

ORIGINAL ARTICLE

In the COVID-19 Pandemic Era: Portray of the Common Causative Pathogens of Community-Acquired Pneumonia in Children

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ABSTRACT

Key words:

Pneumonia, COVID-19, Children, Respiratory Viruses, PCR

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Background: as COVID-19 spreads in a pandemic manner declare the spreading pattern of other viruses inducing lower respiratory tract infection in children is of high diagnostic value due to interfering symptoms where most common being Respiratory syncytial virus, Rhinovirus, Adenovirus, Influenza, and Parainfluenza viruses. Due to the use of the Pneumococcal conjugate and the Hemophilus influenza type b vaccines, Staphylococcus aureus and H. influenza non-type b are emerging as the most common bacterial organisms causing acute community-acquired pneumonia. In low- and middle-income countries, other bacterial organisms are also reported as Klebsiella pneumoniae, E-coli, and Bordetella pertussis. The most frequent symptoms of COVID-19 are fever, cough, dyspnea, anosmia, and gastrointestinal symptoms. Some children may require intensive care unit admission and mechanical ventilation. **Objectives:** to detect the most prevalent viral and bacterial agents causing acute community-acquired pneumonia among children in the era of COVID-19, and to assess their hospital stay length and their clinical outcomes. **Methodology:** This prospective observational study included 100 children presented with community-acquired pneumonia to Cairo University Specialized Pediatric Hospital and 6th October Health Insurance Hospital from October 2020 to September 2021. Respiratory samples were subjected to viral detection by PCR and microbiological isolation. **Results:** The most prevalent pathogens causing community-acquired pneumonia were viruses (44%) followed by bacteria (40%). The most prevalent virus was Influenza B virus (18%). The most prevalent bacteria was Klebsiella pneumoniae (14%). **Conclusions:** Viral agents are the most prevalent pathogen causing acute community-acquired pneumonia in children under 5 years during COVID-19.

INTRODUCTION

Acute community-acquired pneumonia is considered one out of the leading causes of morbidity and mortality in children worldwide. Pneumonia was deliberated the main cause of mortality in children less than 5 years for a long time¹. Since the eighties, the estimations of deaths because of community-acquired pneumonia had improved when respiratory tract infections in children caused around 4 to 5 million children to die annually. The rate of child deaths due to pneumonia has declined from 1,756,000 in 2000 to 809,000 in 2017. In Egypt in 2021, about 13.9% of deaths occurred in children below 5 years of age and were due to pneumonia². Viral agents are the most prevalent cause of acute community-acquired pneumonia among children³. The most common viruses causing lower respiratory tract infection are Respiratory Syncytial Virus (RSV),

Rhinovirus, Adenovirus, Influenza, and Parainfluenza viruses⁴.

The most prevalent bacterial causes of acute community-acquired pneumonia were Streptococcus pneumoniae and Hemophilus influenza. They were described as a coinfection with RSV causing increased severity of host inflammation⁵. As a result of the use of both the Pneumococcal conjugate and Hemophilus influenza type b vaccines, Staphylococcus aureus and H. influenza non-type b were emerged as the most prevalent bacterial organisms causing community-acquired pneumonia. In the low- and middle-income countries, other bacterial organisms are reported as Klebsiella pneumoniae, E-coli and Bordetella pertussis⁶. Viral and bacterial co-infections may have abundant leucocytes, more consolidations on chest radiographs, and parapneumonic effusions. They also

had a higher rate of intensive care unit admission, mechanical ventilation, and a longer hospital stay⁷.

The most frequent symptoms of COVID-19 in children were fever, cough, dyspnea, anosmia, and gastrointestinal symptoms⁸. Some children may require pediatric intensive care unit admission and invasive mechanical ventilation⁹. Our work was planned to detect the most prevalent viral and bacterial agents causing acute community-acquired pneumonia among children in the era of *COVID-19*, and to assess the length of hospital stay and the clinical outcome of children admitted with acute community-acquired pneumonia too.

METHODOLOGY

This prospective observational study included 100 children presented with community-acquired pneumonia to the pediatric wards and the PICU of CUSPH and 6th October Health Insurance Hospital in the period from October 2020 to September 2021.

