Journal of Communicable Diseases
Volume 58, Issue 1 - 2026, Pg. No. 80-87
Peer Reviewed & Open Access Journal

Research Article

Molecular Investigation of Hpiv-1 and Hpiv-3 Viral Types in Patients with Seasonal Respiratory Infections in Iraq

Asmaa Haseeb Hwaid

PhD in Virology/ Microbiology, Department of Biology, College of Education for Pure Sciences, University of Diyala, Iraq
DOI: https://doi.org/10.24321/0019.5138.202612

I N F O

E-mail Id:
asmaa.haseeb@ymail.com
Orcid Id:
https://orcid.org/0000-0002-3179-6115.
How to cite this article:
Hwaid A H, Molecular Investigation of Hpiv-1 and Hpiv-3 Viral Types in Patients with Seasonal Respiratory Infections in Iraq. J Commun Dis. 2026;58(1):80-87.

Date of Submission: 2025-11-15
Date of Acceptance: 2025-12-26

A B S T R A C T

Background: Respiratory tract infections in paediatric and adult populations are associated with four Human Parainfluenza Virus (HPIV) serotypes. HPIV-1 and HPIV-3 rank just behind Human Respiratory Syncytial Virus (HRSV) as significant contributors to severe respiratory tract illnesses. Epidemiological studies employing molecular techniques globally have confirmed the frequent circulation of HPIV-1 and HPIV-3 in humans.

Aims: The focus of this study is to analyse the distribution of HPIV-1 and -3 in patients presenting with respiratory infections, and to analyse co-infection with HMPV and HRSV.

Methods: The study was carried out between 2018 and 2020 in the Iraqi province of Diyala. Three hundred and twenty-three patients of various ages who were suspected of having Respiratory Tract Infections (RTIs) were enrolled in the study. A questionnaire created especially for this purpose was used to gather participant data. HPIVs were detected molecularly using the Real-Time PCR assay. Participant privacy was protected by obtaining verbal consent. The Statistical Package for the Social Sciences (SPSS) version 25 was used to perform statistical analysis on the data.

Results: No HPIV-1 infections were found, and the overall molecular detection rate of HPIV-3 among the participants was 5.3% (17 cases). One (6.3%) participant tested positive for both RSV and HPIV-3, indicating co-infection. The highest detection rate (29.4%) was observed in November, and in children under five, with insignificant differences. Despite the fact that females had a higher HPIV-3 detection rate than males, the difference was not statistically significant.

Conclusion: HPIV-3 is the predominant strain, and dual infection with RSV is possible but rare.

Keywords: Human Parainfluenza Virus Type 1 and 3, Children, RTIs, Diyala

Introduction

People of all ages are affected by respiratory viral infections, which are among the most significant causes of disease requiring medical intervention, and can lead to serious health consequences. This is especially true for young children, the elderly, immunocompromised people, and infants.[1,2] A wide range of viruses that commonly infect the upper respiratory tract (URT) and lower respiratory tract (LRT) can lead to diverse clinical syndromes, including the common cold, pharyngitis, croup, otitis media, bronchiolitis, and viral pneumonia.[3,4]

Human Parainfluenza Viruses (HPIVs) are members of the Paramyxoviridae family, which are viruses with an RNA genome. The four major virus serotypes are HPIV-1, -2, -3, and -4. While HPIV-3 is frequently responsible for bronchiolitis and pneumonia, HPIV-1 and HPIV-2 are known for being the main causes of croup.[5,7] Globally, HPIV is a major cause of morbidity and mortality, especially for children in developing countries.[8] Additionally, it is a major contributor to nosocomial infections, which in certain individuals, like transplant recipients or immunocompromised patients, can be fatal.[9] Furthermore, HPIVs frequently co-circulate with influenza virus and respiratory synsytial virus RSV, among other respiratory viruses, making diagnosis and clinical treatment more difficult.[10] New information on the epidemiology, genetic diversity, seasonality, and related clinical manifestations of respiratory pathogens that cause URT and LRT infections has been facilitated by the development of multiplex Polymerase Chain Reaction (PCR) amplification techniques and their expanding application in the detection of these pathogens.[11,12] In the Eastern Mediterranean Region, Acute respiratory tract infections ARIs caused more than 8% of all deaths in 2013, according to World Health Organization estimates. Meanwhile, HPIV infections are responsible for 4% of paediatric ARI-related deaths.[8] HPIV-3 is the most commonly found of the four HPIV subtypes and is a major contributor to ARIs in children. According to a surveillance study carried out in China between 2009 and 2019, HPIV-3 was consistently one of the top three pathogens causing ARIs in children.[13] To date, only a single study has addressed the frequency of HPIV-1 and HPIV-3 in Iraq, underscoring the scarcity of epidemiological data on these viruses in the region. There are a few studies on the frequency of HPIV-1 and -3 in Iraq.[14] This study aims to determine the distribution of HPIV-1 and -3 in the Iraqi province of Diyala and to assess co-infection with HMPV and HRSV.

