scientific reports

Check for updates

OPEN

Clinical and epidemiological changes in severe viral respiratory infections in pediatric patients after the COVID-19 pandemic in Spain

María Luz García-García[1,2,3,7]✉, Patricia Alonso-López[1,2,7], Sonia Alcolea[1], Arroyas María[1,2], Maria Iglesias-Caballero[4], Rocío Sánchez-León[6], Jara Hurtado-Gallego[6], Vicente Mas[4], Francisco Pozo[4,5], Inmaculada Casas[4,5,8] & Cristina Calvo[3,6,8]

The COVID-19 pandemic and associated public health measures disrupted the circulation of respiratory viruses worldwide. However, the long-term impact of these changes on pediatric respiratory tract infections (ARTIs) remains incompletely understood. We conducted a prospective study in children under 14 years hospitalized for ARTIs in Severo Ochoa Hospital (Spain) from January/2006 to September/2023. The cohort was divided into three periods: pre-pandemic (T1), pandemic (T2), and post-pandemic (T3). Clinical and virological results were compared. 6048 children were included (T1:5,101; T2:122; T3:825). Viral detection increased in T3 (91%) compared to T1 (78.7%) and T2 (69.5%), $p < 0.001$, with higher rate of coinfections, $p < 0.001$, and pneumonia diagnoses, $p < 0.001$. HRV and RSV were the most frequent viruses across periods, with HRV maintaining year-round circulation and RSV showing marked seasonal disruption in T2, followed by return to its typical winter pattern in T3. Detection of PIV and HMPV increased in T3, with altered seasonal peaks and a shift toward older age groups. Influenza infections, nearly absent in T2, re-emerged in T3 with delayed seasonal peaks and higher median ages. HBoV circulation declined and became more evenly distributed throughout the year. Clinically, children in T3 were older, with more hypoxia, radiological infiltrates, and pneumonia, while bronchiolitis cases decreased. Most pneumonia cases in T3 had a viral etiology, with HRV, RSV, HMPV, and PIV as the main contributors. Post-pandemic shifts in viral circulation and disease profiles among children with ARTIs highlight the ongoing impact of COVID-19 on pediatric respiratory health. The increased burden of viral pneumonia and the change in seasonal distribution of infections underscore the need for updated surveillance, diagnostic strategies, and prevention programs tailored to the post-pandemic context.

Keywords COVID-19, Respiratory syncytial virus, Metapneumovirus, Rhinovirus, Human bocavirus, Adenovirus, Influenza virus, Parainfluenza virus bronchiolitis, Respiratory infections

Acute respiratory tract infections (ARTI) are a common cause of hospital admission in infants and children[1]. Viruses are the primary agents responsible for ARTIs in children. Among the most frequently implicated are respiratory syncytial virus (RSV), rhinovirus (HRV), adenovirus (AdV), human metapneumovirus (HMPV), parainfluenza virus (PIV), influenza virus (FLU) and human bocavirus (HBoV)[1]. The emergence of the Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) in Wuhan, China, rapidly spread to many countries and caused a potentially severe ARTI in adults[2]. The World Health Organization (WHO) declared SARS-CoV-2 a global pandemic in March 2020[3]. At that time, measures were implemented to mitigate the spread of the virus.

[1]Pediatrics Department, Severo Ochoa University Hospital, Avenida Orellana s/n. 28911, Leganés, Spain. [2]Puerta de Hierro Institute for Health Research (IDIPHISA), C/ Joaquín Rodrigo, 2, 28220 Majadahonda, Spain. [3]Center for Biomedical Research in the Infectious Diseases Network (CIBERINFEC), Instituto de Salud Carlos III (ISCIII), 28029 Madrid, Spain. [4]Reference and Research Laboratory for Respiratory Virus, National Centre for Microbiology, Instituto de Salud Carlos III (ISCIII), 28220 Majadahonda, Madrid, Spain. [5]CIBER de Epidemiología y Salud Pública (CIBERESP), Instituto de Salud Carlos III (ISCIII), 28029 Madrid, Spain. [6]Pediatric Infectious and Tropical Diseases Department, La Paz University Hospital, La Paz Institute for Health Research (IdiPAZ), Pº de la Castellana, 261, 28046 Madrid, Spain. [7]María Luz García-García and Patricia Alonso-López contributed equally to this work. [8]Inmaculada Casas and Cristina Calvo are senior authors of this study. ✉email: marialuz.hso@gmail.com

In Spain, a nationwide lockdown was enforced for two months, and protective measures against SARS-CoV-2 remained in place until May 2021.

Since the onset of the COVID-19 pandemic, the incidence of influenza, RSV, and other respiratory viruses declined or changed in many countries, probably, related with COVID-19 public health interventions, like social distancing and hygiene measurements (hand hygiene, face mask…[4–8]. The effects of COVID-19 on the frequency and severity of viral ARTIs in Spanish children are not totally understood. This study aimed to assess the clinical and virological characteristics of hospitalizations attributable to ARTIs in children, with a particular focus on analyzing the temporal shifts in respiratory viral pathogens observed across the pre-pandemic, pandemic, and post-pandemic periods.

Material and methods

This is a sub-study of an ongoing prospective investigation of respiratory tract infections in children, funded by grants from the Spanish Health Research Fund (FIS) under the reference numbers PI98/0310, PI06/0532, PI09/0246, PI12/01291, PI15CIII/00028, PI18CIII/00009, PI21CIII/00019, and PI21/00377 and approved by the Medical Ethics Committee at Severo Ochoa University Hospital. All methods were carried out in accordance with relevant guidelines and regulations.

Study population

This study included all children under 14 years hospitalized for respiratory infections in Severo Ochoa University Hospital (Madrid, Spain) between January 1st/2006, and September 30th/2023. Informed consent was obtained. The cohort was divided into three time periods based on public health measures implemented in Spain: T1 (Pre-COVID-19, Jan 2006–Mar 2020), T2 (COVID-19, Mar 2020–May 2021), and T3 (Post-COVID-19, May 2021–Sep 2023). Immunoprophylaxis with nirsevimab was introduced as a preventive strategy against RSV in Spain in October 2023.

Study procedures

All patients were assessed by a physician, and clinical and epidemiological data were prospectively recorded. Bronchiolitis was diagnosed in first episodes of expiratory wheezing in children under two years[9]. All other episodes of acute expiratory wheezing were classified as recurrent wheezing/asthma irrespective of etiology[10]. Laryngitis was related to inspiratory dyspnea without wheezing. For analytical purposes, pneumonia was defined as the presence of focal infiltrates or consolidation on chest radiography in the absence of wheezing, to avoid overlapping with bronchiolitis or wheezing-associated respiratory illness. Blood cultures were obtained when bacterial infection was clinically suspected.

Virological study

Nasopharyngeal aspirates (NPAs) were sent to the National Center for Microbiology (ISCIII, Madrid) for virological analysis. Samples were processed within 24 h, and aliquots were stored at − 80 °C. Nucleic acids were extracted and analyzed by four multiplex RT-PCR assays targeting FLU, PIV 1–4, HRV, RSV A/B, HMPV, HBoV, AdV, and HCoVs (229E, NL63, OC43, HKU1) using previously described primers and probes[10].

From 2020 onward, SARS-CoV-2 was detected using a real-time RT-PCR assay adapted from a method targeting the E gene[11]. This method incorporated an internal control and was routinely evaluated for performance through ECDC/WHO and QCMD quality control programs.

Statistical analysis

Data were summarized as mean ± SD for continuous variables and percentages for categorical variables. Comparisons were performed using one-way ANOVA or T-tests for continuous data, and chi-squared or Fisher's exact tests for categorical variables. Logistic regression models were used to assess associations with the post-COVID-19 period. Variables with $p < 0.1$ in univariate analysis were included in multivariate models using backward stepwise regression. Odds ratios (ORs) with 95% confidence intervals (CIs) were calculated. A p-value < 0.05 was considered statistically significant. Multicollinearity among covariates included in multivariable logistic regression models was assessed using correlation matrices and variance inflation factors, with no evidence of relevant collinearity detected. Given the exploratory nature of the analyses, no formal adjustment for multiple comparisons was applied, and results were interpreted based on effect sizes, confidence intervals, and clinical plausibility. All analyses were performed using SPSS v25 (SPSS Inc., Chicago, IL, USA).