Ethical committee approval:

The study was ethically approved by the Research Ethics Committee of the Faculty of Medicine, Cairo University. (Code: MS-328-2020). Written Consent was taken before data collection.

Inclusion criteria:

Patients aged 1 month to 5 years admitted to the Pediatric Wards and the PICU with community-acquired pneumonia which is diagnosed in accordance with the following clinical and radiological criteria:

- **Fever**
- **Clinical criteria: Pneumonia** is a cough or difficulty breathing with tachypnea and/or chest recession. **Severe pneumonia** is cough or difficulty breathing with one or more of the following: (a) central cyanosis or oxygen saturation less than 90% measured with pulse oximetry, (b) severe respiratory distress manifested by grunting, or (c) any general danger sign such as poor breastfeeding or drinking, lethargy, altered mental status, or convulsions^{10,11}.
- **Radiological criteria** showed consolidations, pleural effusion, and/or other infiltrates on chest radiographs⁶.

Exclusion criteria:

Children with respiratory symptoms and signs that did not meet the criteria of community-acquired pneumonia were excluded from the study.

All the patients enrolled in the study were subjected to the following steps as demonstrated in figure 1.

Flowchart of the Studied Cases: (Figure: 1)

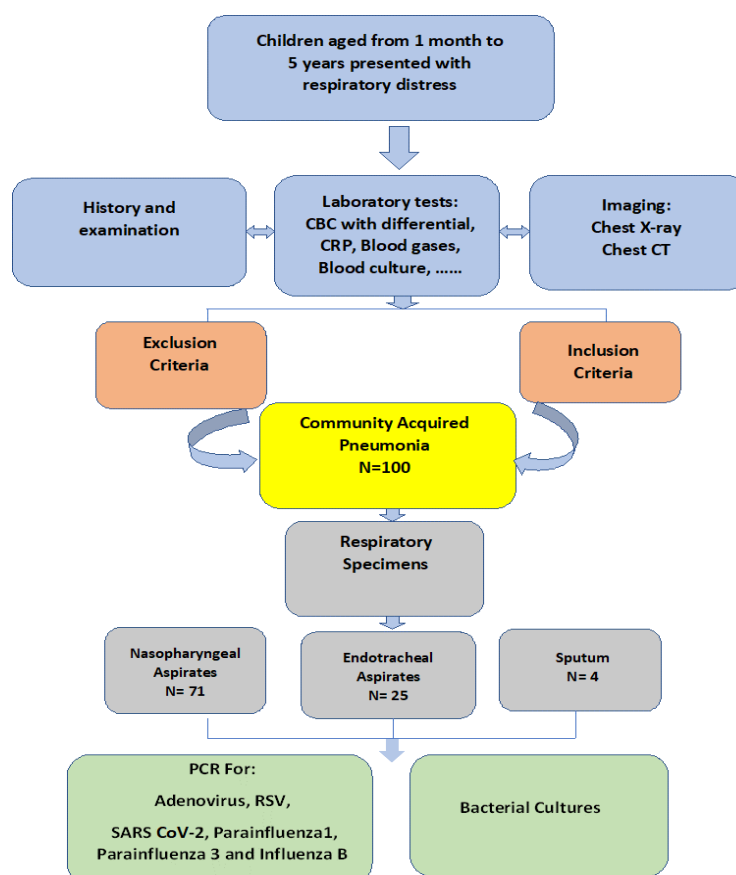


Fig. 1: Flowchart of the Studied Cases

Molecular Analysis:

Each respiratory specimen was divided into two parts:

1. The first part was collected and placed in a tube containing 2 mL of the virus transport medium (Becton Dickinson, USA). An aliquot of 450 µL was submitted for RNA extraction for further testing using multiplex Real-time PCR assay for the presence of *Influenza B*, *RSV*, *Parainfluenza 1*, *Parainfluenza 3*, and single Real-time PCR assay for detection of *SARS CoV-2*. Another aliquot of 450 µL was submitted for DNA extraction for further conventional PCR assay for the presence of the *Adenovirus* (foreword primer, reverse primer, and probe sequences are shown in the table 1. The rest of the

sample was stored with full patient data identification at -80°C if needed ¹².