Methodology

Participants and Study Design

This study employed a cross-sectional design and was conducted in multiple health institutions in Diyala Governorate. A total of 302 patients suspected of having respiratory tract infections (RTIs) were enrolled during two collection seasons in 2018. Data were obtained through a structured questionnaire covering sociodemographic and clinical information. Specimen collection was performed under the supervision of qualified medical professionals. Informed consent was obtained from all participants prior to enrollment, and the study protocol was approved by the relevant institutional authorities.The study period extended from the beginning of 2018 to the end of that year and included multiple health institutions in Diyala Governorate, such as Baqubah Teaching Hospital, Al-Batoul Teaching Hospital and some outpatient clinics. A total of 185 patients were included in the study during the period from January to May, which represented the first season of sample collection, while the number of participants in the second season, which covered November and December, reached 138. Three hundred and twenty-three Three hundred and two patients representing various age groups who had been suspected of having RTIs participated in the study. A questionnaire form created especially for this purpose was used for collecting participant data, including sociodemographic data and clinical observations. The collection of specimens was carried out under the close supervision of qualified medical professionals and practitioners.

Procedure

Three different types of respiratory samples were collected, including swabs from the nasopharynx, nose, and throat. For sampling purposes, the ∑-Virocult swab manufactured by the British company MWE was adopted. The collected swabs were placed in tubes having 1 mL viral transport medium, sourced from MWE (UK) and E. coli Ltd. (Russia), used for sample preservation. The specimens were subsequently transferred to the laboratory in an ice-cooled container and stored at -80°C till they were analysed molecularly using the HPIV-1/ HPIV-3 real-time PCR (RT-PCR/ qPCR).

Statistical Analysis

The Statistical Package for the Social Sciences (SPSS) version 25 was used to analyse the data. To compare categorial data, the chi-square test and Fisher's exact test were adapted. If the p value was equal to or less than 0.05, statistical significance was considered.

Ethics Statement

The research protocols were approved by the Scientific Research Ethics Committee affiliated with the Scientific Department of the researchers' workplace (Ref. No. CEPEC/007- 1/1/2018) and the Research Management Unit of the Diyala Health Department, Ministry of Health (Ref. No. RMU/5878/5/2/2018).

ISSN: 0019-5138
DOI: https://doi.org/10.24321/0019.5138.202612

Results

Between January and December 2018, 323 samples were tested for HPIV-1 and HPIV3 HBV3 over two seasons in the Iraqi province of Diyala. The samples included a total of 71 nasopharyngeal swabs, 161 sinus swabs, and 91 throat swabs. Age distribution over the two seasons shows that the number of study participants under the age of 5 years was higher than in other age groups, and the number of males was higher than that of females. The results shown in Figure 2 visually highlight that HPIV-3 had slightly higher positivity in Season I (5.9%) than in Season II (4.3%), while HPIV-1 had no detected cases in either season (0%) (p = 0.525). The current research did not report HPIV-1 positivity rates in any RTI patient who participated in the study.

The result in Figure (2), visually highlights that HPIV3 had slightly higher positivity in Season I (5.9%) than Season II (4.3%), while HPIV1 had no detected cases in either season (0%), with no statistically significant difference (P = 0.525).

Figure 3 shows that HPIV-3 co-infection was low with both viruses: 6.7% for Human Respiratory Syncytial Virus (HRSV) and 3.3% for Human Metapneumovirus (HMPV), and no statistically significant differences were recorded (p = 0.803 and p = 0.619, respectively).

As shown in Figure 4, the highest positivity was observed in nasal sinus swabs (64.7%), followed by throat swabs (35.3%), while no positive cases were detected in nasopharyngeal swabs. The difference between specimen types was not statistically significant (p = 0.080).

As shown in Figure 5, the results illustrate that the highest positivity was observed in November (29.4%), followed by March (23.5%), while no positive cases were detected in January. The difference showed no statistical significance (p = 0.340).

It is evident from Figure 6 that the age group of under five years showed the highest rate of positivity (82.4%) compared to others, followed by 5-year-olds (11.8%). The difference failed to achieve significance at the conventional threshold (p = 0.504).r

The data in Figure 7 reveal that females accounted for the greatest proportion of positive cases (58.8%), followed by males (41.2%). This difference was not statistically significant (p = 0.246).

