

# Pediatric burden and seasonality of Human Metapneumovirus over five years in Managua, Nicaragua.

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## Abstract

**Background** Human Metapneumovirus (hMPV) is an important cause of pediatric respiratory infection. We leveraged the Nicaraguan Pediatric Influenza Cohort Study (NPICS) to assess the burden and seasonality of symptomatic hMPV infection in children. **Methods** NPICS is an ongoing prospective study of children in Managua, Nicaragua. We assessed children for hMPV infection via RT-PCR. We used classical additive decomposition analysis to assess the temporal trends and Generalized Growth Models (GGMs) were used to estimate effective reproduction numbers. **Results** From 2011-2016 there were 564 hMPV symptomatic infections yielding an incidence rate of 5.74 cases per 100 person-years (95% CI 5.3, 6.2). Children experienced 3,509 Acute Lower Respiratory Infections (ALRIs), of which 160 (4.6%) were associated with hMPV infection. Children under the age of one had 55% of all symptomatic hMPV infections (62/112) develop into hMPV-associated ALRIs and were five times as likely as children over one to have an hMPV-associated ALRI (Rate Ratio 5.5 95% CI 4.1, 7.4  $p < 0.001$ ). Additionally, symptomatic reinfection with hMPV was common. In total, 87 (15%) of all observed symptomatic infections were reinfections. The seasonality of symptomatic hMPV outbreaks varied considerably. From 2011-2016, four epidemic periods were observed, following a biennial seasonal pattern. The mean ascending phase of the epidemic periods were 7.7 weeks, with an overall mean estimated reproductive number of 1.2 (95% CI 1.1, 1.4). **Conclusions** Symptomatic hMPV infection was associated with substantial burden among children in the first year of life. Timing and frequency of symptomatic hMPV incidence followed biennial patterns.

## INTRODUCTION

Human metapneumovirus (hMPV), is a viral respiratory pathogen of global importance <sup>1-4</sup>. First identified in 2001, hMPV is a single-stranded negative-sense RNA Pneumovirus which, based on serologic studies, has circulated worldwide in human populations for at least seven decades <sup>5</sup>. HMPV is divided into two genetic groups: A and B which are further differentiated into 6 known lineages A1, A2a, A2b, A2c, B1, and B2 <sup>6-8</sup> and infects all ages, with severe events occurring in children, the elderly, and the immunocompromised <sup>9</sup>. In children, hMPV is pervasive in early-life, causing both upper <sup>10</sup> and severe lower respiratory infections <sup>1,11</sup>. Indeed, most children are seropositive for hMPV by age five <sup>5,11-13</sup>. Severe hMPV infection is also an important cause in respiratory-associated childhood hospitalization and has globally been estimated to account for 4-18% of Acute Lower Respiratory Infection (ALRI) hospital admissions<sup>2,14,15</sup>.

Despite the importance of hMPV as a childhood respiratory infection, key questions regarding incidence, severity, and seasonality of hMPV infections particularly in Lower- and Middle-Income Countries (LMIC) remain. Globally, there is significant variation in seasonality of hMPV by location, and hMPV infections can occur throughout the year<sup>3,16</sup>. Re-infection and repeat symptomatic episodes of hMPV in both children and adults have also been noted<sup>12,17–19</sup> highlighting the clinical challenge of this ubiquitous pathogen.

Currently no vaccine exists for hMPV. An important step towards this goal is describing the seasonality and burden of hMPV particularly in LMICs. While research on hMPV is increasing, there are few long-standing cohort studies conducted in Central and Latin America<sup>3</sup>. In this study, we describe the burden, symptomatic incidence rate, reinfection, and seasonality of hMPV among a cohort of children in Managua, Nicaragua. We additionally describe estimates of effective reproduction numbers for each of the epidemic peaks observed from 2011–2016.

