Published Online: 2026 May 2 **Research Article**

Post-pandemic Distribution Patterns of Respiratory Pathogens in Erzurum, Turkey: A Retrospective Analysis

Hacı Ahmet Aydemir [1,*], Aslan Mehtap Hülya [2], Abdulkadir Alğan [3]

[1] Department of Family Medicine, Erzurum Faculty of Medicine, Health Sciences University, Erzurum, Turkey
[2] Department of Microbiology, Erzurum Faculty of Medicine, Health Sciences University, Erzurum, Turkey
[3] Health and Ageing Centre, Balıkesir State Hospital, Balıkesir, Turkey

[*] ***Corresponding Author:*** Department of Family Medicine, Erzurum Faculty of Medicine, Health Sciences University, Erzurum, Turkey. Email: haciahmet.aydemir@sbu.edu.tr

Received: 30 December, 2025; **Revised:** 13 March, 2026; **Accepted:** 26 March, 2026

Abstract

Background: This study aimed to investigate post-coronavirus disease 2019 (COVID-19) distribution patterns of respiratory pathogens using data from a tertiary care center in Erzurum, Turkey.

Objectives: This study evaluated the post-pandemic distribution patterns of viral and bacterial respiratory pathogens detected by multiplex real-time polymerase chain reaction and described their associations with age, sex, and seasonal variation in patients with acute respiratory tract infections.

Methods: This retrospective study analyzed respiratory samples submitted to Erzurum City Hospital between 2024 and 2025 for suspected acute respiratory tract infection. Pathogens were identified using a multiplex reverse transcription quantitative polymerase chain reaction panel targeting 15 viral and 5 bacterial agents and were analyzed according to age, sex, and season. A P-value < 0.05 was considered statistically significant.

Results: A total of 3197 samples were analyzed. The median age was 6 years (interquartile range, 2 - 20 years), and 55.9% of the patients were male. Most samples were collected in winter. Respiratory syncytial virus (RSV) was the most commonly detected viral pathogen, followed by severe acute respiratory syndrome coronavirus 2 and influenza A virus. *Streptococcus pneumoniae* and *Haemophilus influenzae* were the predominant bacterial agents. Coinfections were observed mainly in children younger than 10 years, whereas adults more frequently had negative results and lower pathogen diversity. Respiratory syncytial virus, adenovirus, bocavirus, *H. influenzae*, Bordetella pertussis, and *S. pneumoniae* were associated with younger age ($P < 0.05$), whereas coronavirus NL63 was associated with older age ($P < 0.001$). Seasonal patterns showed that RSV and influenza A virus peaked in winter, influenza B virus peaked in spring, and severe acute respiratory syndrome coronavirus 2 was more prevalent in summer and autumn ($P < 0.001$).

Conclusions: These findings demonstrate the re-emergence of RSV and influenza viruses, whereas severe acute respiratory syndrome coronavirus 2 circulation has shifted to lower levels. Bacterial detection by multiplex polymerase chain reaction requires cautious clinical interpretation. These data may inform diagnostic strategies and rational test use in acute respiratory tract infections.

Keywords: Respiratory Tract Infections, Multiplex PCR, Respiratory Syncytial Virus, Influenza, SARS-CoV-2, Epidemiology, Family Practice

1. Background

Respiratory tract infections (RTIs) are among the most common infectious diseases worldwide. They cause a clinical spectrum ranging from asymptomatic infection to fatal disease in all age groups (1, 2). Upper respiratory tract infections are among the leading contributors to the global disease burden, with approximately 17 billion cases annually (3). Consistent with the global situation, RTIs are among the most common reasons for seeking care in primary and

How to Cite: Aydemir HA, Hülya AM, Alğan A. Post-pandemic Distribution Patterns of Respiratory Pathogens in Erzurum, Turkey: A Retrospective Analysis. Jundishapur J Microbiol. 2026;19(4):e169542. doi: https://doi.org/10.5812/jjm-169542

advanced healthcare institutions in Turkey (4, 5). Pathogen identification using broad molecular panels is not performed in primary care in Turkey. This advanced diagnostic procedure is mostly performed in tertiary hospitals. Owing to their molecular diagnostic capabilities, tertiary hospitals play a critical role in defining epidemiological patterns of both community-acquired and hospital-acquired infections. Data obtained from these centers provide important information about pathogen distribution, support clinical decision-making processes, and contribute to public health planning.