Results

A total of 6,048 patients were included in the study: 5,101 during the pre-pandemic period (T1), 122 during the pandemic (T2), and 825 in the post-pandemic period (T3) (Fig. 1). Overall, 4,084 children (67.5%) were under 2 years of age, although this proportion varied across periods (70% in T1, 39% in T2, and 57% in T3), indicating a significant increase in patient age during and after the pandemic ($p < 0.001$).

Regarding overall viral detection and coinfections (Fig. 2), at least one respiratory virus was detected in 4,722 cases (78%). Of them, 2057 (44%) were HRV and 1882 (40%) RSV. AdV accounted for 15% of cases, while detection rates for other viruses, including HBoV, PIV, HMPV, FLU, HCoV, and SARS-CoV-2, were each below 10%. In total, 311 HCoV infections were identified (6.6% of all positive viral detections), of which 66 corresponded to SARS-CoV-2. Viral coinfections were identified in 1503 (31.8%) cases, most commonly RSV + HRV (294/19.5%), HRV + AdV (155/10%), HRV + HBoV (72/5%), RSV + HBoV (71/5%) and RSV + AdV (70/4.6%). Overall, HBoV showed the highest rate of viral coinfection (341/77%).

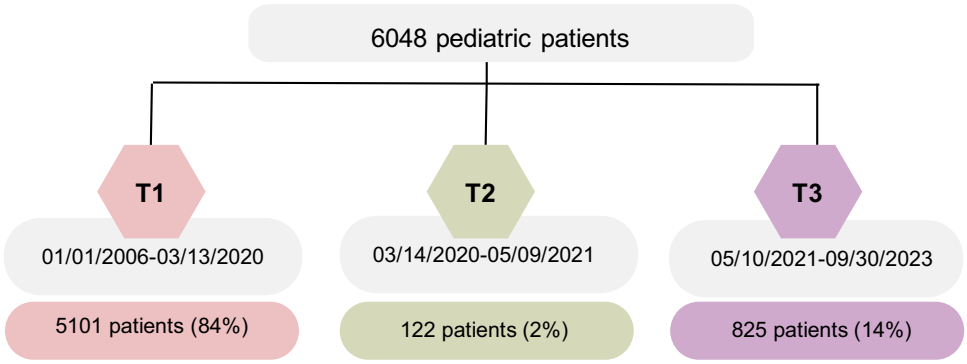

Fig. 1. Distribution of hospitalized children with respiratory viral respiratory infections in the three study periods.

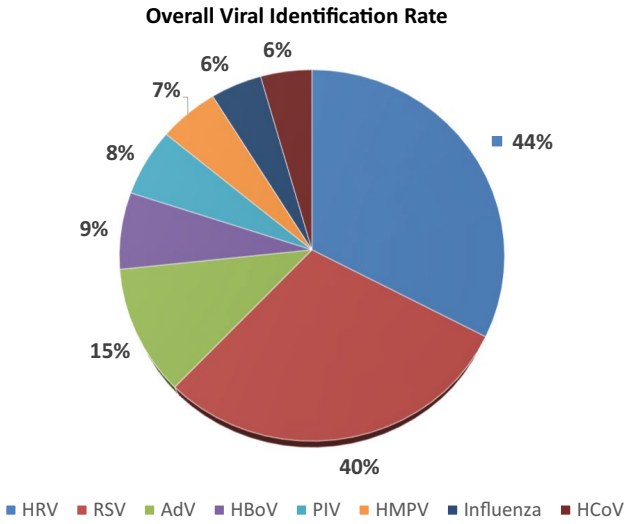

Fig. 2. Overall Viral detection rate in children hospitalized with respiratory tract infection with positive viral detection throughout the study. RSV: respiratory syncytial virus; HRV: rhinovirus; HBoV: human bocavirus; AdV: adenovirus; HMPV: human metapneumovirus; PIV: parainfluenza virus; FLU: influenza virus HCoV: human coronavirus.

Respiratory viruses seasonality before, during and after the COVID-19 pandemic

The viral detection rate increased significantly in T3 (91%) compared to T1 (79%) and T2 (69.5%), $p < 0.001$, with more coinfections in T3 (33%), $p < 0.001$. (Table 1). In T1, HRV (33%) and RSV (32.4%) were predominant, while HRV (51.7%) predominated in T2, when RSV nearly disappeared. In T3, HRV remained the most frequent, RSV returned to T1 levels, and both PIV (10%) and HMPV (8%) increased compared to T2 and T1 ($p < 0.001$ and $p = 0.004$, respectively) (Table 1).

Age-related differences regarding virus detection were observed (Table 2). The likelihood of RSV detection increased by 20% in T3 *vs.* T1, but only in children under 2 years ($p = 0.032$). The probability of HRV infections doubled in T3, mainly in children > 2 years ($p < 0.001$). PIV and HMPV increased across all ages, while HBoV circulation declined in older children ($p = 0.01$).

RSV infections: from disruption to a gradual return to winter dominance

Overall, the proportion of RSV detection in T3 (33%) was similar to T1 (32.5%) (Table 1). During T1, RSV displayed a typical seasonality with a peak in December (814; 51%). In T2, only one case was detected. RSV reemerged out of season in April 2021, with an unusual increase in cases in May (12%) and June (20%). By late 2021, RSV returned to its usual seasonal pattern, peaking in December (29%), although with lower intensity than in pre-pandemic period. In 2022, RSV activity declined early in the year, but surged sharply in November (63%), before dropping by half in December. In 2023, up to October, RSV circulation was minimal, with just a few winter cases. When comparing the entire T1 and T3 periods, RSV detection during the winter months was significantly higher in T1 (74%) compared to T3 (32%). Conversely, in T3, most RSV cases were identified in autumn (46% *vs.* 23% in T1; $p < 0.001$; Fig. 3A).

	Positive viral detection N: 4722	Viral coinfection N: 1503	RSV N:1882	HRV N:2057	HMPV N:350	PIV N:370	AdV N:703	FLU N:283	HBoV N:444
T3 (N = 820)	745 (91%)	272 (33%)	272 (33%)	360 (44%)	68 (8%)	82 (10%)	579 (12%)	243 (5%)	40 (5%)
T2 (N = 122)	82 (69.5%)	22 (18.6%)	1 (0.8%)	61 (51.7%)	1 (0.8%)	2 (1.7%)	14 (14%)	0	13 (11%)
T1 (N = 4952)	3895 (79%)	1209 (24.4%)	1609 (32.5%)	1636 (33%)	281 (5.5%)	286 (5.8%)	107 (13%)	40 (5%)	391 (8%)
p-value	< 0.001	< 0.001	< 0.001	< 0.001	0.001	< 0.001	0.381	0.048	0.004
p-value T3 vs T1	< 0.001	< 0.001	0.701	< 0.001	0.004	0.004	0.266	0.972	0.002
OR (CI95%) T3 vs T1	2.7 (2.1– 3.4)	1.5 (1.3–1.8)	1.0 (0.9–1.2)	1.6 (1.4–1.8)	1.5 (1.1–2.0)	1.8 (1.4–2.3)	1.1 (0.9–1.4)	0.9 (0.7–1.4)	0.6 (0.4-0.8)

Table 1. Comparison of viral detection in hospitalized children in T3 (May 10, 2021, to September 30, 2023) T2 (March 14, 2020 to May 9, 2021) and T1 (January 1, 2006, to March 13, 2020). RSV: respiratory syncytial virus; HRV: human rhinovirus; HMPV: human metapneumovirus. PIV: parainfluenza virus; AdV: adenovirus; FLU: influenza virus; HBoV: human bocavirus.