Nucleic acid Extraction:

Viral nucleic acids were extracted from samples using QIAamp Viral RNA Mini Kit and QIAamp DNA Micro Kit (Qiagen, Germany) according to the manufacturer's instructions. Regarding cDNA 200 ng of extracted RNA using Omniscript RT Kit (Qiagen, Germany) was used for reverse transcription. cDNA Product was used in multiplex assay for influenza B, RSV, and parainfluenza 1 & 3 ¹². SARS CoV-2 was tested using SuperScript™ III Platinum One-Step Quantitative RT-PCR System Invitrogen RT-PCR Kit¹³.

Table 1: Foreword Primer, Reverse Primer, and Probe Sequences of *Influenza B*, *RSV*, *Parainfluenza 1*, *Parainfluenza 3*, and *SARS CoV-2*.

Virus	Primers and Probes Sequences
<i>Influenza B</i>	Forward primer: 5'-AAATACGGTGGATTAATAAAAAGCAA Reverse primer: 5'-CCAGCAATAGCTCCGAAGAAA Probe: 5-CACCCATATTGGGCAATTCCTATGGC- texas red
<i>Respiratory Syncytial Virus (RSV)</i>	Forward primer: 5'-GGAAACATACGTGAACAAGCTTCA Reverse primer: 5'-TCATCATCTTTTCTAGAACATTGTACTGA Probe 6: 5TGTGTATGTGGAGCCTT- Fam
<i>Parainfluenza 1</i>	Forward primer: 5'-ACAGATGAAATTTTCAAGTGCTACTTTAGT Reverse primer: 5'-GCCTCTTTTAATGCCATATTATCATTAGA Probe: 5-ATGGTAATAAATCGACTCGCT- cy5
<i>Para influenza 3</i>	Forward primer: 5'-TGCTGTTTCGATGCCAACAA Reverse primer : 5'-ATTTTATGCTCCTATCTAGTGGAAGACA Probe: 5-TTGCTCTTGCTCCTCA- HEX
<i>SARS CoV-2</i>	GCTGGTGCTGCAGCTTATTA (495-520nm) AGGGTCAAGTGCACAGTCTA fam SARS-CoV-2_IBS_N1 CAATGCTGCAATCGTGCTAC GTTGCGACTACGTGATGAGG hex (535-556nm)

Finally testing Human *Adenovirus* extracted DNA was detected by nested PCR of the hexon gene. The first-round amplification was done by the forward primer 5'-GCC GAG AAG GGC GTG CGC AGG T -3' and the reverse primer 5'-TAC GCC AAC TCC GCC CAC GCG C - 3'. Producing amplicon size of 301 bp. The second-round amplification was performed by the forward primer 5'-TGA CTT TTG AGG TGG ATC CAT G -3' and the reverse primer 5'-GGT CTC GAT GAC GCC GCG GTG -3, both 'targeting a portion of the HAdV hexon gene including 171bp ¹².

2- The second part was processed for routine bacterial culture and antimicrobial susceptibility testing (AST) according to the manual of clinical microbiology ¹⁴. Each specimen was checked for bacterial growth after 24 hours of incubation. Colony counts of more than 1×10^4 CFU/ml were considered a diagnostic threshold for infection ¹⁵. AST was performed using Kirby-Bauer's disk diffusion method and was interpreted

according to the clinical and laboratory standards institute ¹⁶.

Statistical Analysis:

The collected data were computerized and statistically analyzed using SPSS version 24 and NCSS 12, LLC, USA. All statistical comparisons were two-tailed with a significance level of P-value ≤ 0.05 indicating significance, $p < 0.001$ indicates a highly significant difference while $P > 0.05$ indicates a non-significant difference.

RESULTS

One hundred patients were included in this study. Patients presented with community-acquired pneumonia were recruited from pediatrics wards and PICU of CUSPH and 6th October Health Insurance Hospital. Their demographic data and clinical data are illustrated in tables (2) and (3) respectively.

