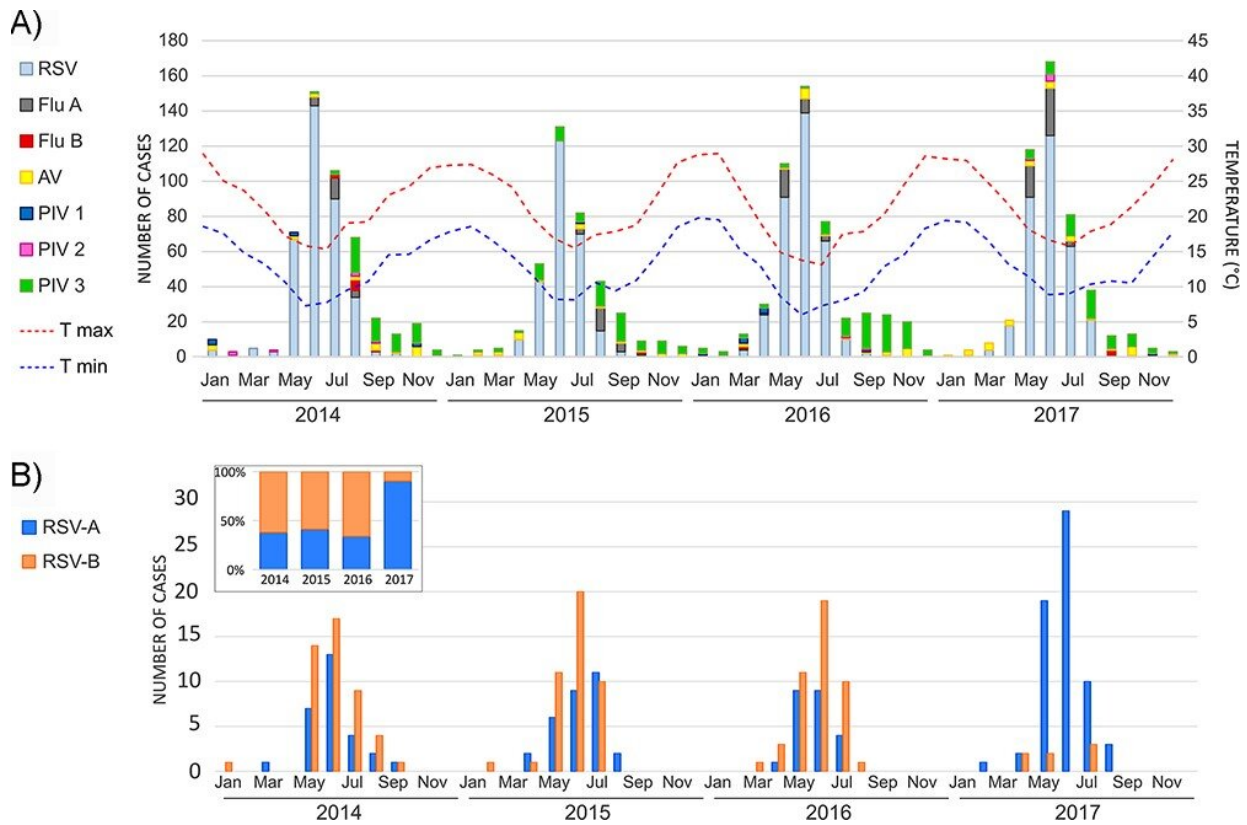


Study finds RSV may evade vaccines via rapid mutation

March 10 2023, by Bill Snyder



Seasonality of RSV cases in children hospitalized with lower respiratory tract infection in Buenos Aires between 2014 and 2017. (A) A cumulative bar graph of the number of positive cases of respiratory viruses detected per month per year. Dotted lines represent the minimum and maximum temperatures recorded per month per year published by the Argentine National Weather Service. (B) The seasonality of the RSV-positive cases for subgroups A and B. Credit: *Virus Evolution* (2023). DOI: 10.1093/ve/vead006

For most people, respiratory syncytial virus (RSV) is about as dangerous as the common cold. But for children younger than six months old, and for people whose immune defenses have been weakened by age, disease, chemotherapy or transplantation, RSV can be fatal.