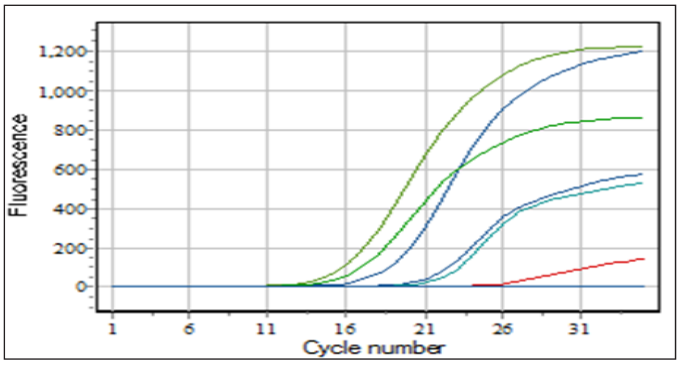

Figure 1.Positive Results for HPIV-3 Recorded Within a Cycle Threshold Range of 15.4 to 25.5 According to a Real-Time PCR Amplification Log Plot

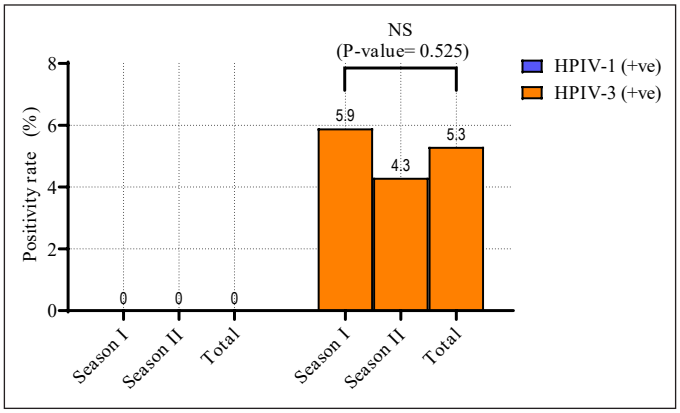

Figure 2.Season-Wise Distribution of the Positivity Rate of Human Parainfluenza Viruses

ISSN: 0019-5138
DOI: https://doi.org/10.24321/0019.5138.202612

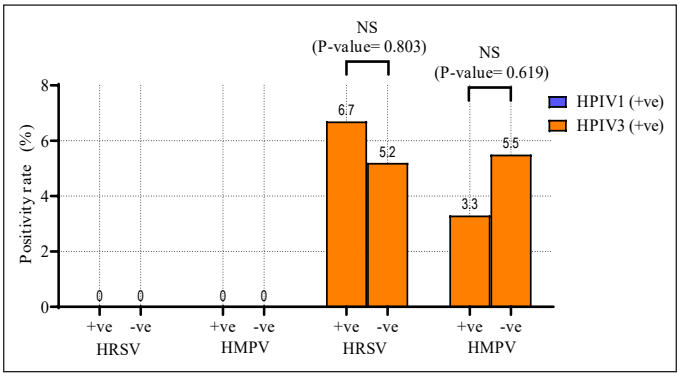

Figure 3.HPVI and HPIV-3 Co-Infection Rates with Other Respiratory Viruses (HRSV and HMPV)