	≤ 2 years N = 3974				> 2 years N = 1796			
	T3 N = 468	T1 N = 3506	*p* value	Odds ratio (95% confidence interval)	T3 N = 352	T1 N = 1444	*p* value	Odds ratio (95% confidence interval)
Positive viral detection	434	2934	< 0.001	2.5 (1.7–3.6)	311	960	< 0.001	3.8 (2.7–5.4)
	92.7%	83.7%			88.4%	66.5%		
Viral coinfection	171	980	< 0.001	1.5 (1.1–1.5)	101	229	< 0.001	2.1 (1.6–2.8)
	36.5%	28%			28.8%	16%		
RSV infection	213	1414	0.032	1.2 (1.0–1.5)	59	195	0.116	1.3 (0.9–1.8)
	45.5%	40.3%			16.8%	13.5%		
HRV infection	165	1107	0.109	1.2 (0.9–1.1)	195	529	< 0.001	2.1 (1.7–2.7)
	35.3%	31.6%			55.4%	36.6%		
HBoV infection	33	315	0.165	0.7 (0.5–1.1)	7	75	0.010	0.4 (0.1–0.8)
	7.1%	9.0%			2%	5.2%		
HMPV infection	45	240	0.029	1.4 (1.1–2.0)	23	41	0.001	2.4 (1.4–4.0)
	9.6%	6.8%			6.5%	2.8%		
AdV infection	55	413	0.827	1.0 (0.8–1.4)	52	179	0.232	1.2 (0.9–1.7)
	11.8%	8.8%			14.8%	12.4%		
PIV infection	53	231	< 0.001	1.8 (1.3–2.5)	29	55	< 0.001	2.3 (1.4–3.3)
	11.3%	6.6%			8.2%	3.8%		
FLU infection	13	164	0.060	0.6 (0.3–1.0)	27	79	0.116	1.4 (0.9–2.3)
	2.8%	4.7%			7.7%	5.5%		

Table 2. Comparison of Viral Detection Rates in Hospitalized Children in T3 (May 10, 2021–September 30, 2023) and T1 (January 1, 2006–March 13, 2020), Stratified by Age (< 2 Years and ≥ 2 Years). RSV: respiratory syncytial virus; HRV: human rhinovirus; HMPV: human metapneumovirus. PIV: parainfluenza virus; AdV: adenovirus; FLU: influenza virus; HBoV: human bocavirus.

Coinfections involving RSV were more frequent in T3 than in T1 among children > 2 years (35/59; 59% *vs.* 73/195; 37%, $p = 0.002$), mainly with HRV, AdV, and HBoV. Additionally, RSV-infected children in T3 were older than in T1 (15.4 ± 18.6 *vs.* 11.1 ± 13.7 months, $p < 0.001$).

HRV and AdV infections: continuous circulations across all seasons

In contrast to RSV, HRV and AdV were consistently detected across all three-study periods, showing a year-round circulation pattern (Fig. 3B, C). HRV prevalence increased significantly from T1 to T2 and T3 (33%, 51.7%, and 44% of all identified viruses, $p < 0.001$) (Table 1), particularly among children over 2 years where the detection rose from 36.6 to 55.4% ($p < 0.001$, Table 2). Although HRV infections declined during summer months in all periods, this reduction was less marked in T3 than in T1 and T2 (12%, 5%, 2%, $p < 0.001$) (Fig. 3B).

AdV identification remained stable over time across T1, T2 and T3 (13%, 14%, and 12%; $p = 0.381$) (Table 1), with differences in seasonal distribution. Notably, more AdV cases were recorded in T3 during both winter and summer months compared to T1 (46% *vs.* 39% in winter; 18% *vs.* 8.5% in summer; $p = 0.004$). In contrast, most cases in T2 were detected in autumn (53%) and spring (41%). (Fig. 3C).

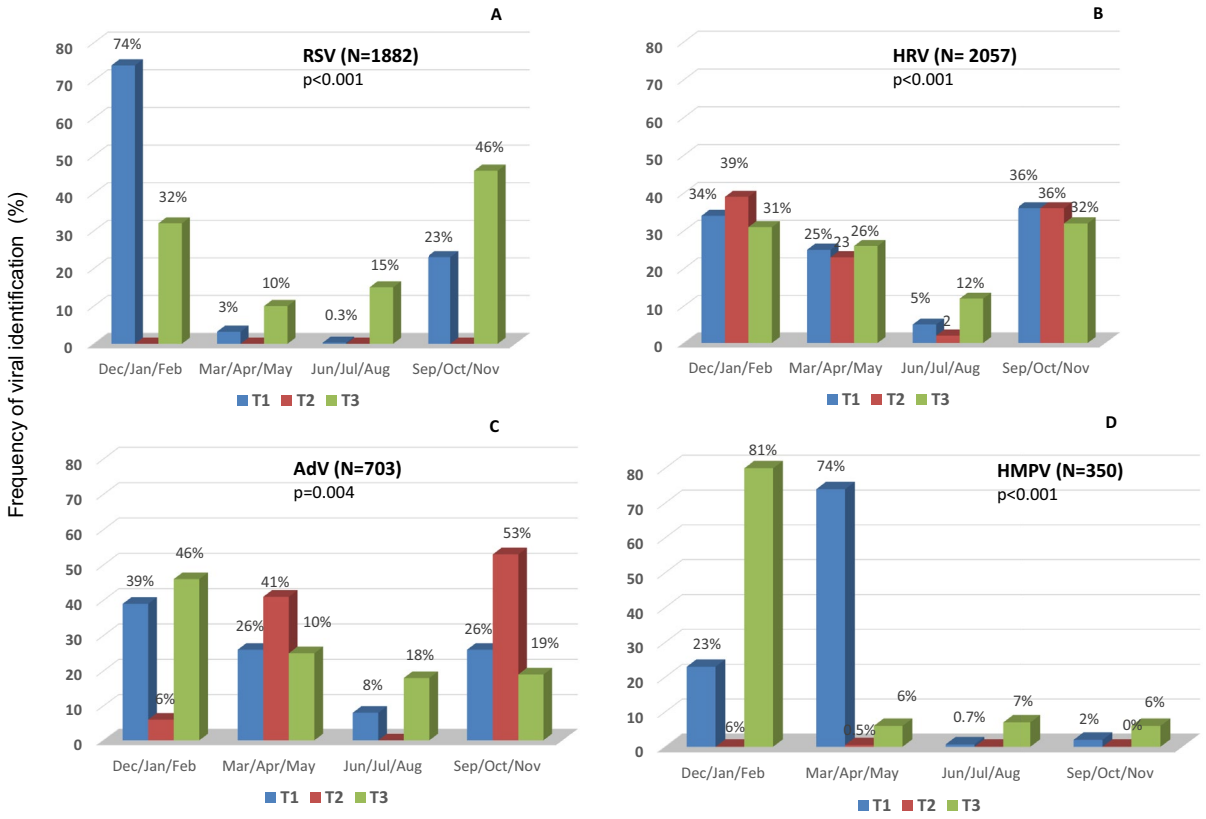

Fig. 3. Time trends of monthly respiratory admissions in the Severo Ochoa Hospital, Madrid, Spain, T3 (May 10, 2021, to September 30, 2023) T2 (March 14, 2020 to May 9, 2021) and T1(January 1, 2006, to March 13, 2020). (**A**) RSV (Respiratory syncytial virus). (**B**) HRV (Rhinovirus). (**C**) AdV: (Adenovirus). (**D**) HMPV (Metapneumovirus).

Coinfections involving HRV or AdV were more frequent in T3. HRV-coinfections increased from 46% (749/1636) in T1 to 53% (192/360) in T3 ($p < 0.001$), while AdV-coinfections were significantly more common only in children > 2 years [59% (105/179) vs. 81% (42/52) $p = 0.004$]. The most common coinfecting viruses were HRV, RSV, and HBoV. Children infected with HRV and AdV in T3 were older than in T1 (HRV: 39.2 ± 38.0 *vs.* 23.0 ± 26.7 months; AdV: 32.5 ± 32.3 *vs.* 21.2 ± 19.6 months; both $p < 0.001$).

