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## Supplementary information

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# The effects of the COVID-19 pandemic on community respiratory virus activity

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## Contents

## Supplementary Table 1 Community Endemic Viruses Associated with Respiratory Infections in Humans

| Name | Taxonomy | Virology | Clinical Features | Seasonality | Methods of Transmission | Community Activity Changes During the COVID-19 Pandemic |
|---|---|---|---|---|---|---|
| Adenovirus[1] | **Family:** *Adenoviridae*<br>**Genus:** *Mastadenovirus*<br>**Species:** *Human mastadenovirus A-G*<br>**Seroptye:** > 80 serotypes | Double-stranded, non-enveloped DNA virus | Range of clinical disease phenotypes including upper and lower respiratory tract and gastrointestinal disease that may differ by serotype; systemic disease in those who are immunocompromised; exacerbation of underlying conditions; can cause latent infections and reactivate when the immune system is compromised[2-8] | Year-round circulation with peaks in the winter and early spring in temperate climates; possible species and serotype-specific seasonality[2] | Transmission likely influenced by clinical disease phenotype including respiratory droplets, mucosal and conjunctival inoculation, fecal-oral spread, fomite transfer and exposure to bodily fluids; can have long shedding period | • Adenoviruses experienced a decrease in community activity at the beginning of the COVID-19 pandemic, but detections increased and persisted despite ongoing use of non-pharmaceutical interventions in some locations.[9-12] |
| Human bocavirus[13,14] | **Family:** *Parvoviridae*<br>**Genus:** Bocaparovirus<br>**Species:** Human bocavirus 1-4 | Single-stranded, non-enveloped DNA virus | Respiratory tract disease frequently accompanied by other viral co-infections; may also be associated with gastrointestinal disease in some people; exacerbation of underlying conditions[13,15,16] | Not well described, but in temperate climates appears to circulate year-round with highest prevalence in the autumn to spring[13,17] | Thought to be primarily transmitted via respiratory droplets, may also be transmitted via fecal-oral transmission; found in respiratory secretions, blood and feces; theoretical fomite transmission given its resistance to environmental factors on frequently touched surfaces[15,18-20] | • Across most locations, human bocavirus activity decreased at the onset of the COVID-19 pandemic with reports of infection resurgences later in 2020.[12,21-24] |
| Human coronavirus, seasonal[20,25,26] | **Family:** *Coronaviridae*<br>**Genus:** *Alphacoronavirus*<br>**Species:** HCoV-229E, HCoV-NL63 | Single-stranded, positive-sense, enveloped RNA virus | Upper and lower respiratory tract disease; exacerbation of underlying conditions; likely species-specific clinical disease phenotypes[27-29] | Contributes to annual winter peaks with alternating predominance of species; HCoV-OC43 typically shows an annual peak in winter | Transmitted primarily through respiratory droplets and aerosols and less commonly through direct contact or self-inoculation through | •All four seasonal human coronaviruses experienced marked reductions early in the COVID-19 pandemic and remained suppressed through the end of 2020 in the US.[36,37] |

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| | **Family:** *Coronaviridae*<br>**Genus:** *Betacoronavirus*<br>**Species:** HCoV-HKU1, [38] HCoV-OC43 | | | months; Tropical climates and in temperate sites in China, there is less of a defined seasonality with HCoV circulation[27,30,31] | fomites; has been recovered in feces, although oral-fecal route is not considered to be a significant transmission mode in humans[32-35] | •In the US, seasonal epidemics of all four seasonal human coronavirus occurred early in 2021. Timing of these peaks varied by geography and species with elevated detection extending into summer in most locations.[37] |
| Enterovirus[39] | **Family:** *Picornaviridae*<br>**Genus:** *Enterovirus*<br>**Species:** *Enterovirus A-D* | Single-stranded, positive-sense, non-enveloped RNA virus | Respiratory tract and gastrointestinal disease, systemic infection, acute cardiovascular events and central nervous symptom infection, dermatologic disease; clinical phenotype frequently associated with specific species and serotypes; exacerbation of underlying conditions[39,40] | Regional variations by latitudinal gradients; in the US southern states have more year-round circulation while seasonal peaks occur more in northern regions and a national peak typically during summer months; shifting patterns of serotypes with possible unique seasonality (e.g. Enterovirus D68 with biennial regional circulation) [41,42] | Transmission can vary by species and serotype affected by the clinical disease phenotype, Transmission via respiratory droplets or the fecal-oral route are most common; possible vertical transmission perinatally[43] | •Most molecular tests are not able to distinguish between enteroviruses and rhinoviruses.<br>•Reports across different countries and regions demonstrated decreased rhinoviruses and respiratory enterovirus activity associated with broad non-pharmaceutical intervention implementation early in the COVID-19 pandemic.[44-46]<br>•Unlike other respiratory viruses that remained suppressed, respiratory enterovirus and rhinovirus detection increased back to or above baseline seasonal levels in the middle of 2020. Activity levels persisted despite the ongoing use of non-pharmaceutical interventions in most localities and may reflect inherent viral properties that allow infections to quickly return when NPI implementation is loosened. [9,22,24,45,46] |
| Influenza virus[47,48] | **Family:** *Orthomyxoviridae*<br>**Genus:** *Alphainfluenzavirus*<br>**Species:** *Influenza A Virus*<br>**Subtype:** *A(H3N2), A(H1N1)pdm09* | Single-stranded, negative-sense, enveloped segmented RNA virus | Influenza A and B viruses cause upper and lower respiratory tract disease; associated with extrapulmonary manifestations including neurologic complications and acute cardiovascular events; exacerbation of underlying conditions; Influenza C virus infection typically associated with mild upper respiratory tract | Seasonal epidemic peaks in temperate climates with variability of seasonality in tropical locations including year-round circulation; Species, subtype, and virus strain predominance may vary by year[48,52-55] | Transmission by respiratory droplets including aerosols from infected individuals at the onset of symptoms; fomite transmission possible as well although not thought to be a large contributor to | •Global seasonal influenza activity including healthcare burden associated with influenza virus infection abruptly decreased at the onset of the COVID-19 pandemic coinciding with broad non-pharmaceutical intervention implementation.[11,44,59-64]<br>•Influenza activity remained low |