Following the COVID-19 pandemic, significant changes occurred in the circulation of respiratory pathogens. Pandemic measures, such as isolation and social distancing, reduced the circulation of classic pathogens, including influenza virus and respiratory syncytial virus (RSV). This created a temporary immunity gap for these agents (6). As these pathogens re-emerged after the pandemic, changes also occurred in their seasonal and age-related distributions (7).

In Turkey, influenza vaccination is administered annually to specific risk groups. Similarly, vaccination against Streptococcus pneumoniae is recommended for certain population groups. However, although routine vaccination programs are recommended for RSV and other viral and bacterial respiratory pathogens, they are not yet routinely implemented. Although COVID-19 vaccination has largely ceased, the risk persists because of declining community immunity and the emergence of new variants. This is particularly important for older adults and individuals with chronic illnesses. Therefore, reassessment of COVID-19 booster doses or targeted vaccination strategies remains important (8).

The data for this study were obtained from Erzurum City Hospital, which serves as a key healthcare facility for Turkey's eastern region, neighboring provinces, and neighboring countries. Respiratory samples sent to the microbiology laboratory between 2024 and 2025 were retrospectively analyzed. This study aimed to define the spectrum of respiratory pathogens during the post-pandemic transition period and to describe their dynamics according to age group, sex, and season.

2. Objectives

This study aimed to provide evidence-based data to support the improvement or updating of national diagnostic strategies and vaccination programs.

3. Methods

3.1. Study Design and Sample Collection

This retrospective study was conducted at the Erzurum City Hospital Medical Microbiology Laboratory. Respiratory samples collected from patients with a preliminary diagnosis of acute respiratory tract infection between January 2024 and June 2025 were analyzed. The study population included individuals from all age groups who sought care at this tertiary center.

3.2. Molecular Pathogen Detection

Pathogen identification was performed using the Bio-Speedy® Respiratory Tract RT-qPCR MX-24 Panel (Bioeksen, Turkey). This multiplex real-time polymerase chain reaction (PCR)-based system allows simultaneous detection of a comprehensive range of viral and bacterial agents.

Bacterial targets: *Streptococcus pneumoniae*, *Haemophilus influenzae*, *Mycoplasma pneumoniae*, *Legionella pneumophila*, and *Bordetella pertussis*.

Viral targets: RSV, influenza viruses A and B, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), adenovirus, bocavirus, human metapneumovirus (hMPV), parainfluenza viruses (PIV) 1 - 4, and coronaviruses 229E, NL63, OC43, and HKU1. Respiratory syncytial virus results were reported as combined RSV A/B.

Laboratory procedures: Total nucleic acid extraction and RT-qPCR amplification were performed according to the manufacturer's validated protocols. The reactions were performed on CFX96 (Bio-Rad) real-time PCR platforms compatible with the Bio-Speedy® system.

3.3. Ethical Approval

Ethics committee approval was obtained from the Research Ethics Committee of Health Sciences Universty, Erzurum Faculty of Medicine on December 11, 2024, with approval number BAEK 2024/12-218. The study was conducted in accordance with Good Clinical Practice principles and the Declaration of Helsinki.

3.4. Statistical Analysis

All statistical analyses were performed using IBM SPSS Statistics for Windows, version 30.0. The

distribution of continuous variables was assessed using the Kolmogorov-Smirnov test. Normally distributed data are expressed as mean ± standard deviation, whereas nonnormally distributed data are expressed as median and interquartile range (IQR). Categorical variables are presented as numbers (No.) and percentages (%). The Mann-Whitney U test was used for comparisons between 2 groups because the data were not normally distributed. The Pearson chi-square test and Fisher exact test were used to evaluate categorical variables. A P-value < 0.05 was considered statistically significant.

4. Results

The study included 3197 respiratory tract samples. The median age of the patients was 6 years (IQR, 2 - 20 years). Overall, 44.1% of the patients were female, and 55.9% were male. When the seasonal distribution was examined, 26.68% of the samples were collected in spring, 12.11% in summer, 22.87% in autumn, and 38.35% in winter (Table 1).

Table 1. Sociodemographic Characteristics of the Study Population [a]

Variables	Overall
Sample size	3197
Age	6 [2 - 20]
Gender	
Female	1410 (44.1)
Male	1787 (55.9)
Season	
Spring	853 (26.68)
Summer	387 (12.11)
Autumn	731 (22.87)
Winter	1226 (38.35)

[a] Values are expressed as No. (%), No. or median [Q1 - Q3].