HMPV and PIV infections: altered seasonality and increased detection in T3

HMPV and PIV infections showed marked differences between the study periods, with minimal circulation during T2 and increased detection in T3. HMPV accounted for 5.5% of all viral infections in T1, peaking consistently from January to May, with a maximum in March (40.6%). In contrast, in T3 (8% of infections), the peak shifted to December (44%), with no cases in March–April and sporadic detections throughout the rest of the year, $p < 0.001$. (Table 1. Figure 3D).

PIV infections followed a similar trend, increasing from 5.8% in T1 to 10% in T3 ($p < 0.001$), with PIV-3 as the dominant type (Table 1). Circulation remained similar in both periods, with most cases detected in autumn and spring (Fig. 4A).

Coinfections were more frequent in T3 for both viruses. HMPV-coinfections rose significantly only among children > 2 years [61% (14/41) vs. 34% (14/23), $p = 0.03$), most commonly with HRV (54%) and RSV (21%). In contrast, PIV-coinfections increased overall in T3 [78% (141/286) vs. 49% (64/82), $p < 0.001$], frequently involving HRV (49%), AdV (26%), RSV (22%), and HBoV (12.7%).

As observed with other viruses, children infected with HMPV or PIV in T3 were significantly older than in T1 (HMPV: 25.5 ± 32.8 *vs.* 14.1 ± 17.1 months, $p < 0.001$; PIV: 23.7 ± 26.6 *vs.* 14.8 ± 18.0 months, $p = 0.006$).

HBoV: widespread coinfections and irregular seasonal pattern

HBoV was detected across all three study periods, although only 13 cases were identified in T2. The highest prevalence was observed in T1, accounting for 8% of all detected viruses, followed by a significant decline in T3, where HBoV represented 5% of cases ($p = 0.002$) (Table 1). During T1, HBoV exhibited a clear seasonal pattern, with most cases occurring in winter and autumn. In contrast, during T3 the distribution was more uniform throughout the year, with a significantly higher proportion of cases detected in summer compared with T1 (20% vs. 2%, $p < 0.001$). Figure 4B.

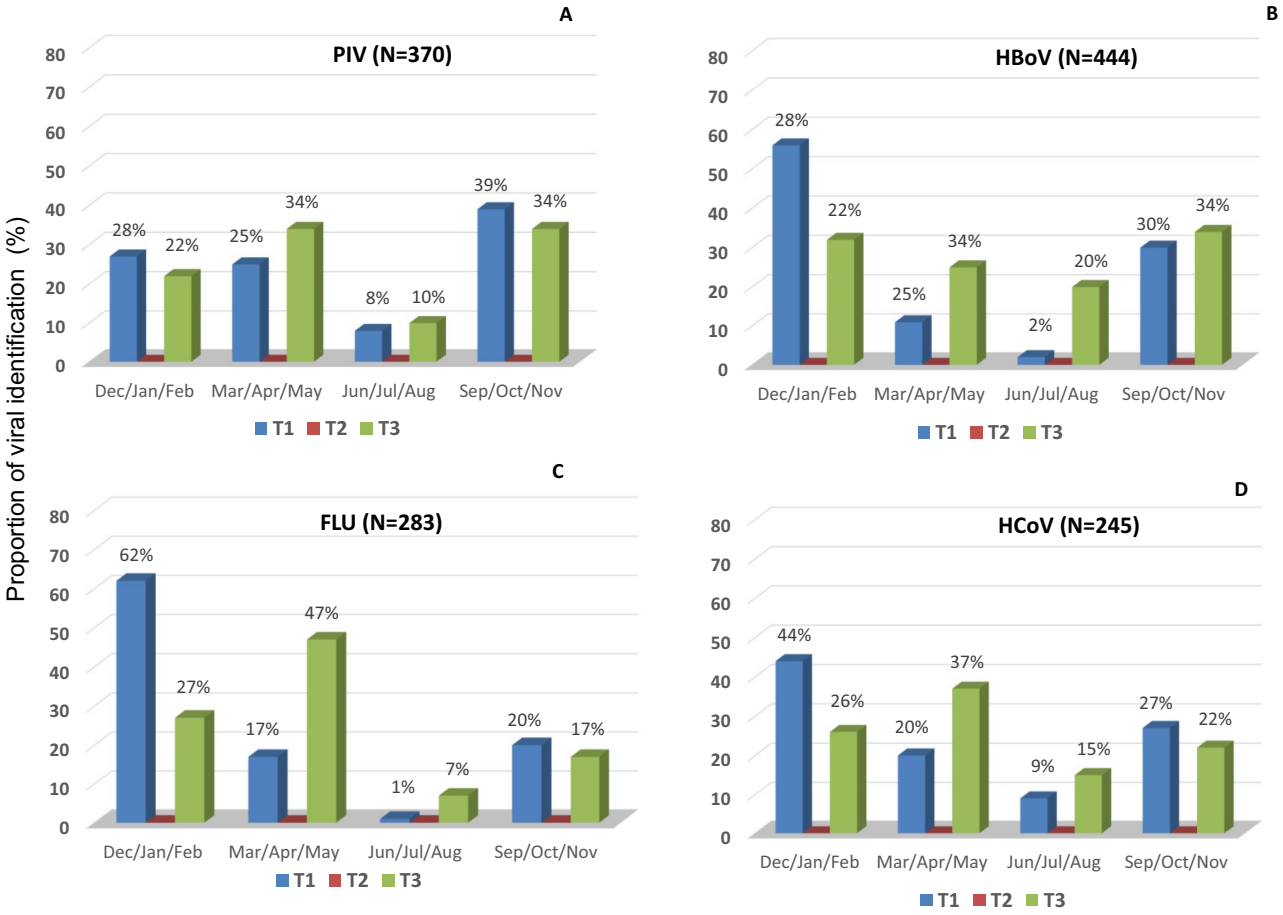

Fig. 4. Time trends of monthly respiratory admissions in the Severo Ochoa Hospital, Madrid, Spain, T3 (May 10, 2021, to September 30, 2023) T2 (March 14, 2020 to May 9, 2021) and T1(January 1, 2006, to March 13, 2020). (**A**) PIV (Parainfluenza virus). (**B**) HBoV (Human bocavirus). (**C**) FLU (Influenza virus). (**D**) HCoV (Human coronavirus).

The mean age of patients infected with HBoV did not differ significantly between T1 and T3 (17.4 ± 15.4 vs. 20.5 ± 15.9 months, respectively; $p = 0.221$). However, in T1, the frequency of HBoV infection was comparable between children younger and older than 2 years, whereas in T3 a significantly higher prevalence was observed among children younger than 2 years ($p = 0.01$).

Coinfections with HBoV were common in all periods (77%), especially in T3 (87%). HRV was the most frequent coinfecting virus across all periods, followed by RSV and AdV. Mean age of HBoV-infected children was similar in T1 and in T3 (17.4 ± 15.4 *vs.* 20.5 ± 15.9 months, $p = 0.221$).

FLU and HCoV: changes in seasonal peaks and age distribution

FLU and HCoV infections were detected at similar rates in T1 and T3 (4.5% and 5%, respectively), with almost no cases in T2. (Table 1). FLU peaked in winter during T1 (62%) and in spring during T3 (47%), $p < 0.001$ (Fig. 4C).

HCoV followed a similar pattern, with higher frequency in winter in T1 (44%) and in spring in T3 (37%), $p = 0.002$ (Fig. 4D).

Coinfections were frequent, especially for HCoV (over 80% in both T1 and T3), and were common for FLU as well (39% in T1, 30% in T3). The most frequently co-detected viruses were RSV and HRV in both groups, followed by AdV and HBoV for HCoV.

FLU-infected children during T3 were significantly older than in T1 (FLU: 52.6 ± 47.8 *vs.* 24.2 ± 30.8 months, $p < 0.001$). A similar trend was observed for HCoV (T3: 32.4 ± 38.3 *vs.* T1: 19.7 ± 26.6 months, $p = 0.006$).

Most SARS-CoV-2 cases were detected in T3 (88%). Among the 66 cases with SARS-CoV-2 infection, 31 (47%) were identified as coinfections with other respiratory viruses, predominantly HRV and RSV. SARS-CoV-2 circulation was observed throughout the entire year, showing a homogeneous distribution across all months. Additionally, 53% of affected children (35/66) were younger than 18 months of age.