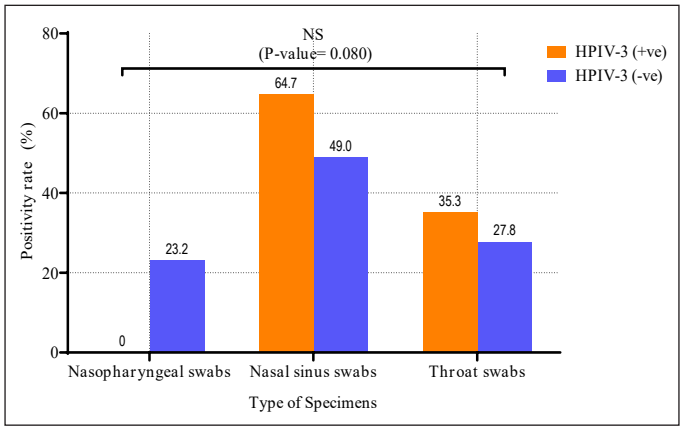

Figure 4.HPIV-3 Positivity Rate by Specimen Type

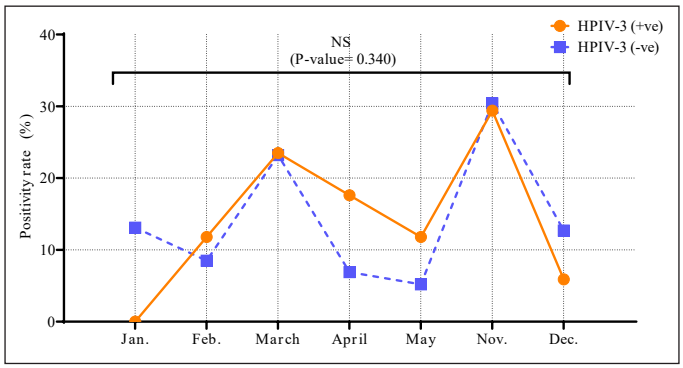

Figure 5.HPIV-3 Positivity Rate per Month

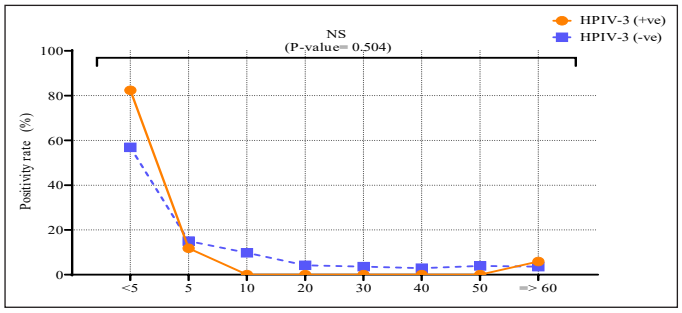

Figure 6.HPIV-3 Positivity Rate by Age (Years)

ISSN: 0019-5138
DOI: https://doi.org/10.24321/0019.5138.202612

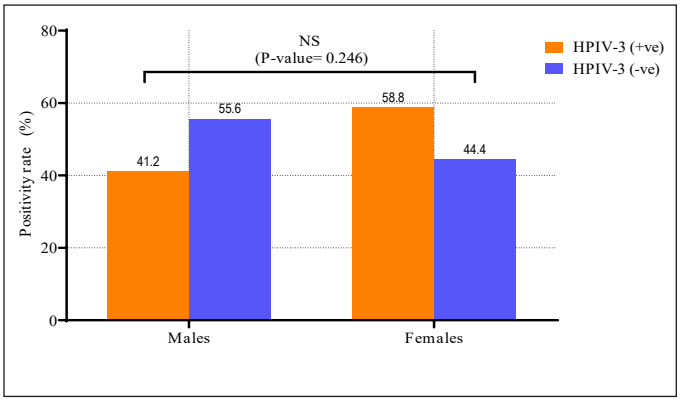

Figure 7.HPIV-3 Positivity Rate According to Gender

Discussion

This study's significance comes from it being the first comprehensive study conducted in the Iraqi province of Diyala, covering the most prevalent viruses causing RTIs and identified using advanced molecular techniques. Measles, diarrhoeal illnesses, and acute lower respiratory infection (ALRI) are among the three main causes of death. About 70% of deaths in children under five years of age are caused by diarrhoea and ALRI. International sanctions, food insecurity and malnutrition, and a lack of high-quality health services constitute the main causes.[15] Other factors that have exacerbated the situation include the presence of refugees and displaced persons, who continue to report inadequate living conditions and neglect of their general health. Other factors which are making matters worse involve the refugee's existence and people who were displaced and continued to complain about inadequate living circumstances and disregard for their general health. Moreover, bacterial pathogens superimposed on viral RTIs, especially those causing pneumonia and LRT infections, exacerbate the condition.[16]

Only a few studies conducted in Iraq evaluated the effects of HPIV-3 in children and other age groups. The current findings revealed that the molecular detection rate of HPIV-3 was 17 (5.3%), which is lower than the findings of Kadim,[14] who reported a higher detection rate of 13.21% in the province of Al-Muthanna, and Hassan et al.,[17] who reported a lower detection rate (4, 1.5%) of HPIV-3 among children in Kurdistan. Additionally, epidemiological studies conducted around the world have reported varying HPIV-3 detection rates; some of these studies are comparable to the present study, while other studies showed higher or lower detection rates. For example, Qatar reported a detection rate of 5.1%, Spain reported a rate of 2%, Beijing in China reported a rate of 4.48%, and Southern Taiwan reported a rate of 73.4%.[18–22] Data from the majority of studies, including the current one, indicated that HPIV-3 is the most common type and accounts for the majority of respiratory infections in various parts of the world.[23]