The most frequently detected viral agent was RSV, which was detected in 5.66% of the samples. This was followed by SARS-CoV-2 (4.44%) and influenza A virus (4.29%). Influenza B virus (2.38%) and parainfluenza virus type 4 (1.31%) were detected less frequently. The positivity rates of other viral pathogens remained below 1%. The most frequently detected bacterial pathogen was *S. pneumoniae*, which was positive in 26.78% of the samples. Haemophilus influenzae (21.24%) was the second most common pathogen. Legionella pneumophila was not detected during the study period. Mycoplasma pneumoniae (2.28%) and B. pertussis (1.19%) were detected at relatively low rates (Table 2).

Table 2. Positivity Rates of Respiratory Viral and Bacterial Pathogens

Pathogens	No. (%)
Viral	
Adenovirus	120 (3.75)
Bocavirus	47 (1.47)
Coronavirus 229E	18 (0.56)
Coronavirus HKU1	7 (0.22)
Coronavirus NL63	7 (0.22)
Coronavirus OC43	53 (1.66)
Influenza A virus	137 (4.29)
Influenza B virus	76 (2.38)
hMPV	3 (0.09)
Parainfluenza 1	21 (0.66)
Parainfluenza 2	2 (0.06)
Parainfluenza 3	38 (1.19)
Parainfluenza 4	42 (1.31)
RSV	181 (5.66)
SARS-CoV-2	142 (4.44)
Bacterial	
Haemophilus influenzae	679 (21.24)
Mycoplasma pneumoniae	73 (2.28)
Bordetella pertussis	38 (1.19)
Streptococcus pneumoniae	856 (26.78)
Legionella pneumophila	0 (0)

Abbreviations: hMPV, human metapneumovirus; RSV, respiratory syncytial virus; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

In the age group younger than 11 years, negative results were followed by bacterial monoinfection (21.25%), viral-bacterial coinfection (15.36%), and viral monoinfection (15.06%), with coinfections being more prominent in this age group. In the 11 - 20-year age group, bacterial monoinfection (24.30%) was the most common finding after negative results, and the rates of viral and bacterial coinfections were relatively lower. In the group older than 20 years, negative results were predominant, followed by viral monoinfection (16.44%) and bacterial monoinfection (10.66%), with coinfections detected at very low rates. Overall, the proportion of negative samples increased with age, whereas infection diversity and coinfection frequency decreased (Figure 1).

When the ages of pathogen-positive and pathogen-negative patients were compared, the ages of patients who tested positive for adenovirus, bocavirus, hMPV, parainfluenza viruses 1 - 3, RSV, *H. influenzae*, B. pertussis, and *S. pneumoniae* were significantly lower than those of

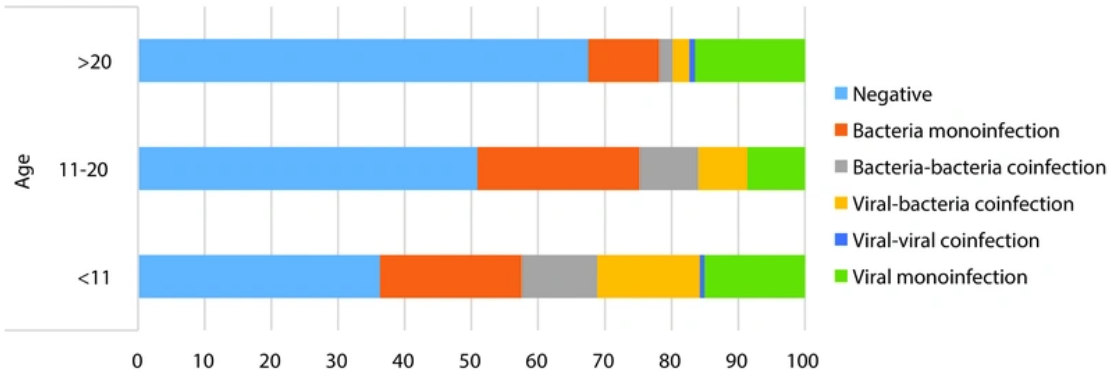

Figure 1. Distribution of bacterial monoinfection, viral monoinfection, and coinfection patterns stratified by age group (< 11, 11 - 20, and > 20 years).