Demographic and clinical characteristics

No differences were observed in sex distribution across the study periods. Compared to T1, hospitalized patients in T2 and T3 were significantly older, with higher mean age and more cases diagnosed in children > 2 years (all

$p < 0.001$; Table 3). In comparison to T1, patients in T3 showed higher and more prolonged rates of hypoxia ($p = 0.006$ and $p = 0.004$, respectively), and increased antibiotic use ($p < 0.001$), while hospital stay duration remained similar ($p = 0.350$) (Table 3).

Among children under 2 years, PICU admissions and antibiotic treatment were more frequent in T3 than in T1 ($p = 0.005$ and $p < 0.001$, respectively; Table 4).

A clear shift in clinical presentation was observed in T3, with higher frequency of pneumonia diagnoses in both age groups (23.5% in T3 *vs.* 11.6% in T1; $p < 0.001$; Table 5), although more pronounced in infants < 2 years (20% *vs.* 6.5%, $p < 0.001$). The rate of viral detection in pneumonia cases was also significantly higher in T3 (89.2% *vs.* 63.9%, $p < 0.001$), as was the frequency of viral coinfections (39% *vs.* 18.2%, $p < 0.001$). While HRV remained the most detected virus in these cases, RSV, HMPV, and PIV were significantly more frequently identified in T3 than in T1, with odds ratios of 3.2, 4.2, and 2.3, respectively (all $p < 0.001$). Blood cultures were performed in 160 out of 194 children with pneumonia in T3. Only three yielded positive results: one *Moraxella catarrhalis*, one *Staphylococcus aureus*, and one coagulase-negative *Staphylococcus*.

During T3, pneumonia was more frequently associated with hypoxia ($p < 0.001$), but was less often accompanied by fever ($p = 0.01$) or PICU admission ($p = 0.035$).

Multivariate logistic regression analysis identified several variables independently associated with the post-COVID period (T3), including age > 24 months, pneumonia, hypoxia, antibiotic use, radiological abnormalities, positive viral detection, viral coinfections, infection with HMPV, PIV, whereas HBoV infection was less frequently identified in T3 (all $p < 0.05$) (Table 6).

The datasets used and/or analysed during the current study are available from the corresponding author on reasonable request.

Discussion

This study offers an in-depth view of the virological and clinical changes in pediatric ARTIs over a 17-year period, covering the pre-pandemic, pandemic, and post-pandemic eras. One of the main findings was the significant increase in respiratory virus detection observed in the post-COVID period (T3). Although changes in diagnostic and/or therapeutic management may have occurred over the years included in the study, these are

	T1 N = 5101	T2 N = 122	T3 N = 825	*p* value	*p* value T1 *vs.*T3	Odds ratio (95% Confidence Interval)
Clinical data						
Sex (male)	2946 (57.8%)	38 (31.1%)	478 (57.9%)	0.898	0.855	
Age (months)	22.5 ± 28.8	43.4 ± 37	32 ± 36.6	**< 0.001**	**< 0.001**	
Age ≥ 2 years	1532 (30%)	74 (60%)	356 (43.2%)	**< 0.001**	**< 0.001**	1.8 (1.5–2.0)
Fever ≥ 38°C	2937 (57.5%)	44 (36%)	459 (55.6%)	**< 0.001**	0.274	
Hypoxia, oxygen saturation < 95%	3098 (60.7%)	95 (77.9%)	533 (64.6%)	**< 0.001**	**0.006**	0.9 (0.8–1)
High oxygen flow	361 (7.1%)	36 (29.5%)	208 (25.2%)	0.08	0.107	
Antimicrobial treatment	1216 (23.8%)	15 (12.3%)	278 (33.7%)	**< 0.001**	**< 0.001**	0.7 (0.6–0.8)
Chest infiltrate	1713 (33.6%)	26 (21.3%)	250 (30.3%)	**< 0.001**	**0.030**	1.3 (1.1–1-5)
Viral coinfection	73 (31.5%)		35 (59%)			
Outcome						
Duration of stay (days)	4.0 ± 2.7	3.0 ± 2.5	3.9 ± 2.6	**0.001**	0.350	
Duration of stay < 3 days	2698 (52.9%)	90 (74%)	447 (54.2%)	**< 0.001**	0.541	
Duration of fever (days)	3.1 ± 2.7	2.1 ± 1.7	3.4 ± 2.9	**0.002**	**0.019**	
Duration of hypoxia (days)	2.9 ± 2.3	1.9 ± 1.5	3.3 ± 2.3	**< 0.001**	**0.004**	
Intensive care unit admissions	108 (2.1%)	4 (3.3%)	27 (3.3%)	0.146	0.063	
Diagnosis						
Bronchiolitis	1592 (31.2%)	14 (11.5%)	219 (26.5%)	**< 0.001**	**< 0.001**	
Asthma	2366 (46.4%)	77 (63.3%)	317 (38.4%)			
Pneumonia	590 (11.6%)	20 (16.4%)	194 (23.5%)			
Laryngitis	87 (1.7%)	2 (1.6%)	8 (1%)			
Blood tests						
Leucocytes (cells/mm^3)	14,734 ± 2505	12,960 ± 5422	13,217 ± 7062	0.401	0.204	
C-reactive protein	46.4 ± 73.5	20.6 ± 29.4	52 ± 72.4	**0.022**	0.137	
Background						
Prematurity	664 (13%)	22 (18%)	99 (12%)	0.183	0.207	
Passive smoking	538 (10.5%)	35 (28.7%)	208 (25.2%)	**0.001**	**0.041**	1.2 (1.1–1.4)

Table 3. Comparison of clinical characteristics of hospitalized children in T3 (May 10, 2021–September 30, 2023), T2 (March 14, 2020 to May 9, 2021) and T1 (January 1, 2006–March 13, 2020). Significant values are in bold.

	≤ 2 years N = 4036				> 2 years N = 1888			
	T3 N = 468	T1 N = 3506	*p* value	Odds ratio (95% confidence interval)	T3 N = 352	T1 N = 1444	*p* value	Odds ratio (95% confidence interval)
Sex (male)	273 58.2%	2095 58.7%	0.829	1.0 (0.8–1.2)	205 57.6%	850 55.5%	0.472	0.9 (0.7–1.1)
Age (months)*	8.6 ± 7.0	8.2 ± 6.6	0.189		62.8 ± 37.1	55.7 ± 32.8	**0.001**	
Fever ≥ 38°C	265 56.5%	2056 57.7%	0.616	0.9 (0.8–1.1)	194 54.5%	880 57.6%	0.294	0.8 (0.7–1.1)
Hypoxia, oxygen saturation < 95%	297 63.6%	2116 59.5%	0.090	1.2 (0.9–1.1)	533 64.8%	3036 59.8%	**0.030**	1.3 (1.0–1.7)
PICU admission	22 4.7%	83 2.4%	**0.005**	1.9 (1.2–3.1)	5 1.4%	25 1.7%	0.060	0.8 (0.3–2.2)
Duration of hypoxia (days)*	3.4 ± 2.3	2.9 ± 2.4	**0.004**		2.3 ± 1.8	1.9 ± 1.7	**0.002**	
Duration of hospital stay (days)*	4.2 ± 2.6	4.3 ± 2.8	0.497		3.5 ± 2.3	3.2 ± 2.2	1.000	
Admission > 5 days	106 22.6%	859 24.1%	0.462	0.9 (0.7–1.1)	55 15.4%	155 10.2%	**0.004**	1.6 (1.2–2.3)
Antibiotic treatment	129 27.6%	708 19.8%	**< 0.001**	1.5 (1.2–1.9)	149 42%	508 33.2%	**0.002**	1.4 (1.1–1.8)
Chest infiltrate	115 24.4%	1027 29.2%	0.09	0.8 (0.6–1.0)	135 38.3%	685 47.7%	**0.001**	0.6 (0.5–0.8)
Diagnosis								
Bronchiolits	218 51.5%	1579 50%			NA	NA	NA	NA
Asthma	114 27%	1301 41.4%			203 64.4%	1063 71.5%		
Pneumonia	85 20%	203 6.5%	< 0.001		109 34.6%	387 26%	0.009	
Laringytis	6 1.4%	63 2%			2 0.6%	24 1.6%		

Table 4. Comparison of clinical features of hospitalized children across T1 (January 1, 2006, to March 13, 2020) and T3 (May 10, 2021, to September 30, 2023) Stratified by Age (< 2 Years and ≥ 2 Years). *mean ± standard deviation. Significant values are in bold.

unlikely to have significantly affected viral detection, as, in this prospective study, nasopharyngeal aspirates for virological analysis using multiplex PCR were systematically obtained from all children under 16 years of age admitted to our hospital throughout the entire study period. Therefore, testing practices remained consistent over time, and the increase in viral detection observed during T3 (post-pandemic period) is unlikely to be explained by changes in healthcare-seeking behavior or hospital admission practices.