The type of clinical specimen is likely one of the factors influencing the detection rate. This is shown in the current investigation by the fact that nasal swabs outperformed nasopharyngeal swabs in identifying HPIV-3. This could be because all positive HPIV-3 samples were found in children younger than five years of age. The researcher used nasal and throat swabs for this group because nasopharyngeal swabs are difficult to use at this age due to discomfort and pain induction. Therefore, only elderly patients were tested using these swabs. Indumathi et al. demonstrated that 26 (11.2%) patients with influenza-like illness tested positive for the HPIV-3 serotype under similar conditions with regard to the use of nasal and throat swabs.[24] According to Hassan et al., a significant number of viral respiratory infections in children occurred in Iraqi Kurdistan between November and March, or late autumn to early spring.[17] Similarly, HPIV-3 exhibited a high detection rate during these months, with a notable peak in March. Global studies have documented seasonal patterns of HPIV-3, yet the incidence of cases in April and May appears to vary across different geographic regions. Some of these studies show that seasonal outbreaks happen in the spring after influenza epidemics, while others indicate that HPIV-3 peaks occur in the spring and summer seasons.[21,22,25,26]

Previous investigation has demonstrated that HPIV-3 is the most frequently diagnosed virus in hospitalised patients, particularly in young children.[5,27] It must be acknowledged that the current study yields comparable results. Other researchers have also reported similar findings.[18,22] In accordance with Jornist et al., HPIV-3 is the third most frequently found respiratory virus in the paediatric population and is the primary cause of respiratory infections in children under the age of five years.[21] In line with a Chinese study by Mao et al., HPIV-3 is the fifth most common virus that causes respiratory infections in children.[28] Furthermore, Argentinean researchers Goya et al. discovered that HPIV-3 was the second most common cause of respiratory viral infections in children, after HRSV.[29] In contrary to the current study's findings, which indicated a slight rise in the HPIV-3 positivity rate among females.

ISSN: 0019-5138
DOI: https://doi.org/10.24321/0019.5138.202612

These findings align with a Korean study [30] In contrary to the current study's findings, which indicated a slight rise in the HPIV-3 positivity rate among females. These findings align with a Korean study.[30] Though the differences in infection rates between the sexes were not statistically significant, a majority of other studies indicated that males had a higher HPIV-3 infection rate.[21,28,31]

Studies have demonstrated that simultaneous RTIs with two or more viruses are generally widespread among hospitalised patients, although it is unclear whether these infections are less serious or more serious than single virus infections.[32] Co-infection of HRSV with other respiratory viruses has been documented in numerous studies, with reported rates ranging from 4% to 53%.[33] As stated in the current study, one patient tested positive for both HPIV-3 and HRSV. In the report by Mao et al., three patients with bronchiolitis and pneumonia had HRSV co-infection with HPIV-3.[28] Additionally, HRSV was the most commonly co-detected pathogen with other viruses, appearing alongside HPIV-3 in five patients in a study.[34] The emergence of co-infection was caused by the overlapping seasonal distribution of these viruses. As was previously known, the co-occurrence of viral infections demonstrated a phenomenon called viral interference, wherein one virus inhibits the growth of another.[32]

Although the role of respiratory virus co-infections in multiple viral RTIs is unclear and debatable, multiple reports have confirmed that there is no correlation between co-viral infections and disease severity.[28,35] Conversely, other research demonstrated that co-infection with these viruses was significantly linked to longer symptom duration. This is particularly true for high-risk populations like children, the elderly, and people with compromised immune systems.[16,36,37] Nevertheless, multiplex RT-PCR showed that HRSV and HMPV were not co-detected. These results therefore contradict the majority of earlier studies, which suggested that most patients presented with dual infections[38–41] . Nevertheless, multiplex RT-PCR showed that HRSV and HMPV were not co-detected, so the current results contradict the majority of earlier research that suggested that most patients had two infections.[38–41]

The seasonal distribution of these viruses in this geographic area is most likely the primary cause of the low co-infection rate in this study. However, one patient was co-infected with HPIV-3 and HMPV. Therefore, the present findings concur with those of Zang et al.[41] and Williams et al.,[42] who showed that one patient had co-viral infection, and those of Mao et al.,[28] who discovered co-infection in three patients. Consequently, the double infection appeared as a result of the seasonal distribution overlapping of two viruses.

Conclusion

The study shows that HPIV-3 is the predominant strain, and dual infection with RSV is possible but rare. Additional prospective research and official monitoring would enhance our comprehension of HPIV in this region.

Authors' Contribution:

The author carried out all stages of the study, including research design, data collection, analysis of results, and drafting of the manuscript, and reviewed and approved the final version for publication

Declaration of Generative AI and AI-Assisted Technologies in the Writing Process: No generative tools or AI-assisted technologies were used in the preparation of this manuscript.