Table 3. Age Distribution According to Pathogen Test Results

Pathogen	Age; Test Negative [a]	Age; Test Positive [a]	P-Value [b]
Adenovirus	7 [2 - 24]	4 [3 - 8]	0.005
Bocavirus	7 [2 - 22]	3 [2 - 4]	< 0.001
Coronavirus 229E	6 [2 - 20]	6 [2 - 36]	0.750
Coronavirus HKU1	6 [2 - 20]	6 [2 - 14]	0.726
Coronavirus NL63	6 [2 - 20]	11 [2 - 69]	< 0.001
Coronavirus OC43	6 [2 - 20]	6 [2 - 17]	0.803
Influenza A virus	6 [2 - 20]	7 [3 - 19]	0.122
Influenza B virus	6 [2 - 21]	7 [4 - 18]	0.376
hMPV	6 [2 - 20]	4 [2 - 4]	0.001
Parainfluenza 1	6 [2 - 21]	4 [2 - 5]	< 0.001
Parainfluenza 2	6 [2 - 20]	2 [2 - 2]	0.024
Parainfluenza 3	6 [2 - 21]	2 [1 - 8]	< 0.001
Parainfluenza 4	6 [2 - 19]	9 [2 - 45]	0.352
RSV	7 [2 - 27]	2 [2 - 3]	< 0.001
SARS-CoV-2	6 [2 - 19]	4 [1 - 52]	0.403
Haemophilus influenzae	8 [2 - 34]	5 [2 - 9]	< 0.001
Mycoplasma pneumoniae	6 [2 - 22]	9 [5 - 13]	0.207
Bordetella pertussis	6 [2 - 22]	2 [1 - 8]	< 0.001
Streptococcus pneumoniae	8 [2 - 36]	4 [2 - 9]	< 0.001

Abbreviations: hMPV, human metapneumovirus; RSV, respiratory syncytial virus; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

[a] Values are expressed as Median [Q1 - Q3].

[b] Mann-Whitney U test.

negative controls ($P < 0.05$). The age distribution of coronavirus NL63-positive patients was significantly higher than that of coronavirus NL63-negative patients ($P < 0.001$) (Table 3).

When the distribution of respiratory pathogens by sex was examined, only *S. pneumoniae* positivity differed significantly between females and males. No significant sex-related difference was detected for any other pathogen (Table 4).

Adenovirus positivity was higher in summer than in autumn and winter ($P = 0.003$). Bocavirus infections were more common in winter than in spring ($P = 0.039$).

Table 4. Positivity Rates of Respiratory Viral and Bacterial Pathogens by Sex

Pathogen	Female (n = 1410) [a]	Male (n = 1787) [a]	P-Value
Adenovirus	51 (3.62)	69 (3.86)	0.718 [b]
Bocavirus	21 (1.49)	26 (1.45)	0.936 [b]
Coronavirus 229E	7 (0.5)	11 (0.62)	0.655 [b]
Coronavirus HKU1	3 (0.21)	4 (0.22)	1.00 [c]
Coronavirus NL63	3 (0.21)	4 (0.22)	1.00 [c]
Coronavirus OC43	24 (1.7)	29 (1.62)	0.862 [b]
Influenza A virus	61 (4.33)	76 (4.25)	0.919 [b]
Influenza B virus	32 (2.27)	44 (2.46)	0.722 [b]
hMPV	3 (0.21)	0 (0)	0.086 [c]
Parainfluenza 1	6 (0.43)	15 (0.84)	0.150 [b]
Parainfluenza 2	1 (0.07)	1 (0.06)	1.00 [c]
Parainfluenza 3	18 (1.28)	20 (1.12)	0.683 [b]
Parainfluenza 4	22 (1.56)	20 (1.12)	0.277 [b]
RSV	88 (6.24)	93 (5.2)	0.208 [b]
SARS-CoV-2	61 (4.33)	81 (4.53)	0.778 [b]
Haemophilus influenzae	278 (19.72)	401 (22.44)	0.062 [b]
Mycoplasma pneumoniae	34 (2.41)	39 (2.18)	0.667 [b]
Bordetella pertussis	16 (1.13)	22 (1.23)	0.803 [b]
Streptococcus pneumoniae	347 (24.61)	509 (28.48)	0.014 [b]

Abbreviations: hMPV, human metapneumovirus; RSV, respiratory syncytial virus; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

[a] Values are expressed as No (%).

[b] Chi-square test.

[c] Fisher exact test.