The included population (n=100) was categorized into 6 groups according to the bacterial culture and PCR results of the respiratory specimens and the radiological findings in the chest CT images.

- **Viral pneumonia group (N=16):** Patients whose respiratory specimens PCR were positive for viral pathogens other than SARS CoV-2 and no bacterial pathogens were detected in the bacterial culture.
- **Bacterial pneumonia group (N=17):** Patients whose respiratory specimens cultures revealed bacterial pathogen and respiratory specimen PCR were negative for viral pathogens.
- **Mixed bacterial/viral pneumonia group (N=17):** Patients whose respiratory specimens PCR were positive for viral pathogens (other than SARS CoV-2) and bacterial pathogens were isolated in the culture as well.

- **COVID-19 pneumonia group (N=11):** Any patient whose respiratory specimen PCR was positive for SARS CoV-2. Some of the patients in this group had coexisting virus evidenced by PCR (36.3%) or bacteria evidenced in the bacterial culture in addition to the SARS CoV-2 (54.5%).
- **Suspected viral pneumonia group (N=17):** Patients whose respiratory specimens PCR were negative for SARS CoV-2 and viral pathogens and no pathogens were isolated in the cultures of the respiratory specimens, however, those patients had radiological findings of viral pneumonia in the chest CT.
- **Unidentified pathogen-pneumonia group (N=22):** Patients having pneumonia evidenced by clinical and uncertain radiological findings whose respiratory specimens PCR were negative for viral pathogens and no bacteria were isolated in the respiratory specimens' cultures.

Table 1: Demographic Data of the Studied Population

	Viral Pneumonia Group N=16	Bacterial Pneumonia Group N=17	Mixed Bacterial/Viral Pneumonia Group N=17	COVID-19 Pneumonia group N=11	Suspected Viral Pneumonia Group N=17	Unidentified Pathogen-Pneumonia GROUP N=22	P
Age (months)	3 (1-36)	4 (1.20-24)	7 (2-48)	3 (1-18)	5 (1-36)	4 (1.40-48)	0.281
Weight (kilograms)	5.25(3.50-16)	5.30(2.50-12)	6(3.75-12)	4.80(2.30-13)	6(3.50-12)	5.55(3-10)	0.508
Sex	13 (81.3%)	8 (47.1%)	8 (47.1%)	4 (36.4%)	9 (52.9%)	15 (68.2%)	0.138
Male							
Contact with a suspected case of COVID-19	3 (18.8%)	4 (23.5%)	3 (17.6%)	2 (18.2%)	5 (29.4%)	1 (4.5%)	0.472
Length of hospital stay (days)	11±6	15±12	13±8	18±10	16±6	8±2	0.004
Outcome	2 (12.5%)	3 (17.6%)	5 (29.4%)	6 (54.5%)	3 (17.6%)	-	0.007
Mortality							