## METHODS

### Study Population

A detailed report on the methods and protocol used for the Nicaraguan Pediatric Influenza Cohort (NPICS) has been described previously<sup>20,21</sup>. Briefly, the primary aim of the NPICS study is to assess the burden, incidence, and seasonality of influenza in Nicaragua. However, while most infectious disease studies focus on a single pathogen or syndrome, NPICS was developed with the goal of assessing multiple respiratory pathogens and can test stored samples for additional pathogens. The NPICS study is an ongoing prospective cohort study initiated in 2011 and includes children aged 0–14 years, residing in District II in Managua, Nicaragua. Legal guardians are encouraged to bring their children to the Health Center Sócrates Flores Vias (HCSFV), at the first sign of illness and receive free medical care and are thus incentivized to use this health outpost as opposed to seeking care at other medical clinics. Initial enrollment for the cohort study was conducted in 2011 by randomly sampling children aged 3–11 years who were enrolled in a previous cohort study for influenza within District II, and additional children aged 0–2 were recruited through house-to-house visits within the catchment area. The age distribution of the NPICS cohort is representative of children of Nicaragua<sup>20</sup> and spatially representative of district II in Managua<sup>20</sup>. Additional children aged 0–2 years were recruited from houses throughout the study catchment area. Children [?] 4 weeks old are enrolled monthly into NPICS and age out of the study on their 15<sup>th</sup> birthday. In this study, we assess those enrolled in NPICS from 2011–2016.

### Case identification

Children aged 0–14 years were followed via annual surveys in addition to clinic visits where care givers were asked to bring their children at the first sign of illness. In this study, our primary outcome is symptomatic real-time reverse-transcription polymerase chain reaction (RT-PCR)-positive hMPV cases of children brought to clinic. Samples were tested using real-time reverse-transcription polymerase chain reaction (RT-PCR) if children met specific clinical features: 1) Reported fever (37.8C) or feverishness with cough, sore throat or runny nose for children aged 2 years and older, 2) Only fever or feverishness for children under 2, 3) Severe respiratory symptoms as evaluated by a physician including wheezing, chest indrawing, apnea etc., and 4) Hospitalization with respiratory symptoms or sepsis.

Our secondary outcome was hMPV-associated Acute Lower Respiratory Infection (ALRI), which was determined as patients that presented with a diagnosis of bronchiolitis, bronchitis, bronchopneumonia, or pneumonia or bronchial hyper-reactivity as determined by study physicians. To assess hMPV-associated ALRI, we selected all clinic visits that met the ALRI criteria occurring up to fourteen days prior to the clinic visit or 28 days after an hMPV-positive RT-PCR. HMPV positive tests spaced more than 30 days apart with different symptom onset dates were considered separate episodes. If the hMPV positive tests were less than 30 days apart, the first symptom onset date was used.

### Sample collection and laboratory testing for hMPV

Nasal Oropharyngeal specimens were collected for all children [?] 6 months for those that met the clinical testing definitions. Combined nasal and oropharyngeal swabs were collected for children > 6 months who

met the testing criteria. RNA was extracted (QIAamp Viral RNA Mini Kit, Qiagen) and then tested by RT-PCR for hMPV using CDC (Center for Disease Control) standardized protocols<sup>22</sup>. Laboratory protocols were unchanged throughout the study.

## Statistics

### Incidence calculations

Incidence was calculated for all symptomatic hMPV infections in addition to stratifying by age, sex, and hMPV-associated ALRI from 2011–2016. Person-time was calculated as the amount of time starting at participant enrollment to December 30, 2016, or withdrawal from the study. Withdrawal for those who were lost to follow-up was calculated as the midpoint of the date of last contact and the date recorded by study personnel as lost to follow-up. Incidence was calculated using generalized linear models with Poisson distributions, participant age was calculated on a weekly basis.

To assess if there were significant differences in hMPV-associated ALRI reported by sex, we used Generalized Estimating Equations (GEE) assuming a dependence on the individual across the sampling weeks. Weeks when hMPV-associated ALRI was not reported was assumed to be negative for hMPV-associated ALRI.