Influenza A virus positivity was significantly higher in winter than in spring, summer, and autumn ($P < 0.001$), whereas influenza B virus positivity was higher in spring than in all other seasons ($P < 0.001$). Parainfluenza 1 infections were more common in autumn than in spring, summer, or winter ($P < 0.001$). Parainfluenza 3 positivity was higher in autumn than in winter ($P = 0.017$). Parainfluenza 4 infections were more frequently observed in spring than in summer and autumn ($P = 0.001$). Respiratory syncytial virus positivity was highest in winter and was higher than in spring, summer, and autumn; it was also higher in spring than in summer and autumn ($P < 0.001$). Severe acute respiratory syndrome coronavirus 2 positivity was higher in summer and autumn than in spring and winter ($P < 0.001$). Among bacterial agents, *H. influenzae* positivity was higher in spring and winter than in summer and autumn ($P < 0.001$). Mycoplasma pneumoniae infections were more common in summer and autumn than in spring and winter ($P < 0.001$). Bordetella pertussis positivity differed significantly across seasons ($P = 0.016$). Streptococcus pneumoniae positivity was higher in winter than in autumn, higher in autumn than in summer, and higher in spring than in summer ($P < 0.001$) (Table 5).

5. Discussion

This study, which included a comprehensive analysis of 3197 respiratory samples, presents the status of respiratory pathogens in eastern Turkey during the post-pandemic transition period. High detection rates of viral agents, such as RSV, influenza virus, and SARS-CoV-2, as well as bacterial agents, such as *S. pneumoniae* and *H. influenzae*, indicate substantial restructuring of the regional respiratory ecosystem. The period covering 2024 - 2025 marked a critical stage in the changes in circulation patterns caused by COVID-19 interventions. High-volume samples collected from a tertiary center,

Table 5. Positivity Rates of Respiratory Viral and Bacterial Pathogens by Season [a]

Pathogen	Spring (1) (n = 853)	Summer (2) (n = 387)	Autumn (3) (n = 731)	Winter (4) (n = 1226)	P-Value/Post Hoc
Adenovirus	39 (4.57)	25 (6.46)	19 (2.6)	37 (3.02)	0.003 [b]/(2 > 3, 4)
Bocavirus	6 (0.7)	5 (1.29)	9 (1.23)	27 (2.2)	0.039 [b]/(4 > 1)
Coronavirus 229E	9 (1.06)	0 (0)	2 (0.27)	7 (0.57)	0.088 [c]
Coronavirus HKU1	1 (0.12)	0 (0)	2 (0.27)	4 (0.33)	0.690 [c]
Coronavirus NL63	0 (0)	0 (0)	2 (0.27)	5 (0.41)	0.203 [c]
Coronavirus OC43	18 (2.11)	2 (0.52)	10 (1.37)	23 (1.88)	0.180 [b]
Influenza A virus	2 (0.23)	0 (0)	1 (0.14)	134 (10.93)	< 0.001 [b]/(4 > 1, 2, 3)
Influenza B virus	57 (6.68)	3 (0.78)	6 (0.82)	10 (0.82)	< 0.001 [b]/(1 > 2, 3, 4)
hMPV	0 (0)	0 (0)	0 (0)	3 (0.24)	0.361 [c]
Parainfluenza 1	0 (0)	0 (0)	16 (2.19)	5 (0.41)	< 0.001 [c]/(3 > 1, 2, 4)
Parainfluenza 2	0 (0)	0 (0)	0 (0)	2 (0.16)	0.620 [c]
Parainfluenza 3	11 (1.29)	6 (1.55)	15 (2.05)	6 (0.49)	0.017 [b]/(3 > 4)
Parainfluenza 4	19 (2.23)	0 (0)	3 (0.41)	20 (1.63)	0.001 [b]/(1 > 2, 3)
RSV	34 (3.99)	1 (0.26)	0 (0)	146 (11.91)	< 0.001 [b]/(4 > 1 > 2, 3)
SARS-CoV-2	33 (3.87)	32 (8.27)	53 (7.25)	24 (1.96)	< 0.001 [b]/(2, 3 > 1, 4)
Haemophilus influenzae	211 (24.74)	51 (13.18)	112 (15.32)	305 (24.88)	< 0.001 [b]/(1, 4 > 2, 3)
Mycoplasma pneumoniae	5 (0.59)	19 (4.91)	28 (3.83)	21 (1.71)	< 0.001 [b]/(2, 3 > 1, 4)
Bordetella pertussis	15 (1.76)	9 (2.33)	5 (0.68)	9 (0.73)	0.016 [b, d]
Streptococcus pneumoniae	241 (28.25)	65 (16.8)	175 (23.94)	375 (30.59)	< 0.001 [b]/(4 > 3 > 2/1 > 2)

Abbreviations: hMPV, human metapneumovirus; RSV, respiratory syncytial virus; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

[a] Values are expressed as No (%).

