Check for updates

OPEN ACCESS

EDITED AND REVIEWED BY Akio Adachi, Tokushima University, Japan

*CORRESPONDENCE Alfonso J. Rodríguez-Morales arodriguezmo@cientifica.edu.pe

RECEIVED 13 November 2024 ACCEPTED 04 December 2024 PUBLISHED 19 December 2024

CITATION

Rodríguez-Morales AJ, Velasco-Hernández JX and Comas-Garcia A (2024) Editorial: Impact of the SARS-CoV-2 pandemic on the evolution and epidemiology of other viruses. *Front. Virol.* 4:1527580. doi: 10.3389/fviro.2024.1527580

COPYRIGHT

© 2024 Rodríguez-Morales, Velasco-Hernández and Comas-Garcia. This is an open-access article distributed under the terms of the Creative Commons Attribution License (CC BY). The use, distribution or reproduction in other forums is permitted, provided the original author(s) and the copyright owner(s) are credited and that the original publication in this journal is cited, in accordance with accepted academic practice. No use, distribution or reproduction is permitted which does not comply with these terms.

Editorial: Impact of the SARS-CoV-2 pandemic on the evolution and epidemiology of other viruses

Alfonso J. Rodríguez-Morales^{1,2*}, Jorge X. Velasco-Hernández³ and Andreu Comas-Garcia^{4,5}

¹Clinical Epidemiology and Biostatistics, Faculty of Health Sciences, Universidad Científica del Sur, Lima, Peru, ²Gilbert and Rose-Mari Chagoury School of Medicine, Lebanese American University, Beirut, Lebanon, ³Instituto de Matemáticas-Unidad Juriquilla, Universidad Nacional Autónoma de México, Querétaro, Mexico, ⁴Microbiology Department, School of Medicine, Universidad Autónoma de San Luis Potosí, San Luis Potosí, Mexico, ⁵School of Medicine, Universidad Cuauhtémoc San Luis Potosí, San Luis Potosí, Mexico

KEYWORDS

SARS-CoV-2, COVID-19, influenza, RSV, evolution, epidemiology

Editorial on the Research Topic

Impact of the SARS-CoV-2 pandemic on the evolution and epidemiology of other viruses

Five years after the onset of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) pandemic, its consequences continue reverberating globally. The Coronavirus Disease 2019 (COVID-19) pandemic has profoundly transformed various aspects of life, including lifestyles, travel, education, economies, food security, environmental pollution, and even mental health. The widespread adoption of telecommuting and social distancing measures has significantly altered social interactions and work environments (1). Additionally, the concept of "immune debt" has emerged, affecting the population's immune responses and altering the epidemiology of numerous diseases and infection patterns (2). The dynamics of COVID-19 transmission may also have influenced the evolution of other pathogens, contributing to the emergence of new variants and reshaping the public health landscape. These collective changes have left a lasting impact on society that we are still working to understand and address. So far, 776 million cases (October 27, 2024) and 7 million deaths worldwide have been reported of SARS-CoV-2/COVID-19.

One intriguing aspect of the pandemic's impact on pathogen evolution can be illustrated by the experience from 2009, when a segment of the G gene of the RSV-A was duplicated, resulting in the emergence of the ON1 genotype (3, 4). Furthermore, during the 2020-21 winter season, the circulation of influenza viruses was notably absent (Figure 1), but even also with the Respiratory Syncytial Virus (RSV) (Figure 1). The Global Influenza Surveillance and Response System (GISRS) reported a significant decline in influenza activity between April and November 2020 (5–7). These examples highlight how the pandemic reshaped the landscape of infectious diseases in ways we are only beginning to comprehend. Therefore, in the Research Topic "*Impact of the SARS-CoV-2*



pandemic on the evolution and epidemiology of other viruses", we analysed how the presence and dominance of SARS-CoV-2 may influence the epidemiology and evolution of other viruses.