### Age and time between repeat hMPV infections

To assess the association between participant age and time between repeat hMPV illnesses, we selected participants with multiple hMPV illnesses. We then calculated the interval in months between infections. We used a Generalized Additive Model (GAM) to assess the relationship between participant age and the interval between infections.

### Seasonality and Seasonal Decomposition Analysis of hMPV

We evaluated the number and incidence of weekly hMPV cases and hMPV-associated ALRI cases from 2011–2016. We used R's<sup>23</sup> (R Version 4.0.4) decompose (part of the stats package) and forecast package<sup>24</sup> to assess the temporal dynamics of hMPV cases and specifically isolate the trend, seasonal, and error components. Since the magnitude of the seasonal fluctuations and the variation around the trend-cycle do not vary proportionally with time, we used an additive time-series decomposition approach to isolate the temporal trend, seasonality, and error components. In additive decomposition we assume:

$$y_t = S_t + T_t + R_t$$

Where  $y_t$  is the data,  $S_t$  is the seasonal component,  $T_t$  is the trend component, and  $R_t$  is the remainder component.

### Effective Reproduction Numbers

We estimated the effective reproduction number (R effective) from the initial growth phase of the local hMPV epidemics using the generalized-growth method<sup>25</sup>, which links the generation interval of the disease with the trajectory of the number of new cases per week to derive our R estimates. This method is especially useful to characterize a range of growth dynamics via 2 parameters: the growth rate ( $r$ ) and the epidemic growth scaling ( $p$ ). This growth dynamics value ranges from constant incidence ( $p = 0$ ) to exponential growth ( $p = 1$ )<sup>25</sup>. We assumed a gamma distributed serial interval of 5 and 7.5 days and a standard deviation of 1 day<sup>26,27</sup>.

## RESULTS

### Study Participation

From 2011–2016, 2576 children were enrolled in NPICS, 1269 (49.3%) were boys and 1307 (49.7%) were girls. The age distribution, enrollment, and reported sex by year are summarized in figure 1. The overall age distribution by cohort year is described in Fig. 1A. The age structure for those under 1 year old are summarized in Fig. 1B. The median age of those entering the cohort after January 2011 was five months old (IQR 0.7–29.4 months), the majority being enrolled in their first year of life (Fig. 1C). The median age

of enrollees exiting the cohort was seven years (IQR 4–11 years). Study participants consistently visited the clinic throughout the study period (Supplemental Fig. 1), across the study period 24.8% of participant clinic visits (11677/47006) met the hMPV testing criteria, and 9.3% (4346/47006) met the criteria for ALRI. The loss-to-follow up throughout the study period was low ranging from 2%-5% per year and are described in detail in Supplemental Table 1.

### Symptomatic hMPV

From 2011–2016, of the 2576 children that participated in the cohort 478 (18.6%) had at least one RT-PCR confirmed hMPV illness episode (Table 1). The overall symptomatic incidence rate was 5.74 (95% CI 5.3, 6.2) per 100 person-years (Supplemental Table 2). Most symptomatic hMPV illness occurred in the first year of life (Fig. 2), with the highest incidence rate occurring between 6–8 months (23.5 cases per 100 person years 95% CI 16.8, 32.0). The lowest incidence was observed in the 10–12 age group (1.0 case per 100 person years 95% CI 0.6, 1.7). Children under one year old had 3.2 times the incidence of children one year or older (Rate Ratio 3.2 95% CI 2.6, 4.0  $p < 0.001$ ). There was no significant difference ( $p > 0.05$ ) observed between sexes (Supplemental Table 2).

Of the total 564 hMPV symptomatic cases, 87 (15%) were symptomatic reinfections (Table 1, Fig. 3). The median time to reinfection was 22 months, or 1.8 years (min 1 month, max 5.1 years), and the median age of reinfection was 40 months, or 3.3 years (min 6 months, max 10.2 years). Participant age was significantly associated with the amount of time between positive RT-PCRs ( $p < 0.001$ ). Most secondary symptomatic infections occurred later in life (4–14 years), compared to the first 3 years of life (Fig. 3B).