Table 2: The Clinical Presentation of the Studied Population

	Viral Pneumonia Group N=16	Bacterial Pneumonia Group N=17	Mixed Bacterial/Viral Pneumonia Group N=17	COVID-19 Pneumonia Group N=11	Suspected Viral Pneumonia Group N=17	Unidentified pathogen Pneumonia Group N=22	Total N=100	P
Fever	13 (81.3%)	11 (64.7%)	13 (76.5%)	9 (81.8%)	14 (82.4%)	17 (77.3%)	77 (77%)	0.844
Oxygen saturation on admission	88.50% (85%-98%)	94% (85%-98%)	93% (85%-98%)	90% (82%-95%)	94% (85%-98%)	95% (89%-98%)	93% (82%-98%)	0.028
Respiratory rate/min	54±11	55±9	52±8	49±7	50±7	51±11	52±9	0.527
Tachypnea	14(87.5%)	15(88.2%)	16(94.1%)	10(90.9%)	16(94.1%)	18(81.8%)	89(89%)	0.827
Intercostal Retractions	15(93.8%)	15(88.2%)	16(94.1%)	11(100%)	14(82.4%)	15(68.2%)	86(86%)	0.088
Grunting	13(81.3%)	10(58.8%)	12(70.6%)	7(63.6%)	8(47.1%)	5(22.7%)	55(55%)	0.006
Cyanosis	8(50%)	4(23.5%)	5(29.4%)	6(54.5%)	4(23.5%)	-	27(27%)	0.005
Wheezes	11(68.8%)	9(52.9%)	10(58.8%)	6(54.5%)	14(82.4%)	8(36.4%)	58(58%)	0.095
Crackles	14(87.5%)	16(94.1%)	17(100%)	7(63.6%)	12(70.6%)	21(95.5%)	87(87%)	0.015
Severity Severe	14(87.5%)	10(58.8%)	13(76.5%)	8(72.7%)	9(52.9%)	6(27.3%)	60(60%)	0.003
Vomiting	2(12.5%)	2(11.8%)	2(11.8%)	-	4(23.5%)	2(9.1%)	12(12%)	0.575
Diarrhea	1(6.3%)	3(17.6%)	1(5.9%)	-	4(23.5%)	4(18.2%)	13(13%)	0.351
Shock	2(12.5%)	2(11.8%)	2(11.8%)	1(9.1%)	2(11.8%)	1(4.5%)	10 (10%)	0.961

The most common pathogens causing community-acquired pneumonia in the studied population were viruses (44%). Figure 2

Laboratory Findings:

Seven percent (7%) of the studied population had positive blood cultures. COVID-19, bacterial, and mixed viral/bacterial pneumonia groups had positive blood cultures. Blood culture grew *Klebsiella pneumoniae* in 2 patients, one of them had COVID-19 pneumonia with coexisting *Klebsiella pneumoniae* and the other one had bacterial pneumonia with *Klebsiella pneumoniae*.

Three patients had positive blood cultures for coagulase-negative Staphylococci; one of them had mixed viral/bacterial pneumonia caused by Parainfluenza 1 and coexisting coagulase-negative Staphylococci. The other 2 samples were considered contaminated as no pathogen was detected when their blood cultures were repeated.

One blood culture revealed methicillin-resistant *Staphylococcus aureus* (MRSA) growth in a patient who had bacterial pneumonia caused by MRSA and *Streptococcus viridans*. One patient had *Pseudomonas aeruginosa*-positive blood culture. He had mixed viral/bacterial pneumonia caused by RSV and *Pseudomonas aeruginosa*.

Imaging Results:

Ground glass opacities in the chest CT were mostly detected in patients of the suspected viral pneumonia group (100%), followed by the mixed viral/bacterial pneumonia group (29.4%), then the COVID-19 pneumonia group (27.3%) ($P < 0.001$).

Clinical Outcome:

Patients presented with severe respiratory symptoms on admission have a poor survival rate (68.3%) compared to patients who did not have severe respiratory symptoms on admission (100%) ($P = 0.021$).

DISCUSSION

The present study enrolled 100 children presenting with community-acquired pneumonia. They were nursed in the Pediatric Wards or PICU of CUSPH and 6th October Health Insurance Hospital during the period from October 2020 to September 2021.

Results of the current study revealed that community-acquired pneumonia among the studied population was caused mostly by viruses (44%) mainly *Influenza B* virus (18%) followed by *SARS-CoV2* (11%) then *RSV* (10%).

Although current evidence suggests that fewer fatal pneumonia cases are due solely to viral infections¹⁷, laboratory investigations of children in developing countries and elsewhere often show that *RSV*, *Influenza* virus, and *Parainfluenza* virus are identified in a large proportion of hospitalized patients with lower respiratory tract illness¹⁷.

Both Jain et al.¹⁷ and O'Brien et al.³ reported that the commonest pathogens causing acute community-

acquired pneumonia in children are viruses agreeing with our results. The most prevalent virus among their studied population was *RSV*, while *Influenza B* was the commonest virus encountered in the current study.

Another finding in China was reported by Liu et al.¹⁸ who reported that during COVID pandemic, the prevalence of common respiratory viruses has been reduced because of the strict infection control measures. However, *Rhinovirus*, *RSV*, and *Parainfluenza 3 virus* were the most commonly detected viruses in children during 2020 (11%, 4.55%, and 2.15% respectively).

