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Human Metapneumovirus Seasonality and Co-Circulation with Respiratory Syncytial Virus — United States, 2014–2024

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Abstract

Human metapneumovirus (hMPV) infections cause acute respiratory illness and lower respiratory tract disease. Respiratory syncytial virus (RSV) is a closely related virus within the *Pneumoviridae* family, and hMPV and RSV infections are associated with similar clinical manifestations. Although no specific antiviral therapies or vaccines exist for hMPV, vaccines and monoclonal antibody products are available to protect against severe RSV disease. This report summarizes hMPV circulation relative to the timing of RSV epidemics before, during, and after the COVID-19 pandemic. Polymerase chain reaction testing results reported to the National Respiratory and Enteric Virus Surveillance System during July 2014–June 2024, were analyzed. Before the COVID-19 pandemic, the median hMPV season onset, peak, and offset occurred in early January, late March, and early June, respectively (median duration = 21 weeks). The 2021–22 season was atypically long (35 weeks); seasonality reverted to more typical patterns during the 2022–23 and 2023–24 seasons. In the two COVID-19 pandemic seasons (2021–22 and 2022–23) and one postpandemic season (2023–24), RSV offsets occurred earlier in January (2021–22 and 2022–23) or March (2023–24) than before the pandemic, when the median offsets occurred in April. The annual interval from peak RSV to peak hMPV circulation increased from a prepandemic median of 11.5 weeks (range = 2–17 weeks) to 19 weeks (range = 19–20 weeks) during and after the pandemic. Fewer than 5 weeks of cocirculation of RSV and hMPV occurred in most regions during the 2022–23 and 2023–24 seasons. Real-time surveillance of RSV and hMPV co-circulation patterns can help guide clinician-directed testing and supportive care, optimize the use of prevention products, prompt detection of and response to outbreaks, and help ensure health care system preparedness for seasonal increases in illnesses.

Introduction

Human metapneumovirus (hMPV) was first identified as a cause of respiratory illness in 2001. Children, older adults, and persons with compromised immune systems are at higher risk for hMPV-associated lower respiratory tract infections (bronchitis, bronchiolitis, and pneumonia) (*1*). hMPV can also exacerbate asthma and chronic obstructive pulmonary disease. Among adults in the United States, an estimated 12.1 hMPV-associated hospitalizations per 100,000 persons occurred each year during 2016–2019 (*2*). hMPV and respiratory syncytial virus (RSV) belong to the *Pneumoviridae* family* and cause similar respiratory illnesses (*3*). During 2008–2014, hMPV circulated from January to May in the United States (*4*). hMPV circulation has consistently followed seasonal RSV epidemics which, before the COVID-19 pandemic, typically occurred during October–April, with winter co-circulation of the viruses. However, the COVID-19 pandemic was associated with disruptions in hMPV and RSV seasonality: the 3% positivity threshold used to calculate the beginning and end of the season, and thus describe seasonality, was not met

* https://ictv.global/report/chapter/pneumoviridae/pneumoviridae

Continuing Education examination available at https://www.cdc.gov/mmwr/mmwr_continuingEducation.html

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during the 2020–21 season (5). This report describes hMPV seasonal circulation patterns during July 2014–June 2024 and identifies changes in national and regional hMPV and RSV co-circulation during and after the pandemic. Understanding co-circulation patterns could help ensure that public health officials detect and respond to outbreaks promptly and help ensure that health care systems are prepared for seasonal increases in the incidence of viral respiratory illnesses.

Methods

Data Source

The National Respiratory and Enteric Virus Surveillance System (NREVSS)[†] is a passive, laboratory-based surveillance system that monitors viruses circulating in the United States. Each week, participating clinical, commercial, and public health laboratories voluntarily report aggregate numbers of tests performed and positive detections to NREVSS by testing method (antigen detection, polymerase chain reaction [PCR] testing, or virus isolation).

Numbers of hMPV and RSV PCR tests and detections reported to NREVSS during July 2014–June 2024 were analyzed. A surveillance year was defined as July–June.[§] Data from laboratories that consistently reported to the system (i.e., with an average of at least 10 PCR tests per week for ≥30 of 52 weeks of the surveillance year) were included in the analyses of each virus. The number of laboratories with consistent reporting of hMPV PCR test results to NREVSS increased from 62 in 34 states during the 2014–15 season to 122 in 38 states during the 2023–24 season. The number of laboratories with consistent reporting of RSV PCR test results increased from 77 in 36 states during the 2014–15 season to 239 in 44 states during the 2023–24 season.

Analysis of Seasonality

For each virus, the weekly percentage of positive test results was calculated[¶] to assess virus circulation, and smoothed trend data were visualized with 3-week (national) and 5-week (regional) centered moving averages. hMPV and RSV season onsets and offsets were defined as the first and last of ≥2 consecutive weeks with ≥3% positive test results, respectively, and the season peak was defined as the week with the highest percentage of positive test results. The median onset, peak, and offset for the prepandemic (2014–15 to 2019–20) seasons were compared with the two COVID-19 pandemic seasons (2021–22 and 2022–23) and one postpandemic season (2023–24). The change in hMPV circulation during the 2020–21 COVID-19 pandemic surveillance year was described, but the season was not analyzed because of the disruption of circulation (i.e., the

[†] https://www.cdc.gov/nrevss/php/dashboard/index.html

[§] For RSV, the typical winter epidemic was absent in 2020–21, and the 2021–22 epidemic began in the spring; therefore, the surveillance years for 2021–22 and 2022–23 (COVID-19 pandemic seasons) were defined from early March (week 9) to late February (week 8) of the following year.

[¶] The weekly percentage of positive test results was calculated by dividing the total number of positive test results by the total number of tests performed each week, multiplied by 100.

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3% positivity threshold was not exceeded) (*5*). The number of weeks when RSV and hMPV seasons overlapped was estimated as each season's interval before the RSV offset week (≥3% positive test results in the last of ≥2 consecutive weeks) and after hMPV onset week (≥3% positive results in the first of ≥2 consecutive weeks), nationally and by U.S. Department of Health and Human Services (HHS) Region.** All data analyses and visualizations were performed using R software (version 4.4.0; R Foundation). This activity was reviewed by CDC, deemed not research, and was conducted consistent with applicable federal law and CDC policy.††

Results

hMPV Circulation

The prepandemic six-season median of the median annual number of tests performed per reporting laboratory was 3,838.5; the three-season median number of tests performed per reporting laboratory during and after the pandemic increased to 4,634 (Table 1). Before the pandemic, a median of 476,169.5 hMPV tests were reported per surveillance year (median positive results = 3.2%). During and after the pandemic, the median number of hMPV tests reported increased by 92% to 914,660 per surveillance year (median positive results = 3.5%). The early COVID-19 pandemic was associated with a 98% decline in hMPV circulation, with 370 (0.07%) of 511,902 hMPV PCR test results reported as positive during the 2020–21 season (Figure).

The prepandemic median hMPV season onset, peak, and offset occurred in early January, late March, and early June, respectively (Table 2), and the median season duration was 21 weeks (range = 15–25 weeks). The 2021–22 hMPV season was atypical, with geographically variable peaks.§§ As a result, the duration of the 2021–22 season (35 weeks) was longer than that of other seasons. In 2022–23 and 2023–24, hMPV seasonality shifted to more typical circulation patterns, similar to prepandemic seasons with peaks in March and April, respectively.