[b] Chi-square test.

[c] Fisher-Freeman-Halton test.

[d] No significant pairwise difference.

such as Erzurum City Hospital, provide a solid basis for interpreting these changing dynamics.

Notably, this study revealed a high frequency of RSV. Although human rhinovirus/enterovirus (HRV/EV) has frequently been identified as the primary agent in many studies conducted in Turkey, the present findings indicate that RSV was the primary viral agent. This difference is not solely the result of epidemiological differences but also reflects methodological differences. The Bio-Speedy® MX-24 panel used in this laboratory does not include HRV/EV targets. In contrast, studies conducted by Uğur and colleagues and Duclos and colleagues used panels with broader viral coverage, which naturally led to higher HRV/EV reporting (9, 10). This highlights the importance of diagnostic panel coverage in interpreting pathogen prevalence in clinical practice. Therefore, panel-specific limitations should not be overlooked when clinicians interpret laboratory reports and compare regional data.

The data presented in this study show that the resurgence of classic respiratory viruses, such as influenza virus and RSV, is consistent with the global resurgence model described in the literature (11, 12). Public health measures, such as mask wearing and social distancing during the COVID-19 pandemic, significantly suppressed the circulation of these pathogens (10). This suppression led to a temporary “immunity gap” or “immunity debt” in the general population (13). The present findings confirm that when protective measures are relaxed, classic pathogens re-emerge at substantial levels. Interestingly, whereas influenza virus and RSV showed sharp and high seasonal peaks, SARS-CoV-2 had a broader and more continuous distribution. These findings suggest that SARS-CoV-2 has become integrated into the respiratory ecosystem as a persistent year-round pathogen (14-16).

When evaluated by age, the data from this study further support the immunity gap theory. The highest pathogen diversity and coinfection rates were detected in the pediatric group. This suggests that children, especially those born during or shortly before the pandemic, had limited exposure to common respiratory viruses for several years because of isolation measures. With the lifting of isolation measures and the resumption of educational activities, this immunologically vulnerable group appears to have encountered multiple pathogens simultaneously. This may explain the high coinfection rates observed in the present data (17, 18). Data from Bukavaz and colleagues and Pizzo and colleagues, showing that the likelihood of detecting multiple pathogens decreases with age, are consistent with the present findings (19, 20). The persistent low-level circulation of SARS-CoV-2 indicates that community immunity has substantially improved through vaccination and previous exposure. Nevertheless, the persistence of SARS-CoV-2 among older adults remains a concern. This situation suggests that older age groups may remain at risk from new variants.

With respect to bacterial agents, the high positivity rates of *S. pneumoniae* and *H. influenzae* in the samples should be interpreted with caution. According to Karabulut et al, these organisms are part of the nasopharyngeal microbiota (21). In this retrospective study design, it was not possible to distinguish asymptomatic colonization from active infection on the basis of PCR results. Reverse transcription quantitative polymerase chain reaction is known to have high sensitivity and may detect bacterial DNA at levels that may not be clinically meaningful. This highlights the need for clinical correlation. Relying solely on molecular detection may lead to overdiagnosis of bacterial infections and unnecessary antibiotic use. Therefore, the correlation between molecular methods and clinical outcomes should be considered when promoting rational antibiotic use.

Regarding seasonal distribution, the results indicated that viral and bacterial positivity peaked during the winter months. These findings are consistent with the literature on the seasonal dynamics of respiratory pathogens in regions with pronounced cold seasons. Respiratory syncytial virus and influenza virus continue to be the main causes of respiratory infections during winter (14, 15). The results are similar in Erzurum, where winter conditions are long and harsh. However, the continued presence of SARS-CoV-2 throughout the year should not be overlooked in relaxed post-pandemic diagnostic strategies.

The transition of SARS-CoV-2 from a pandemic state to a low-level endemic state is among the important epidemiological findings of this study. Vaccination efforts and immunity gained between waves during the pandemic may have contributed to this change. However, the ability of the virus to coexist with classic respiratory pathogens in the ecosystem indicates that a new equilibrium has been reached. This study emphasizes the importance of monitoring this new normal.