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|  | **Family:** *Orthomyxoviridae*<br>**Genus:** *Betainfluenzavirus*<br>**Species:** *Influenza B virus*<br>**Lineage:** *B/Victoria, B/Yamagata* |  | disease with lower respiratory tract and gastrointestinal disease also reported[49-51] |  | infection; asymptomatic or pauci-symptomatic individuals may play a role in community transmission[56-58] | in many localities through 2021 with sporadic outbreaks reported and interseasonal epidemics; relative increase in influenza activity in 2021-2022 influenza seasons in northern temperate zones and countries in the tropics and subtropics.[10,65-68]<br>•Low levels of circulating influenza virus may create challenges for annual vaccine strain selection.<br>•While influenza A(H3N2), A(H1N1)pdm09, B/Victoria viruses have been reported since the start of the COVID-19 pandemic, there have been no confirmed reports of influenza B/Yamagata since March 2020. [69] |
|  | **Family:** *Orthomyxoviridae*<br>**Genus:** *Gammainfluenzavirus*<br>**Species:** *Influenza C virus*<br>**Lineage:** *C/Taylor, C/Mississippi, C/Aichi, C/Yamagata, C/Kanagawa, C/Sao Paulo*[51,70] |  |  | Poorly understood; peaks during colder months with possible biennial epidemics[51] |  |  |
| Human metapneumovirus[71-73] | **Family:** *Pneumoviridae*<br>**Genus:** *Metapneumovirus*<br>**Species:** *Human metapneumovirus*<br>**Lineage:** *A1, A2a, A2b, B1, B2* | Single-stranded, negative-sense, enveloped RNA virus | Upper and lower respiratory tract disease; exacerbation of underlying conditions; common cause of community-acquired pneumonia in hospitalized young children | Annual co-circulation of HMV lineages with alternating predominant lineages that show variability in seasonal peaks; Noted biennial peaks every 2 years in winter and spring[74,75] | Transmission via respiratory droplets and close/direct contact with others; infectious viral particles can be found on frequently touched surfaces but to what extent fomite transmission contributes to community burden is unknown[71] | •Community circulation as well as healthcare burden associated with human metapneumovirus was reduced with the spread of SARS-CoV-2 and remained low through the end of 2020.[9-11,21,76,77] |
| Human parainfluenza virus[78,79] | **Family:** *Paramyxoviridae*<br>**Genus:***Respirovirus*<br>**Species:** *Human respirovirus 1 (HPIV-1), Human respirovirus 3 (HPIV-3)* | Single-stranded, negative-sense, enveloped RNA virus | Upper and lower respiratory tract disease; exacerbation of underlying conditions[78] | HPIV-1: Seasonal peaks in autumn every other year[80,81]<br>HPIV-3: Seasonal peaks in the spring[80,81] | Transmission primarily through respiratory droplets and less likely aerosolized particles; possible self-inoculation through touching of contaminated surfaces[78] | •Along with other enveloped viruses, human parainfluenza virus circulation decreased at the outset of the COVID-19 pandemic and remained low through the end of 2020; this corresponded with reductions in emergency department visits and hospitalizations associated with human parainfluenza virus infection. [9-11,21,76,77] |
|  | **Family:** *Paramyxoviridae*<br>**Genus:***Orthorubulavirus*<br>**Species:** *Human orthorubulavirus 2 (HPIV-2), Human* |  | HPIV-2 most commonly associated with less severe upper respiratory tract disease but can also cause lower respiratory tract disease; HPIV-4 can also cause | HPIV-2: Inconsistent seasonal peaks occasional occurring in the autumn[79-81] |  |  |