RSV Circulation

Before the pandemic, the median onset, peak, and offset for RSV seasons occurred in late October, late December, and late April, respectively (Table 2). In the 2021–22 and 2022–23 seasons, RSV onset shifted to late May and mid-June, but the seasonal peaks during 2021–22 (late July) and 2022–23 (early November) differed considerably. The duration of both the 2021–22 and 2022–23 RSV seasons was longer (33 and 32 weeks, respectively) compared with prepandemic seasons (median = 26.5 weeks; range = 23–28 weeks). The 2023–24 RSV season onset occurred much later in October, but the

** https://www.hhs.gov/about/agencies/iea/regional-offices/index.html
†† 45 C.F.R. part 46.102(l)(2), 21 C.F.R. part 56; 42 U.S.C. Sect. 241(d); 5 U.S.C. Sect. 552a; 44 U.S.C. Sect. 3501 et seq.

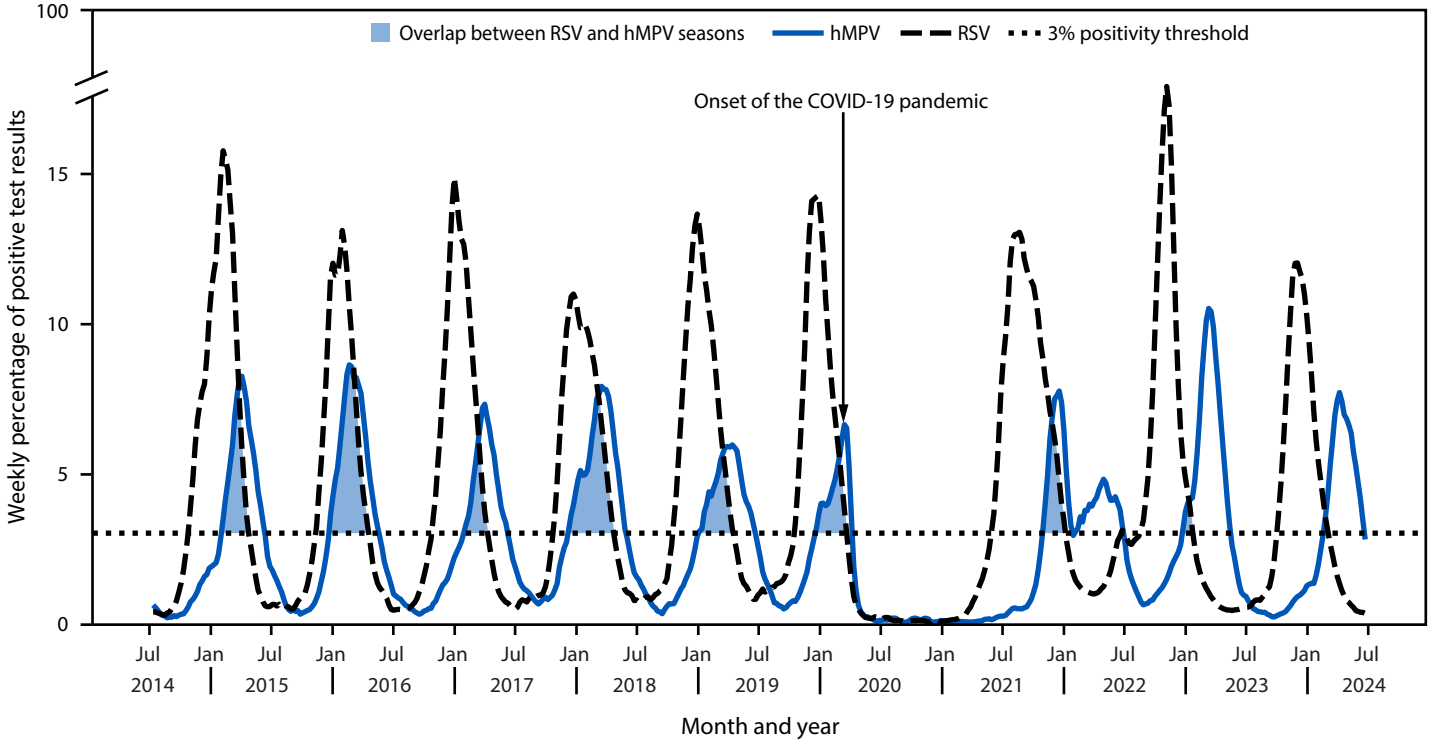
§§ Peaks occurred in early December (weeks 48 and 49) in HHS Regions 4 and 6, early January (week 52) in Region 7, early March (week 10) in Region 9, late March (weeks 11 and 12) in Regions 5 and 8, late April (week 17) in Region 3, late May (week 21) in Region 1, and early June (week 22) in Regions 2 and 10.

TABLE 1. Numbers of reporting laboratories, human metapneumovirus polymerase chain reaction tests performed, and positive test results reported, by surveillance year, before, during, and after the COVID-19 pandemic — National Respiratory and Enteric Virus Surveillance System, United States, 2014–2024

Surveillance yr	No. of states reporting	No. of laboratories consistently reporting	No. of tests performed	Median no. of tests performed per laboratory (IQR)	No. of positive test results (%)	Minimum no. of weekly tests performed	Maximum no. of weekly tests performed	Minimum no. of weekly positive tests (%)	Maximum no. of weekly positive tests (%)
Pre–COVID-19 pandemic									
2014–2015	34	62	297,284	3,620 (3,640)	9,078 (3.1)	2,932	9,475	3 (0.1)	583 (8.4)
2015–2016	37	81	379,594	3,877 (3,609)	15,583 (4.1)	3,559	13,202	10 (0.2)	1,084 (9.2)
2016–2017	40	91	480,520	3,896 (4,461)	14,688 (3.1)	4,347	16,902	19 (0.3)	911 (7.6)
2017–2018	39	92	471,819	3,800 (4,643)	19,524 (4.1)	4,152	16,982	34 (0.6)	1,036 (8.1)
2018–2019	42	97	509,074	3,740 (5,402)	16,610 (3.3)	4,444	14,938	12 (0.2)	895 (6.2)
2019–2020	40	100	560,821	4,206 (5,259)	16,640 (3.0)	4,247	28,290	2 (<0.1)	1,966 (7.0)
Six-season median	39.5	91.5	476,169.5	3,838.5*	16,096.5 (3.2)†	4,199.5	15,920	11 (0.2)†	973.5 (7.8)†
COVID-19 pandemic									
2020–2021	35	109	511,902	3,185 (4,504)	370 (<0.1)	5,005	12,219	1 (<0.1)	37 (0.3)
2021–2022	40	121	897,316	4,479 (6,647)	31,806 (3.5)	12,221	28,216	34 (0.3)	1,795 (7.7)
2022–2023	39	118	914,660	4,634 (6,986)	32,038 (3.5)	10,620	28,436	72 (0.5)	1,927 (10.8)
Post–COVID-19 pandemic§									
2023–2024†	38	122	926,652	4,674 (7,816)	23,889 (2.6)	10,763	25,274	31 (0.2)	1,472 (7.9)
Three-season median¶	39	121	914,660	4,634*	31,806 (3.5)†	10,763	28,216	34 (0.3)†	1,795 (7.9)*

* The median of the median number of tests performed annually per laboratory.
† The median of the number, minimum, and maximum (percentage) of positive test results.
§ The COVID-19 pandemic public health emergency declaration ended May 2023.
¶ During and after the pandemic, the median includes the 2021–22, 2022–23, and 2023–24 seasons.

FIGURE. Weekly percentage of positive test results* for respiratory syncytial virus and human metapneumovirus — National Respiratory and Enteric Virus Surveillance System, United States, July 2014–June 2024†



Abbreviations: hMPV = human metapneumovirus; RSV = respiratory syncytial virus.
* Data were smoothed using a 3-week, centered moving average.
† The overlap between RSV and hMPV seasons represents the period before the RSV offset week (≥3% positive test results in the last of ≥2 consecutive weeks) and after the hMPV onset week (≥3% positive test results in the first of ≥2 consecutive weeks), nationally.