The shift reflects genuine changes in the epidemiology of respiratory infections in children, likely influenced by the widespread disruption of virus transmission and exposure patterns during the COVID-19 pandemic.

As seen in other studies[5,12–16], the implementation of strict public health measures during 2020 coincided with a dramatic decline in ARTIs. RSV, FLU, and HMPV virtually disappeared, while HRV and AdV continued to circulate. This pattern is thought to be associated with structural differences in these viruses; in particular, HRV and AdV are non-enveloped viruses, more resistant to alcohol-based disinfectants[12,15,17]. With the gradual relaxation of mitigation strategies, the landscape began to change again.

After the COVID-19 pandemic, several studies, including ours, have described a shift toward older age among children hospitalized with most respiratory viral infections[18,19].

This pattern is generally attributed to cohort effects following non-pharmaceutical interventions (NPIs), including delayed primary exposure, changes in contact patterns, and disrupted seasonality, which together may have shifted clinically relevant infections to older age groups. These effects have been particularly evident for viruses such as RSV and FLU, which usually cause acute, self-limited infections and for which delayed first exposure may result in clinically significant disease at older ages[20]. In contrast, HBoV did not show a comparable age shift in our post-pandemic cohort, with fewer detections observed among children older than 2 years. This distinct pattern is consistent with known differences in the epidemiology of HBoV compared with other respiratory viruses, including differences in transmission dynamics, the absence of pronounced epidemic waves, frequent coinfections, and a less clearly defined association between age at primary infection and disease severity[21]. Accordingly, post-pandemic changes in viral circulation, ecological interactions among respiratory viruses, and healthcare-seeking and diagnostic practices may have differentially influenced the detection of HBoV in older children.

RSV showed the most striking disruption in seasonality. Although absent during T2 [12–15], it reappeared in T3 with an atypical off-season peak[6,22], later returning to a more common winter circulation. These findings are in line with international data[23–26] showing irregular RSV activity following the easing of restrictions. Our observation of a significantly older age among RSV-infected children in T3 has been reported in other settings as well[27,28] and may have implications for future vaccination strategies or prophylaxis programs.

	T3 N = 194	T1 N = 590	*p* value	Odds Ratio (95% Confidence Interval)
Sex (male)	109 (56.2%)	300 (50.8%)	0.197	1.2 (0.9–1.7)
Aged (months)	36.9 ± 32.3	43.5 ± 34.7	**0.016**	
Aged ≥ 2 years	109 (56%)	387 (65.6%)	**< 0.018**	0.7 (0.5–0.9)
Antimicrobial treatment	154 (79%)	500 (85%)	**0.081**	0.7 (0.5–1.0)
Pleural effusion	15 (7.8%)	55 (9.3%)	0.508	
Fever ≥ 38°C	169 (87%)	547 (93%)	**0.010**	0.5 (0.3–0.8)
Duration of fever (days)	3.9 ± 2.4	4.5 ± 3.5	**0.019**	
Hypoxia, oxygen saturation < 95%	131 (68%)	191 (32.5%)	**< 0.001**	4.4 (3.1–6.2)
Duration of hypoxia (days)	3.0 ± 2.0	3.2 ± 2.9	**0.434**	
Duration of stay (days)	4.3 ± 2.4	4.5 ± 3.1	**0.535**	
Duration of stay > 5 days	48 (24.7%)	121 (20.5%)	**0.213**	1.3 (0.9–1.9)
Intensive care unit admission	2 (1%)	24 (4%)	**0.036**	0.2(0.6–1.0)
Leucocytes (cel/mm^3)	14,036 ± 7000	17,910 ± 20,100	**0.012**	
PCR (mg/L)	78.0 ± 87.2	114.5 ± 115.4	**< 0.001**	
Viral detection				
Positive viral detection	173 (89%)	358 (64%)	**< 0.001**	4.6 (2.9–7.5)
Viral coinfection	76 (39%)	102 (18%)	**< 0.001**	2.9 (2.0–4.1)
RSV	64 (33%)	74 (13%)	**< 0.001**	3.2 (2.2–4.8)
HRV	70 (36.1%)	146 (26.1%)	**0.008**	1.6 (1.1–2.3)
HMPV	34 (17.5%)	27 (4.8%)	**< 0.001**	4.2 (2.5–7.2)
PIV	24 (12.4%)	33 (5.9%)	**0.003**	2.3 (1.3–3.5)
AdV	40(20.6%)	77 (13.8%)	**0.023**	1.6 (1.1–2.5)
HBoV	13 (6.7%)	49 (8.8%)	**0.371**	0.7 (0.4–1.4)
FLU	13 (6.7%)	44 (7.9%)	**0.600**	0.8 (0.4–1.6)

Table 5. Comparison of clinical and virological features of hospitalized children diagnosed with PneumoniaAcross T1 (January 1, 2006, to March 13, 2020) and T3 (May 10, 2021, to September 30, 2023). Significant values are in bold.

Clinical characteristic	*p*-Value	Adjusted OR (95% CI)
Pneumonia	< 0.001	5.6 (4.0–7.7)
Age older than 24	< 0.001	2.4 (1.9–2.9)
Hypoxia	< 0.001	1.6 (1.3–1.9)
Antibiotic treatment	< 0.001	2.4 (1.9–2.9)
Infiltrate/atelectasis	< 0.001	0.5 (0.4–0.6)
Positive viral detection	< 0.001	2.6 (1.9–3.6)
Viral coinfection	< 0.001	1.6 (1.3–2.0)
HMPV infection	0.038	1.4 (1.1–1.9)
PIV infection	0.002	1.7 (1.2–2.3)
HBoV infection	< 0.001	0.5 (0.3–0.7)

Table 6. Factors independently associated with T3 post-pandemic period compared to T1 pre-pandemic period: multivariate analysis. OR: odds ratio; CI: confidence interval. HMPV: human metapneumovirus; PIV: parainfluenza virus; HBoV: human bocavirus.

HRV remained a dominant virus throughout all periods, including during the peak of the pandemic[8,14,29], and became even more prominent in T3. Also, it showed changes in its seasonal behavior, with less pronounced summer declines and more frequent detection among older children. These trends, observed in other studies[8,30,31], highlight the ecological adaptability of HRV.

AdV maintained a relatively stable frequency but demonstrated changes in monthly distribution, with more cases detected in atypical months during T3. Both viruses were frequently involved in coinfections, particularly HRV, which consistently emerged as the most common co-detected virus across all periods.

In contrast, HMPV and PIV were barely detected during T2. Their resurgence in T3 has also been reported elsewhere[27,32,33] and likely reflects resumed viral transmission following the loosening of restrictions. Interestingly, both viruses showed altered seasonality and infected older children more frequently[32]. HMPV,

typically peaking between January and May, circulated primarily in winter during T3, with sporadic detections year-round. These patterns are consistent with findings from China, The Netherlands, and other European cohorts[32,34,35]. PIV retained its bimodal distribution, with peaks in autumn and spring, but showed a substantial increase in detection compared to the pre-pandemic period, as seen in other respiratory viruses.