Last winter an unusual spike in RSV infections filled the wards of children's hospitals around the country. Fortunately, several RSV vaccines are in the final stages of clinical testing and two have been recommended for use in [older adults](#) by an advisory panel of the U.S. Food and Drug Administration.

According to Suman Das, Ph.D., associate professor of Medicine in the Division of Infectious Diseases at Vanderbilt University Medical Center, that may not solve the problem.

In a paper published in the journal *Virus Evolution*, Das and colleagues in Buenos Aires, Argentina, concluded that RSV's ability to mutate rapidly to escape detection by the body's immune system makes it more challenging to design and develop vaccines that can stop it from spreading.

"Once the [vaccine](#) comes, this is the beginning and not the end," Das said. "If we have the vaccine, the virus will evolve faster. The same thing happened with COVID-19. We need to understand what kind of mutation is happening, and whether (it) will affect the efficacy of the vaccines."

Das' lab is among the world leaders in sequencing the RSV genome. The goal is to better understand the diversity, or changes in the viral genetic code that produce different strains of the virus.

The report of RSV diversity, co-authored by Mariana Viegas, Ph.D., and colleagues at the R. Gutierrez Children's Hospital in Buenos Aires,

detailed how the persistence of a predominant RSV strain in Argentina's capital city enabled, in 2017, the sudden emergence and successful spread of a previously unrecognized strain.

The same thing happened with SARS-CoV-2, which causes COVID-19. When delta was the predominant strain of the virus, most people developed immunity to it. But when a new strain called omicron emerged, their immune systems were not primed to recognize it.

"When we're missing an [immune response](#) to something new coming in," Das said, "it's more apt to spread." Diversity, or rather the lack of it, may be a signal that a new strain of virus is on its way. "If we're already looking at other genotypes," he said, "maybe one of them is going to come to us."

The other paper, published Feb. 23 in the *Journal of Virology*, extends collaborative work by Das, Stokes Peebles, MD, the John Murray Professor of Medicine, and Tina Hartert, MD, MPH, the Lulu H. Owen Professor of Medicine, director of the Center for Asthma Research and VUMC Vice President for Translational Research, and colleagues at the J. Craig Venter Institute in Rockville, Maryland, and Emory University School of Medicine in Atlanta that documented increased severity of RSV infections in male babies and a link between RSV and asthma. The current study found an increased frequency of infection by a particular strain of RSV in male babies associated with the presence of co-occurring bacterial infections in the nose.

"Understanding how different RSV genotypes and host factors contribute to disease severity is vital for creating an effective vaccine," the researchers concluded. It also may help identify those at greatest risk who need to be vaccinated first.

Surveillance and sequencing programs thus become critical to ensuring

that RSV vaccines are effective. "We can track where the new variants are coming from," Das said, and if the vaccines that are expected to be approved later this year do not cover them, they can be updated.

"We need to know where the [virus](#) is evolving, and how vaccines are driving evolution," he added. "We want to be ahead of the game."

More information: Stephanie Goya et al, Evolutionary dynamics of respiratory syncytial virus in Buenos Aires: Viral diversity, migration, and subgroup replacement, *Virus Evolution* (2023). [DOI: 10.1093/ve/vead006](https://doi.org/10.1093/ve/vead006)

Yi Tan et al, Influence of Sex on Respiratory Syncytial Virus Genotype Infection Frequency and Nasopharyngeal Microbiome, *Journal of Virology* (2023). [DOI: 10.1128/jvi.01472-22](https://doi.org/10.1128/jvi.01472-22)

Provided by Vanderbilt University

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