5.1. Study Limitations

This study has several limitations. First, it had a retrospective design, and variables such as clinical findings, disease severity, antibiotic or antiviral use, and vaccination status were not included in the analysis. The multiplex PCR panel used in this study does not include some common respiratory pathogens, such as HRV/EV, in its target spectrum, which limits the interpretation of viral agent distribution. Furthermore, it was not possible to distinguish colonization from actual infection among the bacterial agents screened, and the clinical correlation of detected bacterial positivity could not be evaluated. The single-center design and reliance on data from a tertiary hospital may limit the direct generalizability of the findings to community-based and primary care settings. However, the center's service to a large geographical area may partially mitigate these limitations.

5.2. Conclusions

This study provides current regional epidemiological information on the distribution patterns of respiratory pathogens during the transition from the pandemic period to the post-pandemic period in Turkey. The results showed that the distribution patterns of RSV and influenza viruses have returned to a dominant pattern, whereas SARS-CoV-2 shows lower prevalence and broader seasonality. The detection of *S. pneumoniae* and *H. influenzae* as the major bacterial agents indicates that bacterial results obtained by multiplex PCR should be interpreted carefully in the clinical setting. The high prevalence of coinfection, especially in the pediatric group, emphasizes the importance of appropriate diagnostic approaches for this age group. These results

may help define diagnostic strategies for the treatment of acute respiratory infections.

Footnotes

AI Use Disclosure: DeepL was used for the translation of the entire manuscript, while Gemini was utilized for minor text editing specifically in the introduction and Abstract sections.

Authors' Contribution: H. A. A. contributed to the study design and manuscript drafting. M. H. A. contributed to data acquisition and manuscript drafting. A. A. performed the statistical analysis and contributed to manuscript drafting. H. A. A., M. H. A., and A. A. contributed to the investigation, resources, and writing, review, and editing.

Conflict of Interests Statement: The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data Availability: The dataset presented in the study is available on request from the corresponding author during submission or after publication. The data are not publicly available due to patient confidentiality and institutional data protection policies.

Ethical Approval: Ethical committee approval was obtained from the Research Ethics Committee of Health Sciences University Erzurum Medicine Faculty dated 11 December 2024 and numbered BAEK 2024/12-218.

Funding/Support: No financial support was received for the conduct of this study.