Source of Funding: None

Conflict of Interest: None

References

1. Hijano DR, Maron G, Hayden RT. Respiratory viral infections in patients with cancer or undergoing hematopoietic cell transplant. Front Microbiol. 2018;9:3097. [PubMed] [Google Scholar]
2. Li YT, Liang Y, Ling YS, Duan MQ, Pan L, Chen ZG. The spectrum of viral pathogens in children with severe acute lower respiratory tract infection: a 3-year prospective study in the pediatric intensive care unit. J Med Virol. 2019;91(9):1633-42. [PubMed] [Google Scholar]
3. Das S, Dunbar S, Tang YW. Laboratory diagnosis of respiratory tract infections in children–the state of the art. Front Microbiol. 2018;9:2478. [PubMed] [Google Scholar]
4. Gottlieb J. Community-acquired respiratory viruses. Curr Opin Organ Transplant. 2019;24(3):311-7. [PubMed] [Google Scholar]
5. Henrickson KJ. Parainfluenza viruses. Clin Microbiol Rev. 2003;16(2):242-64. [PubMed] [Google Scholar]
6. Branche AR, Falsey AR. Parainfluenza virus infection. Semin Respir Crit Care Med. 2016;37(4):538-54. [PubMed] [Google Scholar]
7. Burrell, C., Howard, C. and Murphy, F. (2017) Human parainfluenza virus. In: Burrell, C.J., Howard, C.R. and Murphy, F.A. (eds.) Fenner and White's Medical Virology. 5th ed. Academic Press: Elsevier Inc., pp. 373–390. Burrell C, Howard C, Murphy F. Human parainfluenza virus. In: Burrell CJ, Howard CR, Murphy FA, editors. Fenner and White's medical virology. 5th ed. Academic Press: Elsevier Inc.; 2017. 373 p.
8. Wang X, Li Y, Deloria-Knoll M, Madhi SA, Cohen C, Arguelles VL, Basnet S, Bassat Q, Brooks WA, Echavarria M, Fasce RA, Gentile A, Goswami D, Homaira N, Howie SR, Kotloff KL, Khuri-Bulos N, Krishnan A, Lucero MG, Lupisan S, Mathisen M, McLean KA, Mira-Iglesias A, Moraleda C, Okamoto M, Oshitani H, O'Brien KL, Owor BE, Rasmussen ZA, Rath BA, Salimi V, Sawatwong P,

Scott JA, Simoes EA, Sotomayor V, Thea DM, Treurnicht FK, Yoshida LM, Zar HJ, Campbell H, Nair H; Respiratory Virus Global Epidemiology Network. Global burden of acute lower respiratory infection associated with human parainfluenza virus in children younger than 5 years for 2018: a systematic review and meta-analysis. Lancet Glob Health. 2021;9(8):e1077-87. [PubMed] [Google Scholar]

9. De Zwart A, Riezebos-Brilman A, Lunter G, Vonk J, Glanville AR, Gottlieb J, Permpalung N, Kerstjens H, Alffenaar JW, Verschuuren E. Respiratory syncytial virus, human metapneumovirus, and parainfluenza virus infections in lung transplant recipients: a systematic review of outcomes and treatment strategies. Clin Infect Dis. 2022;74(12):2252-60. [PubMed] [Google Scholar]
10. Rafeek RA, Divarathna MV, Noordeen F. A review on disease burden and epidemiology of childhood parainfluenza virus infections in Asian countries. Rev Med Virol. 2021;31(2):e2164. [PubMed] [Google Scholar]
11. Nelson PP, Papadopoulos NG, Skevaki C. Respiratory viral pathogens. In: Janes SM, editor. Encyclopedia of respiratory medicine. Academic Press; 2022. p. 129-37. [Google Scholar]
12. Kim H, Hur M, Moon HW, Yun YM, Cho HC. Comparison of two multiplex PCR assays for the detection of respiratory viral infections. Clin Respir J. 2014;8(4):391-6. [PubMed] [Google Scholar]
13. Li ZJ, Zhang HY, Ren LL, Lu QB, Ren X, Zhang CH, Wang YF, Lin SH, Zhang XA, Li J, Zhao SW, Yi ZG, Chen X, Yang ZS, Meng L, Wang XH, Liu YL, Wang X, Cui AL, Lai SJ, Jiang T, Yuan Y, Shi LS, Liu MY, Zhu YL, Zhang AR, Zhang ZJ, Yang Y, Ward MP, Feng LZ, Jing HQ, Huang LY, Xu WB, Chen Y, Wu JG, Yuan ZH, Li MF, Wang Y, Wang LP, Fang LQ, Liu W, Hay SI, Gao GF, Yang WZ; Chinese Centers for Disease Control and Prevention (CDC) Etiology of Respiratory Infection Surveillance Study Team. Etiological and epidemiological features of acute respiratory infections in China. Nat Commun. 2021;12(1):5026. [PubMed] [Google Scholar]
14. Kadim, A.A. (2016) Molecular detection of Parainfluenza virus in infants and young children in Al-Muthanna Governorate. Master's dissertation. College of Science, Al-Muthanna University, Al-Muthanna, Iraq, p. 45 Kadim AA. Molecular detection of Parainfluenza virus in infants and young children in AL-Muthanna Governorate [dissertation]. College of Science, Muthanna University. AL-Muthanna Governorate, Iraq; 2016.
15. World Health Organization. WHO Communicable Disease Profile for Iraq. Communicable Disease Working Group on Emergencies, HQ Division of Communicable Disease Control, EMROWHO Office, Baghdad; 2003, p.