TABLE 2. Respiratory syncytial virus and human metapneumovirus season onset, peak, offset, and duration, by surveillance year, before, during, and after the COVID-19 pandemic — National Respiratory and Enteric Virus Surveillance System, United States, 2014–2024*

	Onset mo (surveillance wk)†		Peak mo (surveillance wk)†		Offset mo (surveillance wk)†		Season duration, wks	
NREVSS yr	**RSV**	**hMPV**	**RSV**	**hMPV**	**RSV**	**hMPV**	**RSV**	**hMPV**
Pre–COVID-19 pandemic								
2014–2015	Oct (43)	Feb (5)	Feb (6)	Apr (14)	Apr (16)	Jun (22)	27	18
2015–2016	Nov (45)	Dec (51)	Feb (5)	Feb (7)	Apr (15)	May (20)	23	22
2016–2017	Oct (42)	Jan (4)	Dec (52)	Mar (12)	Apr (15)	Jun (23)	26	20
2017–2018	Oct (42)	Dec (49)	Dec (51)	Mar (10)	Apr (16)	May (21)	27	25
2018–2019	Oct (41)	Jan (1)	Dec (51)	Apr (16)	Apr (16)	Jun (24)	28	24
2019–2020	Oct (42)	Dec (52)	Dec (51)	Mar (12)	Mar (12)	Apr (14)	23	15
Six-season median	**Oct (42)**	**Jan (53)**	**Dec (52)**	**Mar (12)**	**Apr (16)**	**Jun (22)**	**26.5**	**21**
COVID-19 pandemic§								
2021–2022	May (21)	Oct (43)	Jul (30)	Dec (50)	Jan (1)	Jun (25)	33	35¶
2022–2023	Jun (24)	Dec (52)	Nov (44)	Mar (11)	Jan (3)	May (18)	32	19
Post–COVID-19 pandemic**								
2023–2024	Oct (40)	Feb (8)	Nov (47)	Apr (14)	Mar (9)	Jun (24)	22	17

Abbreviations: hMPV = human metapneumovirus; NREVSS = National Respiratory and Enteric Virus Surveillance System; RSV = respiratory syncytial virus.
* Using crude (unsmoothed) data, hMPV and RSV season onsets and offsets were defined as the first and last of ≥2 consecutive weeks, respectively, with ≥3% positive test results; the season peak was the week with the highest percentage of positive test results.
† MMWR surveillance weeks can be found online. https://ndc.services.cdc.gov/wp-content/uploads/2021/02/MMWR_Week_overview.pdf
§ The 2020–21 hMPV and RSV seasons were excluded because of disruptions in virus circulation associated with the COVID-19 pandemic.
¶ During 2021–22, an atypical hMPV season occurred with peaks in early December (weeks 48 and 49) in U.S. Department of Health and Human Services Regions 4 and 6, early January (week 52) in Region 7, early March (week 10) in Region 9, late March (weeks 11 and 12) in Regions 5 and 8, late April (week 17) in Region 3, late May (week 21) in Region 1, and early June (week 22) in Regions 2 and 10. As a result, the duration of the 2021–22 season (35 weeks) was longer than other seasons. https://www.hhs.gov/about/agencies/iea/regional-offices/index.html
** The COVID-19 pandemic public health emergency declaration ended May 2023.

Summary

What is already known about this topic?

Human metapneumovirus (hMPV) and respiratory syncytial virus (RSV) are members of the *Pneumoviridae* family and cause similar illnesses. In the United States, RSV typically circulates from fall until spring, and hMPV typically circulates from winter through spring.

What is added by this report?

Circulation of both hMPV and RSV declined significantly during the 2020–21 respiratory virus season when the COVID-19 pandemic began. During the 2022–23 and 2023–24 seasons, RSV season offsets have been occurring earlier than usual in late winter, and typical hMPV circulation patterns have returned, with peak circulation in spring.

What are the implications for public health practice?

Understanding hMPV and RSV co-circulation patterns could guide timing and prioritization of clinician-directed testing, prompt detection of and response to outbreaks, and help ensure preparedness of health care systems for seasonal increases in respiratory viral illnesses.

November seasonal peak was similar to that during the 2022–23 season. In the two pandemic and one postpandemic seasons, RSV offsets occurred earlier in January or March compared with the prepandemic median offset in April.

Overlap in RSV and hMPV Seasons

Before the pandemic, RSV and hMPV seasons overlapped considerably (Figure), with hMPV season onset occurring a median of 13.5 weeks before RSV offset (range = 11–19 weeks). During and after the pandemic, the median period of overlap in RSV and hMPV seasons was 3 weeks (range = 1–10 weeks). hMPV peak circulation consistently followed that of RSV by a median of 11.5 weeks before the pandemic (range = 2–17 weeks). During and after the pandemic, peak hMPV circulation followed RSV by a median of 19 weeks (range = 19–20 weeks), representing an additional 7.5 weeks between peaks.

RSV and hMPV season overlap varied regionally (Supplementary Figure, https://stacks.cdc.gov/view/cdc/177080#tabs-3). Before the pandemic, the median overlap ranged from 9–13 weeks (HHS Regions 1, 2, 3, 4, 5, 9, and 10) to 14–19 weeks (Regions 6, 7, and 8). During the 2021–22 season, periods of overlap varied from 0 weeks (Regions 2 and 10) and 1–4 weeks (Regions 5 and 9) to 5–8 weeks (Regions 1, 3, 4, 7, and 8) and 12 weeks (Region 6). In the 2022–23 and 2023–24 seasons, an overlap of 0–4 weeks was most common in all regions, except Region 6 (12 weeks) and Region 9 (6 weeks) during the 2022–23 season.

Discussion

Before the COVID-19 pandemic, co-circulation of hMPV and RSV occurred during the winter months. However, seasonality for respiratory viruses was disrupted during the pandemic (*5*,*6*). RSV season offsets in early winter persisted through 2023–24, resulting in minimal overlap in hMPV and RSV circulation and an additional 7.5 weeks between seasonal peaks during and after the pandemic. Because RSV seasonality is returning to typical patterns, a higher degree of co-circulation of RSV and hMPV in 2024–25 and future seasons is expected. As of the week ending March 22, 2025, the RSV (4.4% positive test results) and hMPV (5.5% positive test results) seasons have overlapped for 5 weeks nationally. During future periods of co-circulation, the combined incidence of these respiratory illnesses might be higher than they were during the COVID-19 pandemic, when RSV and hMPV circulated separately. A meta-analysis published in 2020 found that RSV and hMPV co-infections were associated with higher odds of admission to pediatric intensive care units (7).

hMPV and RSV, both members of the *Pneumoviridae* family, cause acute respiratory illnesses and severe disease similarly in older adults and immunocompromised patients. However, risk groups and clinical management are different in pediatric populations. Children hospitalized with hMPV are significantly older than those hospitalized with RSV (*8*,*9*); unlike for hMPV, very young infants are at highest risk for severe RSV-associated disease. Overall, diagnoses of bronchiolitis and requirement of high-flow respiratory support are more frequent in children with RSV, whereas pneumonia diagnoses, and mechanical ventilation requirements are more frequent in children with hMPV (New Vaccine Surveillance Network, unpublished data, 2025).