HBoV exhibited a distinct post-pandemic pattern, characterized by a reduction in overall detection rates, alongside a marked increase in the proportion of coinfections, reaching 87% in our cohort. Recent reports have described high rates of viral coinfection (82.2% and 80%)[36]. Our findings represent one of the highest coinfection rates reported to date, 87% in the post-pandemic period. Tan et al[37], using targeted next-generation sequencing (mNGS), identified 426 HBoV-positive samples in hospitalized children. Of them, 96% exhibited coinfection with other pathogens, not only respiratory viruses, but also bacteria, opportunistic pathogens and fungi. Since its initial description[38], the pathogenic role of HBoV has remained a matter of debate largely due to its frequent detection in association with other respiratory viruses—as also observed in our study—and its well documented prolonged shedding in the respiratory tract. The strongest body of evidence supporting its pathogenic role has been synthesized in two recent comprehensive reviews, which critically reassess more than two decades of research and identify the virological and clinical conditions under which HBoV1 detection is most likely to reflect true pathogenic involvement rather than incidental carriage or prolonged shedding[36,39]. Beyond this conceptual framework, an increasing number of well-documented case reports and case series have described children with severe acute respiratory tract infections in whom HBoV1 is detected at high viral loads and accompanied by viremia, often in the absence of other respiratory pathogens when mNGS techniques are applied[39]. Overall, these data suggest, but do not prove, a potential pathogenic contribution of HBoV to acute respiratory disease in children.

The seasonal pattern of HBoV infections changed after the COVID-19 pandemic, with a more uniform distribution throughout the year, as previously described[40]. In our cohort, HBoV was less frequently identified in the post-COVID period, as has been reported in Qatar[27] and China[41], suggesting a more limited role in severe ARTIs compared with other viruses such as RSV, HMPV, or PIV. Nevertheless, its altered seasonality and sustained presence in coinfections highlight the complex ecological interactions among respiratory viruses in the post-pandemic setting and support continued surveillance to better define its clinical impact.

FLU was completely absent during the pandemic period[12,13,15,42], in line with global surveillance data, and reappeared in T3 with delayed peaks and a shift in age distribution. The March peak observed in our cohort aligns with the findings of Habbous et al.[8] and might be influenced by the broader rollout of FLU vaccination programs during the post-pandemic period.

HCoV followed a similar trend: it was nearly undetected in T2, returned in T3 with altered seasonality, and frequently appeared in coinfections, particularly with RSV and HRV.

From a clinical standpoint, our study found no differences in sex distribution, in contrast with other reports that noted male predominance[40]. However, several changes in patient profiles were observed in T3, including an overall older age and a higher frequency of hypoxia, radiological infiltrates, and antibiotic use. While the length of hospital stay remained stable, a notable rise in pneumonia cases was observed, particularly in children under two years of age. These findings are consistent with previous observations from China[41], where lobar pneumonia diagnoses increased after the easing of restrictions. Interestingly, we observed a reduction in bronchiolitis diagnoses during and after the pandemic, suggesting a reconfiguration of clinical presentation that may be associated with the shift toward older age among infected children, changes in respiratory viral circulation, and potential viral interference.

In nearly all pneumonia cases in T3, a respiratory virus was identified, most commonly HRV and RSV, followed by HMPV and PIV, highlighting the dominant role of viral pathogens in the current clinical landscape. However, we acknowledge that HRV detection by PCR may reflect prolonged viral shedding or asymptomatic carriage and does not necessarily imply causality. This limitation is inherent to molecular diagnostic techniques and may lead to an overestimation of the clinical role of HRV in pneumonia.

Nevertheless, the detection rate of HRV in children with pneumonia was significantly higher in T3 compared to T1 (36% vs. 26%), suggesting a potential increase in its epidemiological relevance during the post-pandemic period.

Children with viral pneumonia in T3 were more frequently hypoxic but less likely to present with fever, pleural effusion, or require PICU admission, which may suggest a milder but more widespread disease burden and a reduced role of bacterial pneumonia in the post-pandemic period. However, antibiotic treatment was more frequent in the post-pandemic period despite higher viral detection rates. This pattern may be partly explained by the increased proportion of pneumonia diagnoses and radiographic infiltrates in our cohort, which likely influenced clinical decision-making toward antibiotic use when presentations were considered compatible with community-acquired pneumonia. Recent reports indicate a rebound in outpatient antibiotic prescriptions particularly among children, supporting the notion that overall antibiotic use has increased in the post-COVID-19 era[42]. Given the limited accuracy of routine diagnostic tests for bacterial pneumonia in children, innovative diagnostic tools such as computer-assisted lung ultrasound, novel host-based diagnostics, and next-generation sequencing may offer improved precision in guiding antibiotic use[43]. A major strength of this study is the availability of a large, prospectively collected pediatric cohort with uniform clinical assessment and molecular diagnostics applied consistently over a 17-year period. This design enables robust comparisons across pre-pandemic, pandemic, and post-pandemic phases within the same healthcare setting, reducing variability related to changes in diagnostic strategies or case definitions. As such, our findings provide a long-term perspective on post-COVID shifts in respiratory virus epidemiology and clinical expression that complement shorter-term or multicenter reports. However, some limitations must be acknowledged. The study was conducted at a single hospital in Spain, which may limit generalizability. Moreover, only hospitalized children were included,

potentially underrepresenting milder ARTIs seen in primary care. Finally, the substantial decline in hospital admissions during the pandemic could have led to under detection of certain pathogens during T2.

In conclusion, HRV remained the leading cause of ARTIs among Spanish children during the COVID-19 pandemic, followed by AdV, as the second most frequent pathogen. The post-pandemic increase in respiratory pathogen positivity rates, particularly HMPV and PIV, presents a new challenge for public health systems. Further research is needed to better understand the clinical and epidemiological shifts in ARTIs in children, as these findings have significant implications for emergency department planning, hospital admission rates, and the development of preventive treatment strategies.

Data availability

The datasets used and/or analysed during the current study are available from the corresponding author on reasonable request.