15. World Health Organization. WHO Communicable Disease Profile for Iraq. Communicable Disease Working Group on Emergencies, HQ Division of Communicable Disease Control, EMROWHO Office, Baghdad; 2003.
16. Hanada S, Pirzadeh M, Carver KY, Deng JC. Respiratory viral infection-induced microbiome alterations and secondary bacterial pneumonia. Front Immunol. 2018;9:2640. [PubMed] [Google Scholar]
17. Hassan DA, Rachid SK, Ziebuhr J. A single-center study of viral respiratory tract infections in hospitalized children from the Kurdistan region of Iraq. Glob Pediatr Health. 2018;5:2333794X18784996. [PubMed] [Google Scholar]
18. Godoy C, Peremiquel-Trillas P, Andrés C, Gimferrer L, Uriona SM, Codina MG, Armadans L, Martín MD, Fuentes F, Esperalba J, Campins M, Pumarola T, Antón A. A molecular epidemiological study of human parainfluenza virus type 3 at a tertiary university hospital during 2013-2015 in Catalonia, Spain. Diagn Microbiol Infect Dis. 2016;86(2):153-9. [PubMed] [Google Scholar]
19. Pan Y, Zhang Y, Shi W, Peng X, Cui S, Zhang D, Lu G, Liu Y, Wu S, Yang P, Wang Q. Human parainfluenza virus infection in severe acute respiratory infection cases in Beijing, 2014-2016: a molecular epidemiological study. Influenza Other Respir Viruses. 2017;11(6):564-8. [PubMed] [Google Scholar]
20. Janahi I, Abdulkayoum A, Almeshwesh F, Alkuwari M, Al Hammadi A, Alameri M. Viral aetiology of bronchiolitis in hospitalised children in Qatar. BMC Infect Dis. 2017;17(1):139. [PubMed] [Google Scholar]
21. Jornist I, Muhsen K, Ram D, Lustig Y, Levy V, Orzitser S, Azar R, Weil M, Indenbaum V, Sofer D, Mendelson E, Mandelboim M, Hindiyeh M. Characterization of human parainfluenza virus-3 circulating in Israel, 2012-2015. J Clin Virol. 2018;107:19-24. [PubMed] [Google Scholar]
22. Wu KW, Wang SM, Shen CF, Ho TS, Wang JR, Liu CC. Clinical and epidemiological characteristics of human parainfluenza virus infections of children in southern Taiwan. J Microbiol Immunol Infect. 2018;51(6):749-55. [PubMed] [Google Scholar]
23. Wang F, Zhao LQ, Zhu RN, Deng J, Sun Y, Ding YX, Tian R, Qian Y. Parainfluenza virus types 1, 2, and 3 in pediatric patients with acute respiratory infections in Beijing during 2004 to 2012. Chin Med J (Engl). 2015;128(20):2726-30. [PubMed] [Google Scholar]
24. Indumathi CP, Gunanasekaran P, Kaveri K, Arunagiri K, Mohana S, Sheriff AK, SureshBabu BV, Padmapriya P, Senthilraja R, Fathima G. Isolation & molecular characterization of human parainfluenza virus in Chennai, India. Indian J Med Res. 2015;142(5):583. [PubMed] [Google Scholar]
25. Fry AM, Curns AT, Harbour K, Hutwagner L, Holman RC, Anderson LJ. Seasonal trends of human parainfluenza