In a study of Avolio et al.¹⁹ who tracked the most common viruses in Italy during 2020 and 2021, they found that the most prevalent pathogens were *Rhinovirus* (9.79%) followed by coronaviruses other than *COVID 19* (1.51%) then *Bocavirus* and *Enterovirus* (both were 0.63%).

O'Brien et al.³ explained that etiological results in their study varied substantially by the site, for example, the *Influenza* virus did not exceed 3% in any site, but it was more common in Zambia center (6.1%). They also documented that some pathogens exhibit multi-year epidemic cycles and some pathogens as *Influenza* subtypes and *Parainfluenza* viruses have periods of inactivity.

Bacteria were responsible for community-acquired pneumonia in 40 % of the studied population. The most common bacterial pathogen is *Klebsiella pneumoniae* (14%) followed by *Streptococcus viridans* (11%) then *Streptococcus pneumoniae* (4%). Regarding bacterial pneumonia, Jain et al.²⁰ reported that *Streptococcus pneumoniae* was the most common bacteria followed by *Staphylococcus aureus* and *Streptococcus pyogenes*.

Marangu et al.⁶ found that after the introduction of the pneumococcal conjugate and *Hemophilus influenza* type b vaccines, *Staphylococcus aureus* and *H. influenza* non-type b are emerging as the most prevalent bacterial organisms. Other bacterial organisms are reported in their studies such as *Klebsiella pneumoniae* and *E-coli* and *Bordetella pertussis* disagreeing with our results in which *Klebsiella pneumoniae* was found to be the commonest bacteria causing acute community-acquired pneumonia among our studied population.

In the current study, 13% of the studied population had pneumonia caused by 2 or more coexisting viruses. The most prevalent viruses that co-existed with other viruses is *Influenza B* in 7% followed by *RSV* in 6% then *SARS CoV-2* in 4%.

Nolan et al.⁷ reported that *RSV* and the human *Rhinovirus* were the most frequently detected viruses coexisting with other viruses and or bacteria.

Viral and bacterial coinfection was documented in 23% of the studied population. *Klebsiella pneumoniae* is the most common bacteria that coexisted with viruses in the present study. *Klebsiella pneumoniae* coexisted with viruses in 9% of patients mostly with *SARS CoV-2* in

4% followed by *Influenza B* in 3%. Disagreeing with our results, Nolan et al.⁷ reported that *Streptococcus pneumoniae* was the most prevalent bacteria detected with other major viruses.

Sixty four percent of the *COVID-19* pneumonia group had coinfection with other viruses and bacteria. 36 % of this group had coinfection with other viruses influenza B in 18% and adenovirus in 18% while 56% of this group had coinfection with bacteria mainly *Klebsiella pneumoniae* in 36%.

Mania et al.²¹ agreed with our results documenting that patients with *COVID-19* may have co-infection with other bacterial or viral pathogens. However, they reported that *Mycoplasma pneumoniae* is the most frequent bacteria which coexisted with SARS CoV2 virus in their population; on the other hand, in the present study SARS CoV2 was coexisting with *Influenza* virus and *RSV*.

Massey et al.²¹ concluded that the more comorbidities, the higher the co-infections with SARS coV-2. Also, Patel et al.²³ documented that gram-negative bacillus infections coexisted with *COVID-19* disease mainly in patients with intravenous access devices and genitourinary foci leading to more severe disease and prolonged hospital stay.

In the present study, cyanosis was predominant in the *COVID-19* pneumonia group (54.5%) reflecting the most severe spectrum of pneumonia among *COVID-19* patients followed by the viral pneumonia group (50%) then the mixed bacterial/viral pneumonia group (29.4%). Nolan et al.⁷ supported this finding as they reported that *RSV* co-infections with human *Adenovirus* and *Influenza* virus necessitated higher oxygen therapy when compared to pneumonia caused by a single virus infection.