### hMPV-Associated ALRI

During the study period, 3,509 ALRI events were recorded at the study clinics. Of those events, 160 (4.6%) were associated with hMPV. Out of the total 564 hMPV positive cases, 160 (28%) were associated with an ALRI diagnosis (Supplemental Table 2). The incidence rate for hMPV-associated ALRI was 2.1 cases per 100 person-years (95% CI 1.9, 2.4). Of the 160 ALRI events, 7 (4.4 %) were severe enough to transfer the children to a hospital for further treatment. Like symptomatic hMPV cases, there were more ALRI events reported in males ( $N = 116$ , 42% of males with hMPV) in our study compared to females ( $N = 94$ , 33% of females with hMPV), however this difference was not significant. There was a significant difference in incidence rate observed between hMPV-associated ALRI episodes in those under one year of age compared to those over a year (Rate Ratio 5.5 95% CI 4.1, 7.4  $p < 0.001$ ). For children under the age of one, 55% of all symptomatic hMPV episodes resulted in an ALRI event compared to just 33% for children over one.

### Seasonality and Seasonal Decomposition Analysis of hMPV

HMPV epidemics alternated years (Fig. 4). Years with the highest hMPV incidence were 2011, 2013, and 2015. Cases tended to peak during July–August, however there was additional variation of incidence throughout the year, which was particularly notable in 2015 (Fig. 4 and Supplemental Fig. 2). In 2012 and 2014 there was no major epidemic. There was a rise in case numbers in 2016 in September–January which differs from peaks in previous years, however it is possible that the peak epidemic period occurred later into 2017 (Fig. 4, Supplemental Fig. 2).

When the trend ( $T_t$ ) was isolated from the seasonal and remainder components in Classical Additive Decomposition, there was no overall observable increase or decrease in the number of monthly symptomatic hMPV cases (Fig. 5B). When the seasonality and remainder were extracted from the trend there was a distinct decrease of the number of cases in 2012 and 2014 (Fig. 5B), and an increase in cases in 2013 and 2015. This trend was also noted in the remainder component where there were significant increases and decreases that were not explained by the trend ( $T_t$ ) or seasonal component ( $S_t$ ) (Fig. 5C, D). The increases in symptomatic hMPV cases when annual seasonal patterns ( $S_t$ ) and longitudinal trend were extracted ( $T_t$ ) revealed a biennial residual pattern.

### Effective Reproduction Numbers

Four main epidemic periods were observed (in 2011, 2013, 2015, and 2016) and are described in detail in Figure 2 and Supplemental Table 3. The mean ascending phase of the epidemic periods were 7.7 weeks. Effective reproduction numbers ranged from 1.1 – 1.7 with a mean effective reproduction number of 1.3, depending on epidemic period and estimated serial interval (Fig 2B, Supplemental Table 3).

## DISCUSSION

In this prospective cohort, we demonstrate substantial burden of symptomatic-hMPV infection in children (5.7 cases per 100 person-years) and is an important cause of ALRI particularly for children in their first year of life. While the seroprevalence of hMPV in children varies globally, ranging from <5% to >30%<sup>3</sup>, the overall incidence among all children in the Nicaraguan cohort is one of the highest recorded in Central and South America<sup>28,28–33</sup>. Few prospective cohort studies assess for hMPV in children, and studies that screen for hMPV primarily occur at surveillance hospitals making precise comparisons of incidence across communities and countries challenging. To our knowledge, this study is the longest running clinical-based community cohort in Central or South America assessing hMPV in children.