Limitations

The findings in this report are subject to at least three limitations. First, the threshold of 3% positive test results is an imprecise measure of seasonality, particularly at the local level, where the timing of circulation varies (*10*). Second, NREVSS is a passive and voluntary surveillance system; therefore, participating laboratories vary from season to season and might not be representative of all geographic areas (*4*). More laboratories reporting during and after the pandemic and increasing numbers of tests contributed to a larger number of hMPV detections and a higher percentage of positive results over time. These changes likely represent the combined effects of increased testing capacity and broader use of multipathogen testing panels driven by COVID-19 testing. This expanded ability to identify

hMPV might have led to the detection of cases that would have otherwise remained etiologically undiagnosed in previous years. Thresholds for seasonality could also be affected by increased testing. Finally, patient demographic data are not collected in NREVSS, precluding analysis of hMPV circulation patterns across different population groups (e.g., proportions of tests performed for children and adults are unknown).

Implications for Public Health Practice

Near real-time surveillance data are vital for monitoring hMPV, RSV, and other causes of seasonal surges in respiratory illness. Understanding hMPV seasonality and the timing of hMPV and RSV co-circulation, especially that co-circulation has declined since the COVID-19 pandemic, can guide the timing and prioritization of clinician-directed testing, supportive care needs, and health care system preparedness. Currently, no licensed antiviral therapies or vaccines are available for hMPV, whereas licensed RSV vaccines and monoclonal antibody products are expected to reduce the incidence of severe RSV disease in infants and older adults in the coming years. Future incidence studies could estimate the effect of prevention products during periods of co-circulation.

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Epidemiology of Symptomatic Human Metapneumovirus Infection in the CASCADIA Community-Based Cohort — Oregon and Washington, 2022–2024

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Abstract

Human metapneumovirus (hMPV) is an important cause of respiratory illness. However, information about hMPV incidence, patient characteristics, and symptoms outside hospital settings is limited. During June 2022–March 2024, participants aged 6 months–49 years who were enrolled in the CASCADIA community-based cohort study submitted weekly illness surveys and nasal swabs, and completed follow-up illness surveys. Swabs collected 0–3 days before reporting new or worsening symptoms were tested for hMPV and other respiratory viruses by multiplex polymerase chain reaction. Incidence was analyzed using an exponential survival model. Among 3,549 participants, 306 had symptomatic hMPV infection, representing an average of 7.5 cases per 100 persons per year (95% CI = 6.7–8.4). Incidence was highest during January–March (adjusted hazard ratio [aHR] = 4.3; 95% CI = 3.0–6.0) compared with October–December, and among those aged 2–4 years (aHR = 5.8; 95% CI = 3.8–9.0) compared with those aged ≥40 years. The most frequently reported symptoms were cough (80.4%) and nasal congestion (71.9%). Among 252 (82.4%) participants who completed a post-illness follow-up survey, 68 (27.0%) missed work, school, or child care facility attendance. Together, these findings indicate that hMPV is a common cause of respiratory illness during late winter to spring, particularly among young children, and frequently disrupts daily activities. Understanding hMPV epidemiology can guide surveillance definitions, clinical testing, and prioritization of prevention strategies.

Introduction

Infection with human metapneumovirus (hMPV), a member of the *Pneumoviridae* family, causes respiratory illness among children and adults, leading to substantial burdens of hospitalizations worldwide (*1*). However, health care providers do not routinely test for hMPV in most clinical settings, treatment remains supportive, and information about the epidemiology of symptomatic infections outside health care settings is limited. Although no currently approved vaccines or treatments are available for hMPV in the United States, several such products are under development (*2*). This report summarizes the epidemiology of symptomatic hMPV infection among participants in a cohort study designed to characterize respiratory virus infections in the community.

Methods

Data Source

During 2022–2023, Oregon and Washington residents aged 6 months–49 years were invited to enroll in CASCADIA, a prospective, community-based cohort study (*3*). Participants in households with multiple members were prioritized for enrollment, although participation was not required for all household members. During June 2022–March 2024, participants completed an enrollment survey, followed by weekly nasal swabs (collected by participants or caregivers) and weekly electronic surveys that asked whether participants had experienced any new illness. Swabs were routinely tested for SARS-CoV-2, respiratory syncytial virus, and influenza virus; swabs that tested positive for these viruses or that were associated with new illness were also tested for hMPV and other respiratory pathogens using multiplex polymerase chain reaction (PCR)* (*3*).

Identification of hMPV Infections

A symptomatic hMPV infection was defined as the occurrence of any new or worsening symptoms† reported by a participant 0–3 days after collection of an hMPV-positive nasal swab, provided that the swab was collected 2 days before through 7 days after reported illness onset.§ Participants who reported new illness were invited to complete a 14-day follow-up survey to assess health care usage and absenteeism from work, school, or child care facility.

Calculation of hMPV Incidence and Identification of Factors Associated with Infection

Incidence of symptomatic hMPV infection was calculated as cases per 100 persons per year of follow-up. Follow-up time

* Real-Time PCR OpenArray assay tested for hMPV; SARS-CoV-2; influenza A, B, and C; respiratory syncytial viruses A and B; adenovirus; *Chlamydophila pneumoniae* or *Mycoplasma pneumoniae*; human enterovirus (type unspecified); human enterovirus D68; human coronavirus 229E, HKU1, NL63, and OC43; human parainfluenza virus; rhinovirus; and *Streptococcus pneumoniae*.

† Included one or more of the following: fever or chills; cough; shortness of breath or difficulty breathing; fatigue; muscle or body aches; headache, new loss of taste or smell; sore throat; congestion or runny nose; nausea or vomiting; diarrhea; persistent pain or pressure in the chest; and pale, gray, or blue-colored skin, lips, or nail beds.

§ Date of a new hMPV infection was based on reported illness onset, when the onset was ≥30 days since any previous hMPV infection.

was included between qualifying survey responses for each participant. To enable ascertainment of the analysis outcome, qualifying responses were defined as those indicating no new illness, or new illness with a nasal swab collected 0–3 days before the survey, provided that the swab was also collected 2 days before through 7 days after illness onset and had multiplex PCR test results. Follow-up time was censored in the event of a gap between qualifying survey responses of >14 days, and from onset of any symptomatic hMPV infection until 30 days later.

To assess factors associated with risk of symptomatic hMPV infection over time, incidence was modeled as a survival function using an exponential distribution. A random effects term (θ) with a gamma distribution (a continuous probability distribution used to model time-to-event data) was used to allow incidence to cluster within households; household clustering was assumed to occur if θ was greater than zero, using a significance threshold of $p<0.05$.

The model was adjusted for age group, sex, race and ethnicity, year, quarter of the year,[¶] reported household size, household income, and presence of underlying health conditions,[**] all defined a priori.[††] Detections of hMPV alone and codetections with other respiratory pathogens were included in the main analysis.

Among all infections with detection of hMPV, univariable logistic regression was used to compare differences in symptoms, health care usage, and illness-related absenteeism between persons aged <18 and ≥18 years.[§§] To exclude symptoms or illnesses with codetected pathogens, analyses were repeated and restricted to the subset of participants with detections of only hMPV. Data were analyzed using Stata (version 18.5; StataCorp). This study was reviewed and approved by the Kaiser Permanente Northwest Region Institutional Review Board; CDC deferred to this institution's determination. All participants in the study provided written consent.[¶¶]

Results

Characteristics of Study Participants

Among 19,096 illness episodes reported by the 3,620 enrolled participants, 16,508 (86.4%) reported by 3,549 participants were linked to a swab that was tested for hMPV and met analysis criteria. Median follow-up time was 1.3 years per participant (IQR follow-up = 0.9–1.5 years; 4,072 person-years total). Among those included, median age at enrollment was 17 years (IQR = 9–41 years), 2,072 (58.4%) participants were female, and 2,496 (70.3%) were non-Hispanic White. Overall, 2,450 (69.0%) participants had an annual household income ≥$100,000, and 3,307 (93.2%) reported living in households with three or more members. The median number of household members included in the analysis was three (range = one to eight), with a median of two adults (range = one to four) and two children (range = one to six) per household.