Received: 15 June 2025; Accepted: 5 May 2026
Published online: 18 May 2026

References

1. Global Burden of Disease Child and Adolescent Health Collaboration; Kassebaum, N. et al. Child and adolescent health from 1990 to 2015: findings from the Global Burden of Diseases, Injuries, and Risk Factors 2015 Study. *JAMA Pediatr.* **171**, 573–592 (2017).
2. Lozano, R. et al. Global and regional mortality from 235 causes of death for 20 age groups in 1990 and 2010: a systematic analysis for the Global Burden of Disease Study 2010. *Lancet* **380**, 2095–2128 (2012).
3. Zhu, N. et al. A novel coronavirus from patients with pneumonia in China, 2019. *N. Engl. J. Med.* **382**, 727–733 (2020).
4. WHO Director-General's opening remarks at the media briefing on COVID-19 - 11 March 2020. https://www.who.int/director-general/speeches/detail/who-director-general-s-opening-remarks-at-the-media-briefing-on-covid-19-11-march-2020.
5. Nascimiento, M., Baggio, D., Fascina, L. & do Prado, C. Impact of social isolation due to COVID-19 on the seasonality of pediatric respiratory diseases. *PLoS ONE* **15**, e0243694 (2020).
6. Zhu, L. et al. Epidemiological characteristics of respiratory viruses in hospitalized children during the COVID-19 pandemic in southwestern China. *Front Cell Infect. Microbiol.* **13**, 1142199 (2023).
7. Binns, E. et al. Influenza and respiratory syncytial virus during the COVID-19 pandemic: Time for a new paradigm?. *Pediatric Pulmonol.* **57**, 38–42 (2022).
8. Habbous, S., Hota, S., Allen, V. G., Henry, M. & Hellsten, E. Changes in hospitalizations and emergency department respiratory viral diagnosis trends before and during the COVID-19 pandemic in Ontario, Canada. *PLoS ONE* **18**, e0287395 (2023).
9. Mcconnochie, K. M. Bronchiolitis: What's in the name?. *Am. J. Dis. Child.* **137**, 11–13 (1983).
10. Garcia-Garcia, M. L. et al. Role of viral coinfections in asthma development. *PLoS ONE* **12**, e0189083 (2017).
11. Corman, V. M. et al. Detection of a novel human coronavirus by real-time reverse-transcription polymerase chain reaction. *Eurosurveillance.* **17**, 20285 (2012).
12. Díaz, D., Reina, J., Arcay, R. M. & Osona, B. Changes in the incidence and clinical manifestations of paediatric respiratory infections of viral aetiology during the SARS-CoV-2 pandemic. *Enferm. Infecc. Microbiol. Clin.* **40**, 463–464 (2022).
13. Kuitunen, L. et al. Effect of social distancing due to the Covid-19 pandemic on the incidence of viral respiratory tract infections in children in Finland during early 2020. *Pediatr. Infect. Dis. J.* **39**, e423–e427 (2020).
14. Bermudez, L. et al. Impact of the COVID-19 pandemic on admissions for respiratory infections in the Pediatric Intensive Care Unit. *Med. Intensiva (Engl Ed).* **46**, 281–285 (2022).
15. Lucion, M. F. et al. Impact of COVID-19 on the circulation of respiratory viruses in a children's hospital: An expected absence. *Arch. Argen. Pediatr.* **120**, 99–105 (2022).
16. Burrell, R., Saravanos, G. & Britton, P. N. Unintended impacts of COVID-19 on the epidemiology and burden of paediatric respiratory infections. *Paediatr. Respir. Rev.* **53**, 3–13 (2023).
17. Bermudez, L. et al. Influence of the COVID-19 pandemic on the epidemiology of acute bronchiolitis. *Enferm. Infecc. Microbiol. Clin. (Engl Ed)* **41**, 348–351 (2023).
18. Liang, D. F. et al. Changes in the epidemic patterns of respiratory pathogens of children in Guangzhou, China during the COVID-19 pandemic. *BMC Infect Dis.* **25**, 833 (2025).
19. Hong, S. et al. Post-pandemic resurgence of respiratory virus infections: age and department-specific patterns in a Chinese tertiary hospital (2020–2024). *BMC Infect Dis.* **25**, 1431 (2025).
20. Park, M., Suk, W. & Cowling, B. Shifts in influenza and respiratory syncytial virus infection patterns in Korea after the COVID-19 pandemic resulting from immunity debt: Retrospective observational study. *JMIR Public Health Surveill.* **11**, e68058 (2025).
21. Schildgen, O. et al. Twenty years of human bocavirus research: from an unculturable virus of unclear pathogenicity to a culturable human pathogen with distinct clinical associations. *Clin. Microbiol. Rev.* **38**, e0017324 (2025).
22. Foley, D. A. et al. The interseasonal resurgence of respiratory syncytial virus in Australian children following the reduction of Coronavirus disease 2019-related public health measures. *Clin. Infect. Dis.* **73**, e2829–e2830 (2021).
23. Principi, N., Autore, G., Ramundo, G. & Esposito, S. Epidemiology of respiratory infections during the COVID-19 pandemic. *Viruses* **15**, 1160 (2023).
24. Torres, A. R. et al. Resurgence of respiratory syncytial virus in children: An out-of-season epidemic in Portugal. *Acta Med Port.* **36**, 343–352 (2023).
25. Ujiie, M., Tsuzuki, S., Nakamoto, T. & Iwamoto, N. Resurgence of respiratory syncytial virus infections during COVID-19 pandemic, Tokyo, Japan. *Emerg. Infect. Dis.* **27**, 2969–2970 (2021).
26. Britton, P. N. et al. COVID-19 public health measures and respiratory syncytial virus. *Lancet Child Adolesc. Health.* **4**, e42–e43 (2020).
27. Abushahin, A. et al. Impact of COVID 19 pandemic restrictions and subsequent relaxation on the prevalence of respiratory virus hospitalizations in children. *BMC Pediatr.* **24**, 91 (2024).
28. Rao, R. et al. Shifting epidemiology and severity of respiratory syncytial virus in children during the COVID-19 pandemic. *JAMA Pediatr.* **177**, 730–732 (2023).
29. Liu, P. et al. Impact of COVID-19 pandemic on the prevalence of respiratory viruses in children with lower respiratory tract infections in China. *Virol J.* **18**, 159 (2021).
30. Zhang, R. X. et al. Surges of hospital-based rhinovirus infection during the 2020 coronavirus disease-19 (COVID-19) pandemic in Beijing. *China World J. Pediatr.* **17**, 590–596 (2021).
31. Poole, S., Brendish, N. J., Tanner, A. R. & Clark, T. W. Physical distancing in schools for SARS-CoV-2 and the resurgence of rhinovirus. *Lancet Respir Med.* **8**, e92–e93 (2020).

32. Kuang, L. et al. Changes in the epidemiological patterns of respiratory syncytial virus and human metapneumovirus infection among pediatric patients and their correlation with severe cases: A long-term retrospective study. *Front. Cell. Infect. Microbiol.* **14**, 1435294 (2024).
33. Huang, J. et al. Epidemiological, clinical, and genomic traits of PIV in hospitalized children after the COVID-19 pandemic in Wuhan. *China. J Med Virol.* **96**, e70117 (2024).
34. Riepl, A. et al. The surge of RSV and other respiratory viruses among children during the second COVID-19 pandemic winter season. *Front. Pediatr.* **11**, 1112150 (2023).
35. Kivit, C. et al. An off-season outbreak of human metapneumovirus infections after ending of a COVID-19 lockdown. *J Infect.* **84**, 722–746 (2022).
36. Trapani, S., Caporizzi, A., Ricci, S. & Indolfi, G. Human bocavirus in childhood: A true respiratory pathogen or a "passenger" virus? A comprehensive review. *Microorganisms* **11**, 1243 (2023).
37. Tan, J. et al. Human bocavirus-1 infection in hospitalized pediatric patients with acute respiratory tract infections. *Microbiol. Spectr.* **13**, e0298524 (2025).
38. Allander, T. et al. Cloning of a human parvovirus by molecular screening of respiratory tract samples. *Proc. Natl. Acad. Sci. U S A.* **102**, 12891–12896 (2005).
39. Schildgen, O., Qiu, J. & Söderlund-Venermo, M. Twenty years of human bocavirus research: From an unculturable virus of unclear pathogenicity to a culturable human pathogen with distinct clinical associations. *Clin. Microbiol. Rev.* **38**, e000XX–24 (2025).
40. Kampenusa, I. et al. Circulation and Codetections of influenza virus, SARS-CoV-2, respiratory syncytial virus, Rhinovirus, adenovirus, bocavirus, and other respiratory viruses during 2022–2023 season in Latvia. *Viruses* **16**, 1650 (2024).
41. Li, S. et al. Epidemiological characteristics of eleven common respiratory viral infections in children. *BMC Pediatr.* **24**, 827 (2024).
42. Ma, E. S. et al. Rebound of antibiotic use and respiratory infections after resumption of normalcy from COVID-19 in Hong Kong. *Infect Drug Resist.* **18**, 1325–1337 (2025).
43. van de Maat, J., Redfern, A., Bacha, T., Schouten, J. & Ruizendaal, E. Diagnostic testing and antibiotic stewardship for pneumonia in children worldwide: Current developments and next steps. *Curr. Opin. Pediatr.* **37**, 517–526 (2025).

Acknowledgements

We thank Noelia Reyes, Silvia Moreno, Vanessa Montero and Mar Molinero from the Reference and Research Laboratory for Respiratory Virus, National Centre for Microbiology for their exceptional technical support.

Author contributions

*María Luz García-García and Patricia Alonso-López contributed equally to this work.

Funding

This research was partially funded by Instituto de Salud Carlos III through the Projects PI21CIII/00019 and PI21/00377. In addition, funding was received from EU4H-2022-Grant Agreement-101113109, by UNESPA "COVIDSEQ-UNESPA" (MPY 226/22), and by CLARITY-Horizon Europe Programme-GA-101137201.

Declarations

Competing interests

The authors declare no competing interests.

Additional information

Correspondence and requests for materials should be addressed to M.L.G.-G.