In Ghana, Asante et al. reported a decrease in influenza activity during 2020. Using a sentinel surveillance strategy, they evaluated the percentage of influenza positivity from 2017 to 2021. Influenza activity was low between weeks 1 and 10 of 2020, similar to levels seen in 2019. However, there were no detections of influenza until week 40. Overall, influenza activity in late 2020 was lower than in the other periods studied. These results were consistent with data reported by the CDC and other researchers (5–7). It is essential to mention that the world is experiencing multiple independent outbreaks of influenza A/H5N1 in various birds and mammals, with some cases reported in humans. This event raises the question of whether the increase in atypical circulation of influenza A/H5N1, a consequence of the COVID-19 pandemic, could be (8). Hayek et al. conducted a retrospective cohort study in Tennessee between 2018 and 2022. During the pandemic, the proportion of RSV detections in children under 5 years decreased from 63.7% to 59.5%. The study also reported changes in codetection patterns between RSV and other viruses. Like influenza, the authors noted a delay in RSV cases during 2020-2021. We concur with the authors' assertion that the disruption in the circulation of respiratory viruses during the COVID-19 pandemic may explain the observed differences in RSV detection. Other articles showed an increase in paediatric and adult hospitalization and detection comparable to prior seasons (9).

The changes in epidemiology and potential viral evolution due to COVID-19 are not the only intriguing phenomena. Another important question to explore is whether the circulation of SARS-CoV-2 has altered the clinical manifestations or severity of diseases caused by other viruses, particularly influenza and RSV. For example, reports from the USA indicate an increased risk of ICU admission for hospitalised adults due to RSV infection. Researchers have observed concurrent mutations in the RSV-B fusion protein at antigenic sites, especially in clusters detected during 2021-22. These mutations may reduce the neutraliation potency of nirsevimab by 0.5-fold (I206M), 1.2-fold (Q209R), and 29.9-fold (K68N) (10). This phenomenon is similar to the convergent evolution observed in the G gene of the RSV-A ON1 genotype following the 2009 pandemic (4, 11).

The COVID-19 pandemic has altered the epidemiology of respiratory viruses and transformed diagnostic and therapeutic strategies and technologies. In this Research Topic, there is a comprehensive review of SARS-CoV-2 viral proteins and their significance in diagnostics and therapeutics (Chung et al.). Chung et al. describe the spike protein and provide an in-depth characterization of the other eight viral proteins. The review evaluates surface and internal proteins' roles as diagnostic targets and platforms for developing antibodies or vaccines. Additionally, it emphasises how diagnostic methods and vaccine technologies operate.

The article of Tirore et al. examines COVID-19 severity among patients in Southern Ethiopia, focusing on factors influencing disease progression. It identifies demographic, clinical, and socioeconomic variables affecting outcomes, emphasising the role of comorbidities like hypertension and diabetes. Strategies to mitigate severity, such as timely diagnosis and management of high-risk groups, are discussed. The study underscores the importance of tailored public health measures in resourcelimited settings.

In conclusion, the SARS-CoV-2/COVID-19 pandemic altered viral evolution and epidemiology by shifting human behaviour, which reduced the transmission of many viruses, especially respiratory ones like influenza and RSV (12, 13). Lower exposure led to waning immunity, resulting in atypical outbreaks and increased viral mutations once restrictions eased. Co-circulation patterns also changed, affecting virus competition and interactions.

Author contributions

AM: Conceptualization, Data curation, Formal analysis, Funding acquisition, Investigation, Methodology, Project administration, Resources, Software, Supervision, Validation, Visualization, Writing – original draft, Writing – review & editing. JV: Conceptualization, Data curation, Formal analysis, Funding acquisition, Investigation, Methodology, Project administration, Resources, Software, Supervision, Validation, Visualization, Writing – original draft, Writing – review & editing. AC: Conceptualization, Data curation, Formal analysis, Funding acquisition, Investigation, Methodology, Project administration, Resources, Software, Supervision, Validation, Visualization, Resources, Software, Supervision, Validation, Visualization, Writing – original draft, Writing – review & editing.

Conflict of interest

ACG has been speaker of AstraZeneca.

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

The author(s) declared that they were an editorial board member of Frontiers, at the time of submission. This had no impact on the peer review process and the final decision.