During the follow-up period, 306 symptomatic hMPV infections were identified among 221 children (aged 6 months–17 years) and 85 adults (aged 18–49 years) (Table 1); 186 (60.8%) detections were of only hMPV, and 120 (39.2%) were detections of hMPV and other pathogens. No participants had repeat infections during the study period. Among 293 (95.8%) symptomatic hMPV infections in households with multiple members included in the analysis, 101 (34%) occurred within 7 days of another symptomatic infection in the same household.

Overall incidence of symptomatic hMPV infection was 7.5 per 100 persons per year (95% CI = 6.7–8.4), peaking during January–March (incidence = 16.3; 95% CI = 14.3–18.7) (Figure). Incidence was highest among children aged 2–4 years (19.5; 95% CI = 14.9–25.7) and lowest among adults aged ≥40 years (3.8; 95% CI = 2.9–5.0). During January–March, incidence among children aged 2–4 years was 41.3 (95% CI = 29.2–58.4) (Supplementary Figure, https://stacks.cdc.gov/view/cdc/177080#tabs-3).

In the adjusted survival model, higher incidence was associated with ages 2–4 years (adjusted hazard ratio [aHR] = 5.8; 95% CI = 3.8–9.0), 6–23 months (aHR = 3.7; 95% CI = 1.8–7.6), 5–11 years (aHR = 3.1; 95% CI = 2.2–4.5), and 12–17 years (aHR = 2.0; 95% CI = 1.4–3.1), compared with age ≥40 years (Table 1). Incidence was also associated with season and, compared with October–December, was highest during January–March (aHR = 4.3; 95% CI = 3.0–6.0) and lowest during July–September (aHR = 0.4; 95% CI = 0.2–0.9). The random effects term (θ) that was used to model variation among households was greater than zero ($p<0.001$), indicating that incidence was correlated within households, and differed among households.[***]

Symptoms reported among persons with symptomatic hMPV infection included cough (80.4%), nasal congestion (71.9%), sore throat (38.6%), and shortness of breath (7.2%) (Table 2). Compared with adults aged ≥18 years, cough and fever were more likely to be reported among children (odds ratio [OR] = 2.9 and 2.6, respectively), whereas nasal

[¶] Quarters were defined as Q1 (January–March), Q2 (April–June), Q3 (July–September), and Q4 (October–December).

[**] Includes asthma, chronic obstructive pulmonary disease, heart disease, congenital heart disease, heart failure, Down syndrome, hypertension, liver condition, weak or failing kidneys, cancer, arthritis, stroke, deep vein thrombosis or pulmonary embolism, sickle cell disease or thalassemia, weakened immune system, depression or anxiety, or thyroid issues.

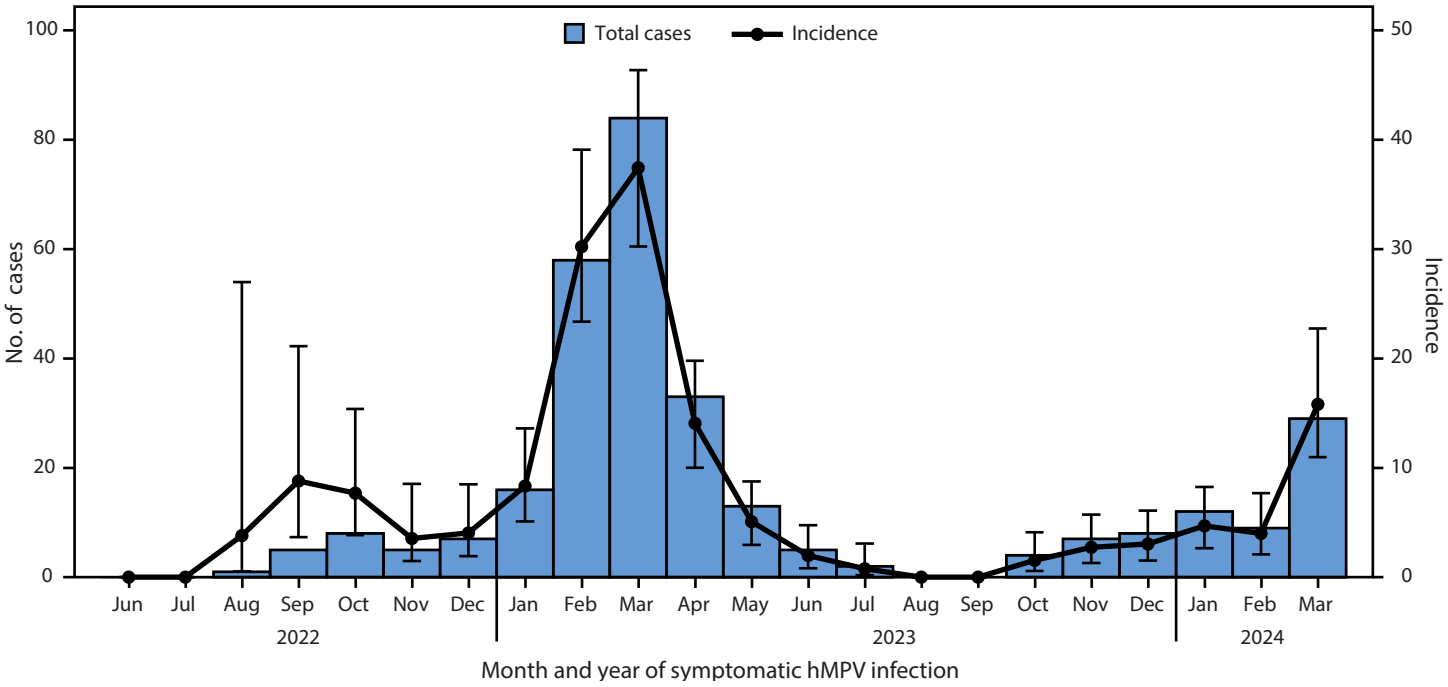
[††] An adjusted model evaluating the association between incidence of symptomatic hMPV infection and the number of children in a household did not include household size (number of household members of any age), because of collinearity.

[§§] Multivariable regression was not performed because of sparseness of data.

[¶¶] C.F.R. part 46.114; 21 C.F.R. part 56.114.

[***] The random effects term (θ) was 0.63 and was statistically above the null value (zero).

FIGURE. Monthly number of symptomatic human metapneumovirus* cases and incidence† — CASCADIA community cohort, Oregon and Washington, June 2022–March 2024



Abbreviation: hMPV = human metapneumovirus.

* A participant was considered to have symptomatic hMPV infection if reporting new or worsening illness 0–3 days after collection of an hMPV-positive nasal swab, provided the swab was also collected during the period 2 days before to 7 days after reported illness onset. The date denotes the date of symptomatic hMPV infection.

† Cases per 100 persons per year, with 95% CIs indicated by bars.

congestion, sore throat, fatigue, and muscle or body aches were less likely to be reported (OR = 0.5, 0.5, 0.4, and 0.4, respectively). Among 252 (82.4%) participants for whom a 14-day post-illness survey was available, 68 (27.0%) missed work, school, or child-care facility attendance, 17 (6.8%) sought medical attention, and two (0.8%) sought in-person health care at a hospital or emergency department. Hazard ratios and illness characteristics were similar when analyses included both hMPV and other pathogens, and when analyses were limited to only hMPV (Supplementary Table 1, https://stacks.cdc.gov/view/cdc/177080#tabs-3) (Supplementary Table 2, https://stacks.cdc.gov/view/cdc/177080#tabs-3).

