consistent with the reported result that *H. influenzae* is the most prevalent pathogen, accounting for 22.58% of sputum culture in severe pneumonia. However, the above report did not study the constituent ratio of *H. influenzae* and its changing trends within different age groups. In this study, we found that the distribution of *H. influenzae* in the

respiratory tract had been increasing until recent years and reflects the age difference. Moreover, this study suggests that the constituent ratio of *E. coli* in the 3–6-years group was significantly lower than that of the younger children's groups. This may be because of the immaturity of immune function in infants and young children, making them more prone to *E. coli* and other opportunistic bacterial infections. It may also be related to the use of nappies in infants and young children.

Sex may also be a factor in the presence of different pathogens in children with respiratory tract infection, but there are few related studies. A study tested 12,359 children (who had acute respiratory infection) from Guangzhou, China, for 9 pathogens (*Mycoplasma*, *Chlamydia*, *Legionella pneumophila*, *Rickettsia* and influenza viruses), revealing that the infection rates of *Mycoplasma* antibody-IgM, influenza B virus and parainfluenza virus in girls were significantly different from those in boys.²⁰ The results showed that the distribution of pathogenic bacteria in children's respiratory tracts differed between sexes. The constituent ratio of gram-negative bacteria was higher than that of gram-positive bacteria in both boys and girls. It should be noted that girls are more susceptible to *H. influenzae* than boys.

The lack of patient baseline characteristics, classification of respiratory infection, consideration of the involvement of viruses and mycoplasma, classification of gram-negative rods and drug susceptibility data, as well as the difficulty in distinguishing whether the detected bacteria represent true infections or are just contaminants and bacteria that cannot grow in these media are limitations of our study. Because of the methods we used to collect specimens, our results need to be further verified. As for the limitations of retrospective analysis, multi-centre studies or more data are needed to refine the results.

Conclusion

Between 2014 and 2021, gram-negative bacteria were the predominant pathogens among school-age children, especially during spring and summer. The proportion of *S. aureus* in children has been decreasing yearly, whereas the proportion of *H. influenzae* in children has increased annually over the past 4 years. Clinicians should pay attention to changes in the pathogenic spectrum and improve the monitoring and management of drug resistance.

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Disclosure

The authors report no conflicts of interest in this work.

References

1. Stensballe LG. Viral nedre luftvejs-infektion hos børn under fem år [Viral lower respiratory tract infection in children under five years of age]. *Ugeskr Laeger*. 2021;183(28):V09200657. Danish.
2. Chen Y, Li Q. Analysis of the effect of nursing intervention on children with respiratory tract infection based on comprehensive nursing. *J Healthc Eng*. 2021;2021:6923823. doi:10.1155/2021/6923823
3. Zhu X, Ye T, Zhong H, et al. Distribution and drug resistance of bacterial pathogens associated with lower respiratory tract infection in children and the effect of COVID-19 on the distribution of pathogens. *Can J Infect Dis Med Microbiol*. 2022;2022:1181283. doi:10.1155/2022/1181283
4. Mai W, Liu Y, Meng Q, Xu J, Wu J. Bacterial epidemiology and antimicrobial resistance profiles of respiratory specimens of children with pneumonia in Hainan, China. *Infect Drug Resist*. 2023;16:249–261. doi:10.2147/IDR.S397513
5. Claassen-Weitz S, Lim KYL, Mullally C, Zar HJ, Nicol MP. The association between bacteria colonizing the upper respiratory tract and lower respiratory tract infection in young children: a systematic review and meta-analysis. *Clin Microbiol Infect*. 2021;27(9):1262–1270. doi:10.1016/j.cmi.2021.05.034
6. Mai WH, Zhuo ZL, Zheng QL, Yu ST. Etiological characteristics and drug resistance of acute lower respiratory tract bacterial infection in children in Haikou. *Chin Tropic Med*. 2021;21(9):833–838.
7. Huang XJ, Lin C, Liu B, Liu B, Zhang H. Sputum culture and drug sensitivity in 372 children with congenital heart disease complicated with community acquired pulmonary infection. *J Pediatr Pharm*. 2021; 12:16–19.
8. Su DQ, Huang HL, Zhuo ZQ. Pathogen distribution and bacterial resistance in children with severe pneumonia: a single-center retrospective study. *Medicine*. 2021;100(35):e27128. doi:10.1097/MD.00000000000027128
9. Wang XL, Zhang ZG, Yu X, Huang HL. Gram-positive pathogen identification and drug-resistance analysis in hospitalized children with lower respiratory tract. *Chin J Postgrad Med*. 2018;41(5):449–451.
10. Same RG, Amoah J, Hsu AJ, et al. The association of antibiotic duration with successful treatment of community-acquired pneumonia in children. *J Pediatric Infect Dis Soc*. 2021;10(3):267–273. doi:10.1093/jpids/piaa055

11. Ruan XF, Qiu L. Distribution characteristics and drug resistance analysis of pathogens from sputum culture of children with infectious pneumonia in our hospital from 2019 to 2020. *Chin J Rural Med Pharm*. 2022;29(4):50–51.
12. Wattal C, Goel N. Pediatric blood cultures and antibiotic resistance: an overview. *Indian J Pediatr*. 2020;87(2):125–131. doi:10.1007/s12098-019-03123-y
13. Liu TT. Study on the composition of main pathogenic bacteria and their resistance to antibiotics in airway sputum samples of children with pneumonia. *Inner Mongol Med J*. 2022;54(1):95–97.
14. Zhou YL, Liu JR, Yi QW, et al. A multicenter retrospective study on the etiology of necrotizing pneumonia in children. *Chin J Pediatr*. 2021;59(8):658–664. doi:10.3760/cma.j.cn112140-20210126-00072
15. Bhuiyan MU, Snelling TL, West R, et al. The contribution of viruses and bacteria to community-acquired pneumonia in vaccinated children: a case-control study. *Thorax*. 2019;74(3):261–269. doi:10.1136/thoraxjnl-2018-212096
16. Wang X, Li Y, O'Brien KL, et al. Global burden of respiratory infections associated with seasonal influenza in children under 5 years in 2018: a systematic review and modelling study. *Lancet Glob Health*. 2020;8(4):e497–e510. doi:10.1016/S2214-109X(19)30545-5
17. Berner R, Huebner J, Huppertz HI, et al. Kinder mit akuter Atemwegsinfektion in Kinderkliniken im Herbst/Winter 2020/21 [Children with acute respiratory tract infections in pediatric hospitals in autumn/winter 2020/2021]. *Monatsschr Kinderheilkd*. 2020;168(12):1138–1141. German. doi:10.1007/s00112-020-01058-9
18. Zhu GH, Xu D, Zhang YY, et al. Epidemiological characteristics of four common respiratory viral infections in children. *Virol J*. 2021;18(1):10. doi:10.1186/s12985-020-01475-y
19. Shu TH, Fu LZ. Analysis on antimicrobial susceptibility tests results of bacteria isolated from sputum culture of neonates with different durations of invasive ventilator assisted ventilation. *Chongq Med*. 2022;51(9):1511–1515.
20. Lai KF, Lian JF, Chen LQ, Lin Z, Ouyang K. Results of detection of 9 pathogens in respiratory tract of 12359 children with acute respiratory tract infection in Guangzhou area. *Matern Child Health Care Chin*. 2018;33(13):2996–2999.

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