In the Nicaraguan study cohort, the majority of symptomatic-hMPV and critically hMPV-associated ALRI occurred in first year of life (Fig 3). Those under one year old were 3.2 times more likely to have a symptomatic hMPV episode compared to those aged 1-14. Worldwide hMPV infection is greatest in those <5 years old<sup>2,3</sup>, however there is considerable variation in age and infection in children under five<sup>11,34–36</sup>. However, in long-running prospective cohort studies in children the burden appears to primarily affect those under a year of age<sup>34,37</sup>. Indeed, recent global modeling studies indicate that infants under one year have disproportionately high risks for hMPV-associated ALRI similar to Respiratory Syncytial Virus (RSV) and influenza<sup>2</sup>. Indeed, the highest incidence for influenza-associated ALRI for children aged 9-11, in the same study cohort was 4.8 influenza-associated ALRI cases (95%CI: 2.8-8.3) per 100 person-year compared to 13.7 hMPV-associated ALRI per 100 person-year for children of the same age (95%CI: 8.7-20.6)<sup>20</sup>. This study also indicates that children under a year six months old in LMICs are at an increased risk of death compared to upper-middle-income countries. In the United States, a long-running cohort found that the hMPV infection was greatest in those under one year of age<sup>37</sup>. Similarly, in Guatemala, a hospital-based cohort similar in size and scope to our study, also found increasing hMPV incidence throughout the first year of life<sup>34</sup>. Our study demonstrates that not only are children at a high risk of acquiring hMPV, but also infection with hMPV is likely to result in an ALRI event, particularly for infants under a year old.

We additionally found that symptomatic reinfection of hMPV was common. In total 87 (15%) of all observed episodes were symptomatic reinfections. While this study did not capture asymptomatic reinfections, the total number of symptomatic reinfections is substantial. Globally reinfection is common, likely due to poor development of T and B cell immunological memory or a lack of sterilizing immunity<sup>12,17–19</sup>. Reinfection was positively associated with age, with most reinfections occurring after age three. However, there was variation in symptomatic reinfections in the study cohort and reinfection occurred across childhood.

Similar to other studies, hMPV-associated ALRI events accounted for a substantial proportion of symptomatic hMPV episodes<sup>3,11,37</sup>. Throughout the study period, hMPV-associated ALRI constituted 27% - 43% of all symptomatic hMPV infections. The likelihood of hMPV-associated ALRI was five-times higher in children under the age of one compared to those older than one. This severity is consistent with other hospital cohort studies<sup>15</sup>. In the United States, the annual rate of hospitalization was highest for infants in the 0–5-month range<sup>15</sup>.

Seasonality of symptomatic hMPV varied considerably year to year. While hMPV infection occurred throughout the study period, four epidemic peaks were identified. Effective reproductive numbers varied based on year and depending on the estimate of serial interval used. We were unable to find other published estimates of the reproductive number for hMPV and while better estimates of generation interval are needed for more precise estimates, this study is an important step forward in estimating the potential spread of pediatric hMPV. During the epidemic periods observed, cases peaked in July or August corresponding to the rainy season which lasts from June to November. This seasonality is similar to other studies conducted

in tropical and subtropical areas where epidemic peaks tended to occur during periods of high rainfall and high relative humidity<sup>35,38,39</sup>, in contrast to temperate areas where hMPV infection predominately peaks in the winter and spring months<sup>3</sup>. Globally, seasonality of hMPV is broadly influenced by climatic features, but local metrological conditions likely influence variation regionally and locally<sup>3,16</sup>.

While longer time scales are needed to assess fixed patterns in seasonality, during the timeframe observed biennial seasonality across the first four years. While most studies observe annual hMPV epidemic cycles<sup>16,29,34–36,39–43</sup>, biennial seasonality in hMPV infection is uncommon<sup>44</sup>, and has not been observed in the tropics. For some infectious diseases, like measles, periodicity resulting in biennial transmission is due to the variation of the proportion of susceptible individuals in a population<sup>45,46</sup>. While age structure and distribution of those entering the cohort was stable throughout the study period, we are unable to broadly assess if the total number of susceptible individuals are changing and if this change influences the seasonality of hMPV.