Discussion

During June 2022–March 2024, among participants aged 6 months–49 years enrolled in a community cohort, overall incidence of symptomatic hMPV was 7.5 per 100 persons per year. This estimate is consistent with other population-based studies, although previous analyses were generally limited to particular age groups or to medically attended illness (*4,5*). hMPV is a leading cause of severe respiratory illness among young children and older adults (*6,7*), and pediatric hospitalization rates are comparable to those reported for influenza (*7*). This analysis indicates a high incidence of symptomatic infection in the community that commonly led to missed school, work, or child care facility attendance.

Overall incidence of hMPV varied by age group and season. Incidence rates of symptomatic hMPV infection were highest among children aged 2–11 years (up to 41.3 per 100 persons per year among those aged 2–4 years during January–March). These findings align with serologic evidence from a 2013 study that found the highest rates of hMPV infection among children aged ≥2 years (*8*); however, children aged <2 years might have higher hospitalization rates because of their elevated risk for severe disease (*7*). Incidence over time was consistent with data from laboratory-based surveillance indicating temperate-region predominance during the late winter and spring months (*9*). Lower incidence during the first quarter of 2024 compared with 2023 might also be consistent with reports of biennial variation in timing and transmission (*1,9*).

Modeled clustering of incidence by household highlights the role of close contacts in hMPV transmission. Although household size was not associated with infection, comparison was generally limited to households with multiple members. Among households with multiple members enrolled, one third of symptomatic hMPV infections were associated with another symptomatic infection in the same household within 7 days. Underlying health conditions have been linked to severe illness (*1*) but were not associated with incidence of symptomatic infection in this study.

TABLE 1. Characteristics associated with incidence of symptomatic human metapneumovirus infection — CASCADIA community cohort (N = 3,549), Oregon and Washington, June 2022–March 2024

Characteristic	Total cases/Total person-years	Incidence* (95% CI)	Hazard ratio (95% CI)	
			Unadjusted	Adjusted†
Overall	**306/4,072**	**7.5 (6.7–8.4)**	—	—
Age group during follow-up				
6–23 mos	**10/74**	13.5 (7.3–25.1)	3.6 (1.8–7.1)	3.7 (1.8–7.6)
2–4 yrs	**51/261**	19.5 (14.9–25.7)	5.3 (3.6–7.9)	5.8 (3.8–9.0)
5–11 yrs	**114/999**	11.4 (9.5–13.7)	3.0 (2.2–4.1)	3.1 (2.2–4.5)
12–17 yrs	**46/6,517**	7.1 (5.3–9.4)	1.9 (1.3–2.8)	2.0 (1.4–3.1)
18–39 yrs	**29/6,234**	4.7 (3.2–6.7)	1.2 (0.8–2.0)	1.2 (0.8–1.9)
≥40 yrs	**56/1,462**	3.8 (2.9–5.0)	Ref	Ref
Sex				
Female	**183/2,369**	7.7 (6.7–8.9)	Ref	Ref
Male	**123/1,703**	7.2 (6.1–8.6)	0.9 (0.7–1.2)	0.8 (0.6–1.0)
Race and ethnicity				
White, NH	**206/2,916**	7.1 (6.2–8.1)	Ref	Ref
Other§	**100/1,156**	8.7 (7.1–10.5)	1.2 (1.0–1.6)	1.1 (0.8–1.4)
No. of persons reported in household¶				
1–2	**18/271**	6.6 (4.2–10.5)	Ref	Ref
3	**61/920**	6.6 (5.2–8.5)	1.0 (0.6–1.7)	0.8 (0.5–1.4)
4	**154/1,995**	7.7 (6.6–9.0)	1.2 (0.7–2.0)	0.9 (0.5–1.5)
≥5	**73/886**	8.2 (6.5–10.4)	1.2 (0.7–2.1)	0.9 (0.5–1.5)
No. of children reported in household**				
0	**5/117**	4.3 (1.8–10.3)	Ref	Ref
1	**76/1,040**	7.3 (5.8–9.1)	1.7 (0.7–4.4)	1.1 (0.4–2.9)
2	**161/2,138**	7.5 (6.5–8.8)	1.8 (0.7–4.4)	1.0 (0.4–2.6)
≥3	**64/776**	8.2 (6.5–10.5)	1.9 (0.8–5.0)	1.1 (0.4–2.8)
Household income (USD)				
<100,000	**63/905**	7.0 (5.4–8.9)	Ref	Ref
100,000–199,000	**105/1,518**	6.9 (5.7–8.4)	1.0 (0.7–1.4)	1.0 (0.7–1.5)
≥200,000	**120/1,381**	8.7 (7.3–10.4)	1.3 (0.9–1.8)	1.2 (0.8–1.7)
Prefer not to answer	**18/268**	6.7 (4.2–10.7)	0.9 (0.5–1.7)	0.9 (0.5–1.6)
Health insurance status				
Employer or individual	**281/3,576**	7.9 (7.0–8.8)	Ref	Ref
Medicaid, Medicare, or other government insurance	**17/296**	5.7 (3.6–9.2)	0.7 (0.4–1.3)	0.6 (0.4–1.2)
Other††	**8/167**	4.8 (2.4–9.6)	0.6 (0.3–1.2)	0.5 (0.2–1.1)
Underlying health condition				
No	**217/2,453**	8.8 (7.7–10.1)	Ref	Ref
Yes	**89/1,619**	5.5 (4.5–6.8)	0.6 (0.5–0.8)	1.1 (0.8–1.5)
Year				
Year 1 (Jun 19, 2022–Jun 18, 2023)	**235/1,757**	13.4 (11.8–15.2)	4.4 (3.4–5.8)	3.5 (2.6–4.6)
Year 2 (Jun 19, 2023–Mar 30, 2024)	**71/2,315**	3.1 (2.4–3.9)	Ref	Ref
Q				
Q1 (Jan–Mar)	**208/1,273**	16.3 (14.3–18.7)	5.0 (3.6–7.0)	4.3 (3.0–6.0)
Q2 (Apr–Jun)	**51/742**	6.9 (5.2–9.0)	2.1 (1.4–3.2)	1.2 (0.8–1.9)
Q3 (Jul–Sep)	**8/860**	0.9 (0.5–1.9)	0.3 (0.1–0.6)	0.4 (0.2–0.9)
Q4 (Oct–Dec)	**39/1,197**	3.3 (2.4–4.5)	Ref	Ref
Study site				
Kaiser Permanente Northwest	**129/1,960**	6.6 (5.5–7.8)	Ref	Ref
University of Washington	**177/2,112**	8.4 (7.2–9.7)	1.3 (1.0–1.6)	1.2 (0.9–1.6)

Abbreviations: NH = non-Hispanic; Q = quarter; Ref = referent group; USD = U.S. dollars.

* Cases per 100 persons per year.

† Models were adjusted for age group, sex, race and ethnicity, year, Q of the year, household size, household income, and presence of underlying health conditions. Household size was omitted from the model of the number of children in the household because of collinearity.

§ Includes NH American Indian or Alaska Native, NH Asian, NH Black or African American, NH Native Hawaiian or Pacific Islander, Hispanic or Latino (Hispanic), NH multiple races, and preferred not to say.

¶ Median of three members enrolled per household (range = one to eight), with a median of two members aged ≥18 years enrolled per household (range = one to four).

** Median of two children aged <18 years (range = one to six) enrolled per household.

†† Includes no insurance, other insurance, don't know, and preferred not to say.

The most frequently reported hMPV symptoms were cough and nasal congestion; shortness of breath was also reported, consistent with involvement of the upper and lower respiratory tracts (*1*). Symptoms varied by age, with children experiencing more fever and cough compared with adults. Because this study was not conditioned on medical attendance or particular symptoms, it might provide a clearer description of symptomatic hMPV infection than that reported in other studies (*1*). Although most participants experienced a relatively mild infection, 27% missed work, school, or child care facility attendance during the 14 days after illness onset, highlighting the impact that even mild infection can have on daily activities.