Lu et al.²⁴ reported that 2.3% of children with *COVID-19* had oxygen saturation below 92% and Göttinger et al.⁹ reported that 13% of patients with *COVID-19* required oxygen therapy. Regarding laboratory findings of the studied population, lymphocytosis was mostly detected in the viral pneumonia group. Absolute lymphopenia was reported in 25% of the studied population. It was mostly detected in the suspected viral pneumonia group (70.6%) followed by the mixed viral/bacterial pneumonia group (29.4%). While relative lymphopenia was observed in 53% of the studied population and it was mostly detected in the *COVID-19* pneumonia group (72.7%).

CRP was positive in 55% of our patients. The highest Mean CRP value is detected in patients of the *COVID-19* pneumonia group followed by the mixed viral /bacterial pneumonia group, and bacterial pneumonia group. On the contrary Bhuiyan et al.²⁵ found that CRP, total leucocyte count, and absolute neutrophil count were higher in children with bacterial pneumonia compared to viral pneumonia.

Miao et al.²⁶ reported that children with *COVID-19* may have normal, or decreased total leukocytes count, and lymphopenia. They also found that CRP and procalcitonin may be increased in case of secondary bacterial infection. Liver transaminases and lactate dehydrogenase may be slightly increased.

Tam et al.²⁷ found that only 9.89% of blood cultures taken are positive in hospitalized children with severe lower respiratory tract infection, with higher false-positive rates because cultures may be taken with concomitant antibiotic use and localized infection in the lung parenchyma. Driscoll et al.²⁸ mentioned that the ability of blood culture to detect microbial organisms is about 2% in a blood culture volume of 1 ml and up to 6% in a volume of 3 ml. Exposure to antibiotics further decreases blood culture detection of microorganisms. Also, El Seify et al.²⁹ found that the blood cultures yield of bacterial pathogens in children with community-acquired pneumonia was very limited (3.3%); *Staphylococcus aureus* in 2.2% and *Klebsiella pneumoniae* in 1.1%.

Included children in our study showed positive blood cultures in 6% of the studied population. One blood culture revealed MRSA growth in a patient with bacterial pneumonia caused by MRSA and Streptococcus viridans. One patient had Pseudomonas aeruginosa-positive blood culture. he had mixed viral/bacterial pneumonia caused by RSV and Pseudomonas aeruginosa.

Garg et al.³⁰ found that the patient who has viral pneumonia with *RSV*, *Adenovirus*, *Cytomegalovirus*, and *Influenza viruses A and B* all had ground glass opacities in the chest CT agreeing with our results. Similarly, Duan et al.³¹ documented that the ground-glass opacities are the commonest findings detected in adults and children with *COVID-19*. They are multifocal, located peripherally, and appear first in the lower lobes. Lu et al.²⁴ mentioned that the ground glass opacities were observed in the chest CT of 32.7% of children with *COVID-19*, 18.7 % had local patchy shadowing, 12.3% had bilateral patchy shadowing, 1.2% had interstitial abnormalities, and 15.8% did not have radiological features of pneumonia.

Also, Tran et al.³² found a significant increase in severity and mortality rate with *Influenza* type B than with *Influenza* type A, agreeing with our results that most severe symptoms were detected in the viral pneumonia group in which *Influenza B* was the most common virus detected.

The unidentified pathogen-pneumonia group is one of the limitations of our study. The assays to determine etiology and define classes of infections did not include all possible viral and bacterial respiratory pathogens. We did not perform any serological testing which may have helped us to point causative agents in this group.

CONCLUSIONS

Respiratory viruses are the most prevalent causative agents of acute community-acquired pneumonia. *Influenza B* virus and *Klebsiella pneumoniae* are the most common virus and bacteria detected in our study respectively. The COVID-19 pneumonia group has the highest mortality rate. High CRP results and decreased oxygen saturation on admission were associated with a prolonged hospital stay.

Declarations:

Consent for publication

Not applicable

Availability of data and material

Data are available upon request

Competing interests

The authors declare that there are no financial or personal relationships with other people or organizations that could inappropriately influence (bias) the authors' actions.

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Contribution:

Heba S. Abdel Aziz: (Corresponding Author) Clinical data collection of the study cases, interpretation of results, and manuscript editing

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