This study was not without limitations. While this study is longer compared to many cohort studies on hMPV, it is not long enough to make to describe temporal patterns accurate of seasonal dynamics. Additionally, we did not assess genetic variation in hMPV, which might offer insight into seasonal dynamics and disease severity. Based on current literature, there are no strong associations between these lineages and disease severity, or when detected, were found in smaller studies lacking substantial power<sup>16,40,43,47</sup>. It is likely that multiple lineages and changes in lineage are occurring during the study period. Studies assessing the seasonality of subgroup types have found alternating subgroup seasonality, with subgroup dominance shifting every 1-3 years while the clinical presentation of hMPV remained unchanged. This is consistent with our study where hMPV-associated ALRI events were consistently proportional to the number of symptomatic events. It is therefore unlikely that changes in lineage effect the number of severe ALRI outcomes. While specific genetic groupings are globally more common in specific regions, for example in Asian countries after 2005 A2c and A2b genetic groupings were more common<sup>6</sup>, than samples derived from Europe, multiple lineages circulating in a specific season are common and found globally<sup>3,6,10,15,16,28,29,36,40,42,48–52</sup> without substantial changes to their yearly seasonal dynamics.

Human metapneumovirus is a ubiquitous childhood respiratory illness. While seroprevalence for hMPV is high globally little is known about hMPV in Latin America or how its dynamics might influence prevention, prediction, and surveillance of hMPV. Here, we demonstrate that hMPV infection is an important cause of ALRI in children and is particularly important for children under one year of age. While hMPV infections occur throughout the year, distinct biennial seasonality for hMPV infection was evident in our cohort and may be important in defining timing of future interventions.

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## TABLES

**Table 1** . Symptomatic hMPV illness and subsequent positive symptomatic episodes. Total number of symptomatic hMPV positive infections and reinfections and summary statistics.

	Number of Symptomatic hMPV Cases	Male sex (%)
All PCR Confirmed Symptomatic hMPV Cases	564	279 (49.4)
Primary Symptomatic Episode	478	240 (50.0)
Secondary Symptomatic Episode	79	34 (44.2)
Tertiary Symptomatic Episode	7	3 (42.9)
Quaternary Symptomatic Episode	1	1 (100)

## FIGURES AND FIGURE LEDGENDS

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**Figure 1 .** Age characteristics of the Nicaraguan Pediatric Influenza Cohort Study (NPICS) from 2011–2016. A) Age of all children enrolled in NPICS from 2011–2016, B) Age structure of NPICS cohort for those under 1 year of age, C) Age of new enrollees by year following the initial enrollment period, D) Reported sex and age distribution of all enrollees.

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**Figure 2.** Incidence of symptomatic-hMPV and hMPV-associated ALRI infection by age category with 95% CI. Incidence rate per 100 person-years of symptomatic hMPV cases and hMPV-associated ALRIs A) by age category and B) stratified by 0–1 year and 2–12 years.

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**Figure 3.** Age of patients with repeat symptomatic-hMPV infections compared to the time since previous infection. A) Fitted Generalized Additive Model (GAM) comparing age of illness in months and the amount of time since previous infections. B) Time interval between last symptomatic-hMPV infection stratified by 0–3 years and 4–14 years.

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**Figure 4.** Weekly hMPV case counts and symptomatic incidence rate from 2011–2016. A) Weekly count of hMPV cases in the NPICS cohort from 2011–2016. B) Weekly symptomatic incidence rate for hMPV cases in the NPICS cohort within a 95% confidence interval from 2011–2016. Yellow bars indicate the ascending phase length for each outbreak and the subsequent estimated mean effective reproductive number based on a 5-day serial number. C) Weekly symptomatic incidence of hMPV cases causing Acute Lower-Respiratory Infection (ALRI) in the NPICS cohort within a 95% confidence interval from 2011–2016.