Publisher's note

All claims expressed in this article are solely those of the authors and do not necessarily represent those of their affiliated organizations, or those of the publisher, the editors and the reviewers. Any product that may be evaluated in this article, or claim that may be made by its manufacturer, is not guaranteed or endorsed by the publisher.

References

1. Onyeaka H, Anumudu CK, Al-Sharify ZT, Egele-Godswill E, Mbaegbu P. COVID-19 pandemic: A review of the global lockdown and its far-reaching effects. *Sci Prog.* (2021) 104:00368504211019854. doi: 10.1177/00368504211019854

2. Munro AP, Jones CE. Immunity debt and unseasonal childhood respiratory viruses. Br J Hosp Med. (2022) 83:1-3. doi: 10.12968/hmed.2022.0349

3. Eshaghi A, Duvvuri VR, Lai R, Nadarajah JT, Li A, Patel SN, et al. Genetic variability of human respiratory syncytial virus A strains circulating in Ontario: A novel genotype with a 72 nucleotide G gene duplication. *PloS One*. (2012) 7. doi: 10.1371/journal.pone.0032807

 Comas-García A, Noyola DE, Cadena-Mota S, Rico-Hernández M, Bernal-Silva S. Respiratory syncytial virus-A ON1 genotype emergence in central Mexico in 2009 and evidence of multiple duplication events. *J Infect Dis.* (2018) 217:1089–98. doi: 10.1093/ infdis/jiy025

5. Power BI report. Available online at: https://app.powerbi.com/view?r= eyJrIjoiZTkyODcyOTEtZjA5YS00ZmI0LWFkZGUtODIxNGI5OTE3Yj M0IiwidCI6ImY2MTBjMGI3LWJkMjQtNGI2OS04MTBiLTNkYzI4MGFmYjU5MCI sImMiOjh9 (accessed November 1, 2024).

6. O'Neill G, Taylor J, Kok J, Dwyer D, Dilcher M, Hua H, et al. Circulation of influenza and other respiratory viruses during the COVID-19 pandemic in Australia and New Zealand, 2020–2021. West Pac Surveill Response J. (2023) 14:13–22. doi: 10.5365/wpsar.2023,14.3.948

7. Chow EJ, Uyeki TM, Chu HY. The effects of the COVID-19 pandemic on community respiratory virus activity. *Nat Rev Microbiol.* (2022), 195–210. Available at: https://www.nature.com/articles/s41579-022-00807-9.

8. CDC. Avian influenza (Bird flu). In: *H5 Bird Flu: Current Situation* (2024). Available at: https://www.cdc.gov/bird-flu/situation-summary/index.html (accessed November 1, 2024).

9. Falsey AR, Cameron A, Branche AR, Walsh EE. Perturbations in respiratory syncytial virus activity during the SARS-CoV-2 pandemic. *J Infect Dis.* (2022) 227:83–6. doi: 10.1093/infdis/jiac434

10. Hultquist J, Rios-Guzman E, Simons L, Dean T, Agnes F, Pawlowski A, et al. Altered RSV epidemiology and genetic diversity following the COVID-19 pandemic (2023). Available online at: https://www.researchsquare.com/article/rs-3712859/v1 (accessed November 1, 2024).

11. Comas-García A, Noyola DE, Bernal-Silva S. Reply to furuse. *J Infect Dis.* (2018) 217:2010–2. doi: 10.1093/infdis/jiy155

12. Bonilla-Aldana DK, Aguirre-Florez M, Villamizar-Peña R, Gutiérrez-Ocampo E, Henao-Martínez JF, Cvetkovic-Vega A, et al. After SARS-CoV-2, will H5N6 and other influenza viruses follow the pandemic path? *Infez Med.* (2020) 28:475–85.

13. Malik YS, Kumar N, Sircar S, Kaushik R, Bhat S, Dhama K, et al. Coronavirus disease pandemic (COVID-19): challenges and a global pserspective. *Pathogens*. (2020) 9:519. doi: 10.3390/pathogens9070519