Limitations

The findings in this report are subject to at least seven limitations. First, follow-up was <24 months; incidence during April–June was only represented in 2023. Second, incidence might be influenced by changes in seasonality after the COVID-19 pandemic. Third, importance of households as a source of transmission might be underestimated because not all eligible household members were enrolled, and because some infections might be asymptomatic. Fourth, hMPV cases might have been missed because of missed swab collections or assay sensitivity. Fifth, hMPV detection does not prove cause of illness, and other pathogens might have contributed; however, detection usually indicates a causal role (*10*). Sixth, because the CASCADIA cohort only included persons aged 6 months–49 years at enrollment, cases of hMPV illness among younger infants or older

TABLE 2. Characteristics associated with symptomatic human metapneumovirus infection among children aged 6 months–17 years and adults aged 18–49 years — CASCADIA community cohort, Oregon and Washington, June 2022–March 2024

Variable	No. (%) Total (N = 306)	Children (n = 221)	Adults (n = 85) (Ref)	Odds ratio* (95% CI)
Sign or symptom				
Cough	**246 (80.4)**	189 (85.5)	57 (67.1)	2.9 (1.6–5.2)
Congestion or runny nose	**220 (71.9)**	151 (68.3)	69 (81.2)	0.5 (0.3–0.9)
Sore throat	**118 (38.6)**	76 (34.4)	42 (49.4)	0.5 (0.3–0.9)
Fatigue	**96 (31.4)**	56 (25.3)	40 (47.1)	0.4 (0.2–0.6)
Fever	**72 (23.5)**	61 (27.6)	11 (12.9)	2.6 (1.3–5.2)
Headache	**70 (22.9)**	44 (19.9)	26 (30.6)	0.6 (0.3–1.0)
Muscle or body aches	**45 (14.7)**	24 (10.9)	21 (24.7)	0.4 (0.2–0.7)
Shortness of breath	**22 (7.2)**	17 (7.7)	5 (5.9)	1.3 (0.5–3.7)
Nausea or vomiting	**21 (6.9)**	16 (7.2)	5 (5.9)	1.2 (0.4–3.5)
Diarrhea	**16 (5.2)**	10 (4.5)	6 (7.1)	0.6 (0.2–1.8)
Loss of taste or smell	**11 (3.6)**	6 (2.7)	5 (5.9)	0.5 (0.2–1.5)
Persistent pain or pressure in the chest	**7 (2.3)**	3 (1.4)	4 (4.7)	0.3 (0.1–1.3)
Pale, gray, or blue-colored skin, lips, or nail beds	**1 (0.3)**	1 (0.5)	0 (—)	—
Care-seeking†	**252**	**183**	**69**	—
No care-seeking	**224 (88.9)**	162 (88.5)	62 (89.9)	0.9 (0.4–2.2)
Remote consult	**8 (3.2)**	6 (3.3)	2 (2.9)	1.1 (0.2–5.8)
Medically attended doctor's office or urgent care	**17 (6.8)**	13 (7.1)	4 (5.8)	1.2 (0.4–4.0)
Pharmacy	**2 (0.8)**	0 (—)	2 (2.9)	—
Visited hospital or emergency department in person	**2 (0.8)**	1 (0.5)	1 (0.5)	0.4 (0–6.1)
Other or unspecified	**3 (1.2)**	3 (1.6)	0 (—)	—

Summary

What is already known about this topic?

Human metapneumovirus (hMPV) causes substantial respiratory illness worldwide. However, information on the epidemiology of symptomatic infection is limited, particularly outside of health care settings.

What is added by this report?

In this community cohort study including participants aged 6 months–49 years, average incidence of symptomatic hMPV infection was 7.5 per 100 persons per year. Incidence was highest during January–March and among children aged 2–4 years, and clustered in households. Although most infections caused mild illness, 27% were associated with absenteeism from work, school, or a child care facility.

What are the implications for public health practice?

Better understanding of the epidemiology of hMPV infection in the community can guide clinical testing and future strategies for prevention and treatment.

TABLE 2. (*Continued*) Characteristics associated with symptomatic human metapneumovirus infection among children aged 6 months–17 years and adults aged 18–49 years — CASCADIA community cohort, Oregon and Washington, June 2022–March 2024

Variable	No. (%) Total (N = 306)	Children (n = 221)	Adults (n = 85) (Ref)	Odds ratio* (95% CI)
Absence from work, school, or child care facility	**252**	183	69	—
Yes	**68 (27.0)**	54 (29.5)	14 (20.3)	1.6 (0.8–3.2)
Days missed from work, school, or child care facility	**76 (31)**	57 (23)	19 (8)	—
Median (range)	**2 (1–8)**	2 (1–8)	1.5 (1–5)	—
Codetection§				
No	**186 (60.8)**	127 (57.5)	59 (69.4)	Ref
Yes	**120 (39.2)**	94 (42.5)	26 (30.6)	1.7 (1.0–2.9)

Abbreviations: Ref = referent group; RSV = respiratory syncytial virus.

* Unadjusted odds ratios for ages 6 months–17 years versus 18–49 years.

† Participant could respond "yes" to one or more categories. Columns might not sum to 100%.

§ Codetection of human metapneumovirus with one or more other pathogens: *Streptococcus pneumoniae* (70); rhinovirus (30); adenovirus 1 (13), adenovirus 2 (11); human parainfluenza virus (four); human enterovirus (five); human coronavirus type HKU1 (three), type 229E (one), type NL63 (eight), and type OC43 (four); SARS-CoV-2 (two); influenza A (two) and influenza C (three); and RSV A (one) and RSV B (one).

adults would not have been captured. Finally, sociodemographics and household size of enrolled participants might not be representative of the general U.S. population.

Implications for Public Health Practice

Symptomatic hMPV infection is frequently associated with cough or nasal congestion, typically occurring during late winter to spring, with high rates of infection among young children. Although hMPV infections are usually mild, illness can have a considerable impact on daily activities, including work, school, and child care facility attendance. Increased testing for hMPV can identify opportunities for infection control measures and optimize public health surveillance. Understanding hMPV disease incidence can help guide the development and future introduction of vaccines, prophylactic and therapeutic antibodies, antivirals, and nonpharmaceutical prevention products (*2*).

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Notes from the Field

Response to a Case of Travel-Associated Lassa Fever — Iowa, October–November 2024

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Introduction

Lassa fever is a viral hemorrhagic fever (VHF) endemic to western Africa. The Lassa virus has a *Mastomys* genus rodent reservoir and is transmitted through contact with excreta or body fluids of infected rodents or humans (*1*); the incubation period is 1–3 weeks.* No licensed vaccine to prevent Lassa fever is currently available. In late October 2024, the Iowa Department of Health and Human Services (HHS) received a telephone call from a local hospital regarding a patient who had recently returned from rural construction-related work in Liberia, where Lassa fever is endemic. The patient's travel history, negative malaria test result, and increasing daily body temperature and hemodynamic instability, despite receipt of empiric broad-spectrum antibiotics, prompted concern for Lassa fever. A blood specimen collected at hospital C was tested within hours at the Nebraska Public Health Laboratory using the BioFire Global Fever Special Pathogens Panel (*2*), which returned a presumptive positive result for Lassa virus. The diagnosis was subsequently confirmed by CDC's Viral Special Pathogens Branch. This represents the first U.S. Lassa fever case in eight years and the ninth U.S. travel-associated Lassa fever case since 1969 (*3*). An investi-gation was undertaken by federal, state, and local partners to identify contacts of the patient who might have been exposed and to prevent further transmission.