References

1. José RJ. Respiratory infections: A global burden. *Ann Res Hospitals*. 2018;**2**:12. https://doi.org/10.21037/arh.2018.09.01.
2. Calderaro A, Buttrini M, Farina B, Montecchini S, De Conto F, Chezzi C. Respiratory Tract infections and laboratory diagnostic methods: A review with a focus on syndromic panel-based assays. *Microorganisms*. 2022;**10**(9). [PubMed ID: 36144458]. [PubMed Central ID: PMC9504108]. https://doi.org/10.3390/microorganisms10091856.
3. Jin X, Ren J, Li R, Gao Y, Zhang H, Li J, et al. Global burden of upper respiratory infections in 204 countries and territories, from 1990 to 2019. *E-Clin Med*. 2021;**37**:100986. [PubMed ID: 34386754]. [PubMed Central ID: PMC8343248]. https://doi.org/10.1016/j.eclinm.2021.100986.
4. İNcİ H. Utilization of family health centers by patients presenting to the internal medicine outpatient clinic. *UNIKA J Health Sci*. 2022;**2**(3):321-31. https://doi.org/10.47327/unikasaglik.67.
5. Yüksel A. Adult emergency department patient profile, diagnostic codes and triage assessment. *Anatolian J Emerg Med*. 2020;**3**(2):37-41.
6. Li X, Ma J, Li Y, Hu Z. One-year epidemiological patterns of respiratory pathogens across age, gender, and seasons in Chengdu during the post-COVID era. *Sci Rep*. 2025;**15**(1):357. [PubMed ID: 39747544]. [PubMed Central ID: PMC11697200]. https://doi.org/10.1038/s41598-024-84586-8.
7. Dimaka K, Karampatakis T, Kachrimanidou M, Katsifa H, Exindari M. Epidemiology of bacterial respiratory tract infections during the pre-pandemic, COVID-19 pandemic and post-pandemic era: A retrospective study of hospitalized adults in northern Greece between 2018 and 2023. *Diagn Microbiol Infect Dis*. 2025;**111**(3):116710. [PubMed ID: 39892369]. https://doi.org/10.1016/j.diagmicrobio.2025.116710.
8. Jin Q, Yu S, Qu J. Epidemiological characteristics of respiratory tract infections during and after the pandemic of COVID-19 from 2021 - 2023 in Shenzhen, southern China. *BMC Public Health*. 2025;**25**(1):1724. [PubMed ID: 40346486]. [PubMed Central ID: PMC12063367]. https://doi.org/10.1186/s12889-025-22884-0.
9. Uğur M, Şahin AM. Distribution of Pathogens of Respiratory Tract Infections By Months and Age Groups. *Cerasus J Med*. 2024;**1**(1).
10. Duclos M, Hommel B, Allantaz F, Powell M, Posteraro B, Sanguinetti M, et al. Multiplex PCR detection of respiratory tract infections in SARS-CoV-2-negative patients admitted to the emergency department: An International Multicenter Study During The COVID-19 pandemic. *Microbiol Spectrum*. 2022;**10**(5). [PubMed ID: 36154273]. [PubMed Central ID: PMC9603986]. https://doi.org/10.1128/spectrum.02368-22.
11. Eden J, Sikazwe C, Xie R, Deng Y, Sullivan SG, Michie A, et al. Off-season RSV epidemics in Australia after easing of COVID-19 restrictions. *Nature Communications*. 2022;**13**(1). [PubMed ID: 35610217]. [PubMed Central ID: PMC9130497]. https://doi.org/10.1038/s41467-022-30485-3.
12. Xiong W, Cowling BJ, Tsang TK. Influenza resurgence after relaxation of public health and social measures, Hong Kong, 2023. *Emerg Infec Dis*. 2023;**29**(12):2556-9. [PubMed ID: 37885047]. [PubMed Central ID: PMC10683823]. https://doi.org/10.3201/eid2912.230937.
13. De Conto F, Rafei R, Osman M, Barake BA, Mallat H, Dabboussi F, et al. Shifting respiratory pathogens: Post-COVID-19 trends in community-acquired infections in underserved communities. *PLOS One*. 2025;**20**(8). [PubMed ID: 40845032]. [PubMed Central ID: PMC12373226]. https://doi.org/10.1371/journal.pone.0329481.
14. Neumann G, Kawaoka Y. Seasonality of influenza and other respiratory viruses. *EMBO Mol Med*. 2022;**14**(4). [PubMed ID: 35157360]. [PubMed Central ID: PMC8988196]. https://doi.org/10.15252/emmm.202115352.
15. Townsend JP, Hassler HB, Lamb AD, Sah P, Alvarez Nishio A, Nguyen C, et al. Seasonality of endemic COVID-19. *mBio*. 2023;**14**(6). [PubMed ID: 37937979]. [PubMed Central ID: PMC10746271]. https://doi.org/10.1128/mbio.01426-23.
16. Kirişci Ö. Investigation of the frequency of viral and bacterial agents in patients with preliminary diagnosis of acute respiratory tract infection in Kahramanmaraş province using multiplex PCR method. *Kahramanmaraş Sütçü İmam Univ Faculty Med J*. 2025;**20**(1):52-7. https://doi.org/10.17517/ksutfd.1500719.
17. Onel M, Uysal HK, Hulikyan A, Ucar YA, Yapar G, Allahverdiyeva A, et al. Syndromic testing in the pandemic era and beyond: Rapid detection for respiratory infections in Istanbul. *Viruses*. 2025;**17**(6).

[PubMed ID: 40573366]. [PubMed Central ID: PMC12197672]. https://doi.org/10.3390/v17060776.

18. Uğur M, Şahin AM. Distribution of Pathogens s of Respiratory Tract Infections By Months and Age Groups. *Cerasus J Med*. 2024;**1**(1):35-41.
19. Bukavaz S, Gungor K, Köle M, Ekuklu G. Adult Patients with Acute Respiratory Viral Infections and the Impact of Humidity Exposure: A Retrospective Study. *Preprints.org*. 2024;**Preprint**. https://doi.org/10.22541/au.173052005.55349734/v1.
20. Pizzo M, Bonura F, Cacioppo F, Palazzotto E, Filizzolo C, Russo S, et al. Post-COVID-19 epidemiology of viral infections in adults hospitalized with acute respiratory syndromes in Palermo, South of Italy. *Pathogens*. 2025;**14**(10). [PubMed ID: 41156608]. [PubMed Central ID: PMC12567287]. https://doi.org/10.3390/pathogens14100997.
21. Karabulut N, Alaçam S, Şen E, Karabey M, Yakut N. The Epidemiological Features and Pathogen Spectrum of Respiratory Tract Infections, Istanbul, Türkiye, from 2021 to 2023. *Diagnostics*. 2024;**14**(11). [PubMed ID: 38893598]. [PubMed Central ID: PMC11171886]. https://doi.org/10.3390/diagnostics14111071.