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| | *orthorubulavirus 4 (HPIV-4)* | | both upper and lower respiratory tract disease but is overall less commonly detected; exacerbation of underlying conditions[78] | HPIV-4: Autumn-winter seasonality[79-81] | | |
| Human parechovirus[82,83] | **Family:** *Picornaviridae*<br>**Genus:** *Parechovirus*<br>**Species:** *Parechovirus A*<br>***Genotype:*** *HPEV 1-19* | Single-stranded, positive-sense, non-enveloped RNA virus | Respiratory tract and gastrointestinal disease; central nervous system infection reported; infection leading to myocarditis reported as well | Year-round circulation with summer peaks[83,84] | Transmitted through respiratory secretions, droplets and feces[85-88] | •Few studies have been published on human parechovirus activity during the COVID-19 pandemic and baseline surveillance data are limited; however available data suggest there was decreased detection of human parechovirus in young children early in 2020.[21] |

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| Respiratory syncytial virus[89] | **Family:** *Pneumoviridae*<br>**Genus:** *Orthopneumovirus*<br>**Species:** *Human orthopneumovirus (RSV)*<br>**Subtype:** *RSV-A, RSV-B* | Single-stranded, negative-sense, enveloped RNA virus | Upper and lower respiratory tract disease; exacerbation of underlying conditions; leading cause of lower respiratory tract disease including bronchiolitis and pneumonia in young children; c primary infectious cause of infant hospitalizations in the US before the COVID-19 pandemic; cause of pneumonia in adults; central nervous system disease has also been reported[90-92] | Seasonal peaks in winter often overlapping with influenza virus circulation in temperate climates; seasonal peaks also seen in tropical climates in colder months[93-95] | Transmission via respiratory droplets between close contacts; self-inoculation through touching of contaminated surfaces; Contact and fomite transmission also possible[96-98] | •In 2020, respiratory syncytial virus (RSV) circulation decreased across geographical regions and climate zone in association with stay-at-home orders which reduced non-household social interactions and limited transmission through close contacts in childcare or school-age environments. [99,100]<br>•During subsequent seasons, countries reported rapid resurgence of RSV infections with some localities experiencing inter-seasonal RSV circulation with uncharacteristic peaks during times of the year not typical of RSV seasonality.[100,101]<br>•RSV-associated emergency department visits and hospitalizations similarly decreased with healthcare burden mirroring community circulation levels as cases returned from 2021 onward.[24,36,77,100-110]<br>•RSV-associated diagnoses including acute respiratory illness and bronchiolitis experienced similar changes with decreases early in the COVID-19 pandemic and then a return to equivalent or higher levels as non-pharmaceutical intervention measures were relaxed.[111]<br>•RSV genomic diversity may have been affected by the reduction in community circulation with regional shifts in subtype predominance; Reports from Australia showed reductions in RSV-A sublineages and emergence of novel lineages.[111] |

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| Rhinovirus[82,112,113] | **Family:** *Picornaviridae*<br>**Genus:** *Enterovirus*<br>**Species:** *Rhinovirus A, Rhinovirus B, Rhinovirus C*<br>**Serotype:** *~ 160 serotypes* | Single-stranded, positive-sense, non-enveloped RNA virus | Upper and lower respiratory tract disease; exacerbation of underlying conditions; causes community acquired pneumonia in young children and elderly adults[91,114-117] | Year-round circulation with occasional seasonal peaks in late summer to autumn and spring; regional variation in seasonality has been reported; seasonality also may be dependent on circulating serotype[113,118-122] | Transmission via respiratory droplets and aerosols between close contacts; long shedding period; self-inoculation via contaminated surfaces, person-to-person contact and fomite transmission also possible[123-126] | •Most molecular tests are unable to differentiate between rhinoviruses and enteroviruses given their genetic relatedness; genomic sequencing is frequently required to differentiate these viral species<br>•Decreases in rhinovirus and respiratory enterovirus activity coincided with the near-simultaneous implementation of COVID-19 community mitigation measures, but early relaxing of these policies was associated with a rebound of activity returning to pre-COVID-19 pandemic levels. [22,24,36,44,127,128]<br>•One genomic study of rhinovirus activity in South Korea showed similar predominance of rhinovirus species before and during the COVID-19 pandemic.[22] |

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