ISSN: 0019-5138
DOI: https://doi.org/10.24321/0019.5138.202612

viral infections: United States, 1990–2004. Clin Infect Dis. 2006;43(8):1016-22. [PubMed] [Google Scholar]
26. Zaki SR, Keating MK. Viral diseases. In: Zander DS, Farver CF, editors. Foundations in diagnostic pathology. 2nd ed. Pulmonary pathology. Elsevier; 2018. p. 244-88. [Google Scholar]
27. Gomez M, Mufson MA, Dubovsky F, Knightly C, Zeng W, Losonsky G. Phase-I study MEDI-534, of a live, attenuated intranasal vaccine against respiratory syncytial virus and parainfluenza-3 virus in seropositive children. Pediatr Infect Dis J. 2009;28(7):655-8. [PubMed] [Google Scholar]
28. Mao N, Ji Y, Xie Z, Wang H, Wang H, An J, Zhang X, Zhang Y, Zhu Z, Cui A, Xu S, Shen K, Liu C, Yang W, Xu W. Human parainfluenza virus-associated respiratory tract infection among children and genetic analysis of HPIV-3 strains in Beijing, China. PLoS One. 2012;7(8):e43893. [PubMed] [Google Scholar]
29. Goya S, Mistchenko AS, Viegas M. Phylogenetic and molecular analyses of human parainfluenza type 3 virus in Buenos Aires, Argentina, between 2009 and 2013: the emergence of new genetic lineages. Infect Genet Evol. 2016;39:85-91. [PubMed] [Google Scholar]
30. Park G, Lee JY, Lee SY, Kim JH, Kang JH, Choi UY. Seroprevalence of human parainfluenza virus types 1–4 among healthy children under 5 years of age in Korea. Viral Immunol. 2018;31(5):352-7. [PubMed] [Google Scholar]
31. Shi W, Cui S, Gong C, Zhang T, Yu X, Li A, Chen M, Luo M, Huang F. Prevalence of human parainfluenza virus in patients with acute respiratory tract infections in Beijing, 2011–2014. Influenza Other Respir Viruses. 2015;9(6):305. [PubMed] [Google Scholar]
32. Pinky L, Dobrovolny HM. Coinfections of the respiratory tract: viral competition for resources. PLoS One. 2016;11(5):e0155589. [PubMed] [Google Scholar]
33. Cai XY, Wang Q, Lin GY, Cai ZW, Lin CX, Chen PZ, Zhou XH, Xie JC, Lu XD. Respiratory virus infections among children in South China. J Med Virol. 2014;86(7):1249-55. [PubMed] [Google Scholar]
34. Liu WK, Liu Q, Chen DH, Liang HX, Chen XK, Huang WB, Qin S, Yang ZF, Zhou R. Epidemiology and clinical presentation of the four human parainfluenza virus types. BMC Infect Dis. 2013;13:28. [PubMed] [Google Scholar]
35. Lim FJ, de Klerk N, Blyth CC, Fathima P, Moore HC. Systematic review and meta-analysis of respiratory viral coinfections in children. Respirology. 2016;21(4):648-55. [PubMed] [Google Scholar]
36. Cho HJ, Shim SY, Son DW, Sun YH, Tchah H, Jeon IS. Respiratory viruses in neonates hospitalized with acute lower respiratory tract infections. Pediatr Int. 2013;55(1):49-53. [PubMed] [Google Scholar]
37. Georgakopoulou VE. Insights from respiratory virus co-infections. World J Virol. 2024;13(4):98600. [PubMed] [Google Scholar]
38. Ali SA, Williams JV, Chen Q, Faori S, Shehabi A, Jundi EA, Khuri-Bulos N, Halasa N. Human metapneumovirus in hospitalized children in Amman, Jordan. J Med Virol. 2010;82(6):1012-6. [PubMed] [Google Scholar]
39. Kouni S, Karakitsos P, Chranioti A, Theodoridou M, Chrousos G, Michos A. Evaluation of viral co-infections in hospitalized and non-hospitalized children with respiratory infections using microarrays. Clin Microbiol Infect. 2013;19(8):772-7. [PubMed] [Google Scholar]
40. Atyah NS, Fadhil HY, Al-Hamadani FG, Auffi IM, Al-azzawi MA. Molecular detection of subfamily Pneumovirinae among children with flu-like illness by using RT-PCR. Curr Res Microbiol Biotechnol. 2017;5(5):1239-44. [Google Scholar]
41. Zhang L, Liu W, Liu D, Chen D, Tan W, Qiu S, Xu D, Li X, Liu T, Zhou R. Epidemiological and clinical features of human metapneumovirus in hospitalised paediatric patients with acute respiratory illness: a cross-sectional study in Southern China, from 2013 to 2016. BMJ Open. 2018;8(2):e019308. [PubMed] [Google Scholar]
42. Williams JV, Edwards KM, Weinberg GA, Griffin MR, Hall CB, Zhu Y, Szilagyi PG, Wang CK, Yang CF, Silva D, Ye D, Spaete RR, Crowe JE Jr. Population-based incidence of human metapneumovirus infection among hospitalized children. J Infect Dis. 2010;201(12):1890-8. [PubMed] [Google Scholar]

ISSN: 0019-5138
DOI: https://doi.org/10.24321/0019.5138.202612