Timeline, Investigation, and Outcomes

The patient returned to Iowa from Liberia during early October 2024 (day 0), and experienced fever, myalgias, and headache on day 8. After an evaluation in the emergency department of hospital A on day 15, the patient was transferred to hospital B for diagnostic evaluation. On day 19, the patient needed specialized care and was transferred to hospital C, the hospital that contacted the Iowa Department of HHS; the patient died on day 21.

The patient's clinical status by the time the diagnosis was recognized at hospital C precluded obtaining detailed previous exposure history. Risk assessments† were completed for 180 contacts (Table). Because illness began >1 week after returning from Liberia, the patient was not considered to have been infectious while in Liberia or during travel from Liberia to Iowa (*4*).

Among the 180 contacts, four household contacts (2%) and three of the four community-associated contacts (2%) were classified as having high-risk exposures, quarantined until day 21 after their last exposure (the maximum incubation period), and monitored twice daily for Lassa fever signs and symptoms.§ Contacts' monitoring results were submitted by local public health and health care facilities to a REDCap database.

Among the 180 contacts, 172 (96%) were health care–associated, and level of risk was determined by use of personal protective equipment (PPE)¶ in relation to the patient's clinical stability, and whether the patient was experiencing bleeding, vomiting, or diarrhea when the contact occurred. Sixty-seven (39%) health care–associated contacts occurred in settings where the patient was clinically stable and without bleeding, vomiting, or diarrhea; among these contacts, 45 (67%) were classified as high-risk on the basis of one or more PPE omissions (i.e., of gown, gloves, eye protection, or face mask); these persons were permitted to continue working in order to maintain local health care capacity. Five of the 67 contacts had direct skin-to-skin contact and one or more PPE omissions and were excluded from work until 21 days after their last exposure. At hospital C, the patient was clinically unstable, and health care providers were at risk for body fluid exposure. Among 68 identified contacts at hospital C, 25 (37%) were classified as high-risk and excluded from work through day 21 from their last exposure; 24 of these 25 contacts had one or more PPE omissions (i.e., gown, gloves, eye protection, or N95 respirator), and one had body fluid contact.

* https://www.cdc.gov/lassa-fever/about/index.html

† https://www.cdc.gov/viral-hemorrhagic-fevers/php/public-health-strategy/people-with-suspected-or-confirmed-vhf-or-high-risk.html

§ Weakness or fatigue, fever, headache, chills, muscle aches, diarrhea, vomiting, unexplained bleeding or bruising, rash, chest pain, sore throat, cough, or dark urine.

¶ Risk was based on the patient's clinical stability and caregivers' use or omission of PPE. Anyone who provided care when the patient was unstable (rapid clinical deterioration, obtundation, or requirement for intubation or vasopressors) would have had to wear gown, gloves, eye protection, and an N95 respirator; omission of any of these would result in classification of the contact as high risk. https://www.cdc.gov/viral-hemorrhagic-fevers/hcp/guidance/ppe-clinically-stable-puis.html; https://www.cdc.gov/viral-hemorrhagic-fevers/hcp/guidance/ppe-clinically-unstable.html

TABLE. Exposure group and risk classifications* of contacts of a patient with travel-associated Lassa fever (N = 180) — Iowa, October–November 2024

Exposure location (no.)	Contact risk level (no.)					
	High exposure, nature of risk			Low exposure, nature of risk	No exposure	
	Household† (4)	Health care setting with ≥1 PPE omission†,§,¶ (95)	Health care setting with ≥1 PPE omission§,¶ and skin-to-skin contact or cleaning of body fluids† (6)	No PPE omission§,¶ (health care setting) or risk for exposure was possible (community-associated)† (50)	None (25)	Total contacts (180)
Household (4)	4**	—	—	—	—	**4**
Community (4)	—	3**	—	1	—	**4**
Health care (172)						
Hospital A (ED)	—	6	2††	1	—	**9**
EMS unit A	—	2	—	—	—	**2**
EMS unit B	—	2	—	—	—	**2**
EMS unit C	—	—	—	—	3	**3**
Hospital B	—	35	3††	7	6	**51**
Hospital C§§	—	24††	1††	36	7	**68**
Postmortem care	—	—	—	—	3	**3**
Laboratory						
A (ED)	—	2††	—	—	—	**2**
B	—	13††	—	1	1	**15**
C	—	4††	—	—	—	**4**
D	—	1††	—	1	—	**2**
E	—	3††	—	3	2	**8**
F	—	—	—	—	3†	**3**

Abbreviations: ED = emergency department; EMS = emergency medical services; PPE = personal protective equipment.
* https://www.cdc.gov/viral-hemorrhagic-fevers/php/public-health-strategy/people-with-suspected-or-confirmed-vhf-or-high-risk.html
† Actively monitored for signs and symptoms, including weakness or fatigue, fever, headache, chills, muscles aches, diarrhea, vomiting, unexplained bleeding or bruising, rash, chest pain, sore throat, cough, or dark urine.
§ https://www.cdc.gov/viral-hemorrhagic-fevers/hcp/guidance/ppe-clinically-stable-puis.html
¶ https://www.cdc.gov/viral-hemorrhagic-fevers/hcp/guidance/ppe-clinically-unstable.html
** Quarantined until 21 days after the last exposure.
†† Excluded from work until 21 days after last exposure.
§§ The patient was clinically stable until arrival at hospital C.

Summary

What is already known about this topic?

Lassa fever is a viral hemorrhagic fever (VHF) endemic to western Africa. Before 2024, eight travel-associated cases had been identified in the United States.

What is added by this report?

A fatal Lassa fever case in a patient returning from Liberia, the first U.S. case diagnosed in eight years and the ninth U.S. travel-associated case since 1969, was identified in Iowa in late 2024. Investigation identified 180 contacts. Lassa fever virus testing was performed for five symptomatic contacts; all laboratory results were negative.

What are the implications for public health practice?

The coordinated public health response to this case underscores the importance of eliciting a travel history from febrile patients, effective VHF planning within public health departments and medical communities, and the importance of rapid local testing capabilities.

Laboratorians were evaluated on the basis of activities performed and the use of appropriate PPE; 34 contacts were identified across six laboratories; 23 (68%) of these were classified as high-risk, and were excluded from work for 21 days, on the basis of published recommendations for biosafety in microbiological and biomedical laboratories (*5*).

All 105 high-risk contacts without contraindications were offered oral ribavirin postexposure prophylaxis (*4*); however, most felt that their exposure did not warrant prophylaxis. Five (5%) contacts began prophylaxis, four stopped because of adverse reactions (e.g., nausea), and one completed the 10-day course. Among 158 monitored contacts, 43 (27%) reported any signs or symptoms, including five whose signs or symptoms were potentially consistent with Lassa fever; these persons were transported to an assessment or treatment hospital** under VHF precautions for evaluation and testing; all test results were negative.

Preliminary Conclusions and Actions

The occurrence of this Lassa fever case and the ensuing public health response underscore the importance of eliciting

** The Iowa Bureau of Preparedness and Response program has used funding from the Hospital Preparedness Program (an Administration for Strategic Preparedness and Response grant) and the Public Health Emergency Preparedness program (a CDC grant) to create a robust Highly Infectious Diseases system comprising four EMS transport agencies, two Level 3 assessment hospitals, and one Level 2 treatment center. This system was established in 2014 during the Ebola virus disease outbreak and has been continuously refined since then.

a travel history from febrile patients, maintaining awareness of high-consequence infectious disease risk, and facilitating close coordination between clinical and public health partners. Well-developed VHF response planning and rapid test turnaround were essential to preventing transmission despite multiple possible exposures to this patient with fatal disease.

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