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**Figure 5.** Classical Additive Decomposition of monthly hMPV infections. Panel A shows the original non-detrended data of symptomatic hMPV episodes per month from 2011–2017. Panel B shows the trend-cycle component for monthly data (seasonal and remainder components extracted). Panel C shows the seasonal component extracted from the original data. Panel D shows the remainder component when the trend-cycle and seasonal component are extracted. The grey bars to the right of the panels denote the scales of each of the components.

## SUPPORTING INFORMATION

**Supplemental Table 1.** Participants entering and exiting in the study cohort by year and reason for exiting the cohort.

Year	Enrolled	Withdrawn	Lost to Follow Up	Died	Total Entering	Total Exiting
2011	1578	3 (0.19%)	33 (2.1%)	1	143+	37
2012	1653	14 (0.85%)	73 (4.4%)	1	113	88
2013	1790	13 (0.72%)	102 (5.7%)	2	225	117
2014	1938	32 (1.6%)	90 (4.6%)	1	265	233
2015	1894	22 (1.2%)	90 (4.8%)	0	188	233
2016	1874	18 (0.95%)	36 (1.9%)	1	213	149

+Total enrolled after the initial January start date

**Supplemental Table 2 .** Incidence rate of symptomatic-hMPV and hMPV-associated ALRI in the NPICS cohort from 2011–2016 by year and reported sex.

	Person years	Symptomatic hMPV- episodes Cases	Symptomatic hMPV- episodes Incidence (95% CI per 100 person-years)	hMPV- associated ALRI episodes Cases	hMPV- associated ALRI episodes Incidence (95% CI per 100 person-years)
All Year	9797.9	564	5.74 (5.3, 6.2)	160	2.1 (1.9, 2.4)
2011	1506.5	119	7.9 (6.6, 9.5)	46	3.1 (2.3, 4.1)
2012	1568.3	16	1.0 (0.6, 1.7)	5	0.3 (0.1, 0.8)
2013	1613.2	153	9.5 (8.1, 11.1)	56	3.5 (2.7, 4.5)
2014	1697.8	5	0.3 (0.1, 0.7)	0	0 (NA)
2015	1689.4	183	10.8 (9.4, 12.5)	79	4.7 (3.8, 5.8)
2016	1722.7	88	5.1 (4.1, 6.3)	24	1.4 (0.9, 2.1)
Sex					
Male	4875.8	279	5.7 (5.1, 6.4)	116	2.4 (2.0, 2.4)
Female	4922.1	285	5.8 (5.1, 6.5)	94	1.9 (1.6, 2.3)
Age					
0–2 months	191.1	14	7.3 (4.0, 12.3)	8	4.2 (1.8, 8.2)
3–5 months	167.7	20	11.9 (7.3, 18.4)	9	5.4 (2.5, 10.2)
6–8 months	169.8	40	23.6 (16.8, 32.1)	22	13.0 (8.1, 19.6)
9–11 months	167.8	38	22.7 (16.0, 31.1)	23	13.7 (8.7, 20.6)
1–2 years	659.4	100	15.2 (12.3, 18.4)	50	7.6 (5.6, 10.0)
2–4 years	1349.6	143	10.6 (8.9, 12.5)	51	3.8 (2.8, 5.0)
4–6 years	1395.8	105	7.5 (6.2, 9.1)	30	2.1 (1.5, 3.1)
6–8 years	1349.9	38	2.8 (2.0, 3.9)	12	0.9 (0.5, 1.6)
8–10 years	1392.3	33	2.4 (1.6, 3.3)	3	0.2 (0.0, 0.6)
10–12 years	1445.6	15	1.0 (0.6, 1.7)	1	0.1 (0.0, 0.4)
>12 years	1509.0	18	1.2 (0.7, 1.9)	1	0.1 (0.0, 0.4)

