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# Rhinovirus and SARS-COV-2 Co-Circulation: A Unique Insight on the Pandemic

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**Abstract:** The interaction of SARS-COV-2 and other respiratory viral pathogens remains an active area of inquiry. Non-pharmaceutical interventions resulted in historically low levels of respiratory viral pathogen infection rates during 2020. In this report, we present evidence that Rhinovirus and SARS-COV-2 demonstrated a negative correlation in their distribution over a period of 98 weeks since the declaration of the pandemic. Rhinovirus infections allow a unique insight into the circulation patterns of SARS-COV-2.

**Keywords:** SARS-COV-2, Rhinovirus, COVID-19, Pandemic, Co-Circulation

## Introduction

The WHO declared the outbreak of COVID-19 a global pandemic on March 11, 2020 (Cucinotta and Vanelli., 2020), which resulted in an unprecedented mobilization of public health resources globally that comprised both pharmaceutical and Non-Pharmaceutical Intervention (NPI) strategies. Models suggest that NPI strategies have been successful in slowing down the spread of SARS-COV-2 (Liu *et al*., 2021). Economic lockdowns, social distancing, and increased emphasis on personal hygiene had a significant impact on the seasonal circulation of other respiratory viral pathogens. Almost all respiratory viruses saw a dramatic decline in their infection rates with Respiratory Syncytial Virus (RSV) and Influenza activity falling to almost zero during 2020 (FluSurv-NET; RSV-NET). Relaxing of social distancing norms and the resumption of in-person teaching resulted in the non-seasonal increase in RSV levels during the summer months in 2021 (Antoon *et al*., 2021). In the present study, we present infection rates of Human Rhinovirus (HRV) and SARS-COV-2 over a two-year period (2020-2022) which shows a statistically significant negative correlation between the co-circulation of the two respiratory viral pathogens.

## Materials and Methods

The data presented is a survey of positive HRV and SARS-COV-2 detections in symptomatic patient samples tested at HealthTrackRX laboratory located in Denton, Texas, over a period of 98 weeks beginning on 16$^{th}$ March 2020. The study was deemed exempt from Institutional Review Board approval as no personal identifying data for the patients were either collated or accessed. The samples were anonymized and only the percent positivity rate of the pathogens in the tested samples was determined. Extraction of nucleic acid and real-time PCR for HRV and SARS-COV-2 were performed according to previously described procedures (Singh *et al*., 2021). Pearson correlation coefficient (R) was calculated using R version 3.6.0 (R Foundation for Computational Computing, Vienna, Austria).

## Results and Discussion

Co-circulation of HRV and SARS-COV-2 demonstrates a pattern wherein every peak in HRV infections is interspersed between SARS-COV-2 infection peaks (Fig. 1). A very clear negative correlation between the two viral species in the population can be observed ($R = -0.21$, P-value = 0.03), even though very low levels of HRV and SARS-COV-2 co-detection within the same sample have been reported previously (Singh *et al*., 2021).

Throughout 2021, as opposed to other respiratory viral pathogens, HRV was detected in patient samples and was the most prominent respiratory viral infection, following SARS-COV-2. The highly resistant nature of the HRV and prolonged viral shedding (Turner, 2007) and potentially decreased surveillance during the pandemic favoring SARS-COV-2 testing only may have contributed to the yearlong persistence of HRV as opposed to other viral pathogens. Similar observations concerning persistent HRV have been reported in Finland (Kuitunen *et al*., 2021) and South Korea (Kim *et al*., 2021).

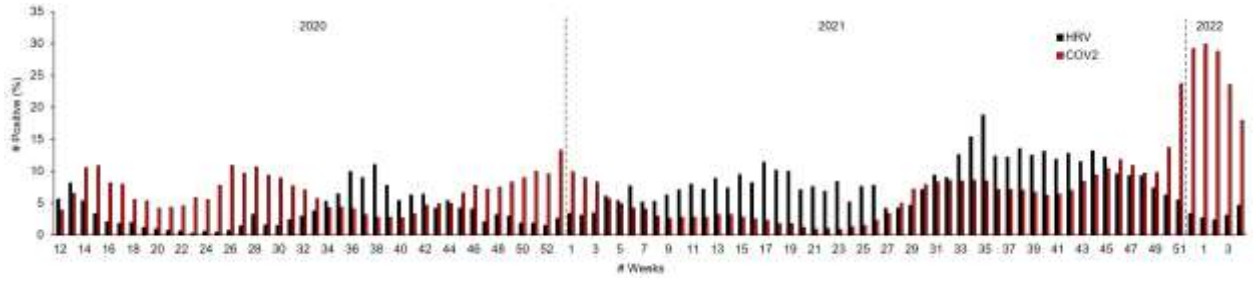


**Fig. 1:** Weekly percent positivity rates of HRV and SARS-COV-2 detected between March 2020 and January 2022

The sustained levels of HRV infections and the lack of equivalent data for other respiratory viruses, during the course of the pandemic in 2020-21 provide a unique blueprint for predicting the course of SARS-COV-2 spread in the population and its potential seasonality. This is reminiscent of the role prior HRV infections played in delaying the 2009 Influenza Virus (IV) pandemic in Europe (Casalegno *et al*., 2010). According to the viral interference theory, previous HRV infection of the respiratory tract results in host defenses being activated that affords protection against other viral pathogens like IV infecting the same tissue (Wu *et al*., 2020). Recently, Cheemarla *et al*. (2021) demonstrated that HRV infection of human bronchial epithelium cells activated interferon-stimulated gene expression that resulted in the prevention of SARS-COV-2 replication.

The novelty of SARS-COV-2 presents both opportunities and challenges. The current pandemic has exposed the vulnerabilities and potentials of our public health resources. With the sporadic success of vaccination drives and the emergence of new SARS-COV-2 variants, IV infections are on the rise in the northern hemisphere, which was not observed in 2020. These developments highlight the need for constant year-round surveillance against respiratory viral pathogens, like HRV, that can help predict the course of the current and future viral epidemics and pandemics.

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## Author's Contributions

**Pallavi Upadhyay:** Data analysis and writing.
**Vijay Singh:** Study concept and writing.

## Ethics

Advarra IRB deemed the study exempt from Institutional Review Board approval, as no personal identifying data for the patients were either collated or accessed.

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