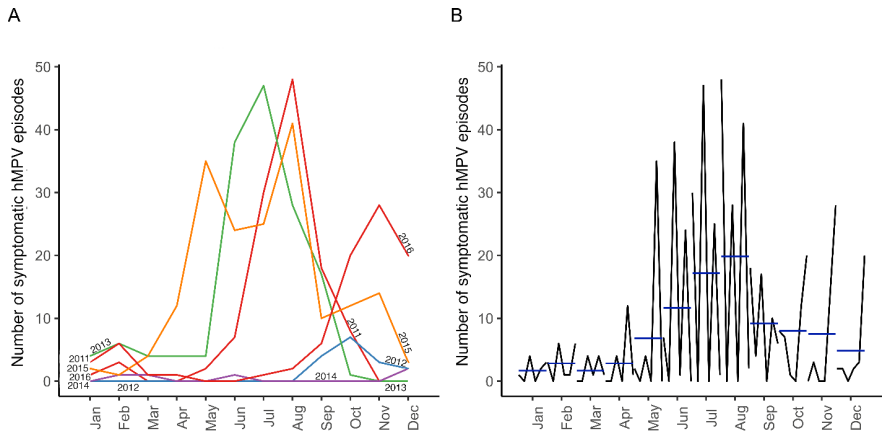
**Supplemental Table 3.** Estimated effective reproduction number for each outbreak period. We assumed a sigma of 1 day and calculated the Growth rate ( $r$ ), scaling growth ( $p$ ), and effective reproduction number for each outbreak using a 5-day and 7.5-day generation interval.

5-Day Mean Generation Interval Week	5-Day Mean Generation Interval Ascending phase length (weeks)	5-Day Mean Generation Interval Growth rate ( $r$ ) Mean (95% CI)	5-Day Mean Generation Interval Scaling of growth ( $p$ ) Mean (95% CI)	5-Day Mean Generation Interval Reproduction number Mean (95% CI)
7/3/2011	7	1.50 (0.56, 3.00)	0.66 (0.38, 1.00)	1.20 (1.10, 1.50)
5/19/2013	9	1.20 (0.48, 2.40)	0.65 (0.40, 0.95)	1.10 (1.10, 1.30)
3/22/2015	7	0.65 (0.51, 1.10)	0.93 (0.64, 1.00)	1.40 (1.10, 1.50)
10/2/16	8	0.74 (0.28, 2.40)	0.76 (0.31, 1.00)	1.20 (1.00, 1.30)
7.5-Day Mean Generation Interval Week	7.5-Day Mean Generation Interval Ascending phase length (weeks)	7.5-Day Mean Generation Interval Growth rate ( $r$ ) Mean (95% CI)	7.5-Day Mean Generation Interval Scaling of growth ( $p$ ) Mean (95% CI)	7.5-Day Mean Generation Interval Reproduction number Mean (95% CI)
7/3/2011	7	1.50 (0.56, 3.00)	0.66 (0.38, 1.00)	1.30 (1.10, 1.80)
5/19/2013	9	1.20 (0.48, 2.40)	0.65 (0.40, 0.95)	1.20 (1.10, 1.40)
3/22/2015	7	0.65 (0.51, 1.10)	0.93 (0.64, 1.00)	1.70 (1.30, 1.90)
10/2/16	8	0.74 (0.28, 2.40)	0.76 (0.31, 1.00)	1.30 (1.10, 1.40)

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**Supplemental Fig 1.** Study participant clinic visits and outcomes. Panel A describes the total monthly counts of clinic visits (grey), visits that met the hMPV testing criteria (purple), and visits with ALRI (light red). Panel B describes hMPV-related outcomes per month where visits that met the hMPV testing criteria (grey), followed by those that were symptomatic RT-PCR confirmed hMPV events (orange), and visits with hMPV-associated ALRI (light blue).



**Supplemental Fig 2.** Time series patterns of monthly symptomatic hMPV infections. Panel A describes the variation of hMPV infection over time with each year plotted separately. Panel B aggregates all the years of data and plots the time series recorded by month; the blue line denotes the mean of the hMPV infections per month.