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Editorial: SARS-CoV-2: virology, epidemiology, diagnosis, pathogenesis and control, volume II

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Editorial on the Research Topic
SARS-CoV-2: virology, epidemiology, diagnosis, pathogenesis and control, volume II

Introduction

SARS-CoV-2 was first described in late December 2019 and rapidly established sustained human-to-human transmission, causing the coronavirus disease 2019 (COVID-19) (1, 2). To date, more than 779 million cases have been documented worldwide, and COVID-19 has had a tremendous impact on global public health, representing one of the greatest crises in human history (3, 4). Remarkably, the rapid response to SARS-CoV-2 brought together the scientific community, biotech companies, and public health authorities to develop effective vaccines, diagnostic tools, new therapies, and coordinated public health measures to control the virus's spread (5).

Yet, despite extensive efforts since its emergence to advance knowledge and address key gaps, several important aspects of the virus and the disease it causes remain incompletely understood. To further expand knowledge of SARS-CoV-2 and COVID-19, we launched Volume II of the Research Topic "*SARS-CoV-2: virology, epidemiology, diagnosis, pathogenesis, and control*," building on the success of the first volume (Volume I). In this Editorial Article, we summarize the main findings of the studies published in this Research Topic.

Epidemiology and transmission dynamics of SARS-CoV-2 across diverse settings

The COVID-19 pandemic was characterized by multiple waves of infection, reflecting the dynamic interplay between viral evolution and population immunity (6, 7). Within this epidemiological perspective, Tayachew et al. conducted a study involving 8,881 participants that demonstrated ongoing SARS-CoV-2 circulation in Ethiopia during the post-pandemic period, with low detection rates but near-universal seropositivity, indicating widespread population exposure. Genomic surveillance revealed exclusive circulation of diverse Omicron sub-lineages, highlighting the importance of sustained, integrated surveillance methods in resource-limited settings.

In another interesting study, Espinosa et al. examined national surveillance data from Ecuador (2020–2024) to model SARS-CoV-2 transmission patterns and assess its transition toward endemicity. Their findings showed a decreasing trend with regular early-year seasonal peaks, indicating a shift toward a stable, seasonally driven transmission pattern likely affected by vaccination.

To address the impact of population mobility on SARS-CoV-2 transmission and healthcare system burden, Guo et al. developed a modeling framework using real SARS-CoV-2 data to assess how inter-regional population mobility influences epidemic spread and healthcare system burden. Using two cities, Taiyuan–Jinzhong and Linfen–Yuncheng, in China as research subjects, the study shows that mobility patterns critically influence transmission dynamics and healthcare congestion, emphasizing the need for coordinated, region-specific intervention strategies.

Complementing these findings, Bao et al. investigated the spatial factors influencing SARS-CoV-2 transmission by analyzing COVID-19 case data from 3,142 U.S. counties using advanced spatial modeling techniques, based on a truncated dataset from March to September 2020. Their results highlight the importance of geographic, environmental, and policy-related factors in shaping transmission dynamics and improving predictive accuracy.

At the individual level, Zeng et al. identified key risk factors driving SARS-CoV-2 transmission by analyzing contact tracing data from 622 primary cases and 31,278 close contacts in China, reporting a secondary attack rate of 1.4% and showing that age, household exposure, and vaccination status significantly influenced the risk of infection.

Translating these epidemiological insights into policy-relevant outcomes, Ertem et al. assessed the impact of non-pharmaceutical interventions on SARS-CoV-2 transmission by analyzing data from 3,970 districts comprising 53,453 schools, finding that lifting school mask mandates was associated with no to modest increases in hospitalizations and deaths at the community level.

Genomic surveillance and viral evolution in regional and global contexts

Since its discovery, SARS-CoV-2 has been characterized by the emergence of variants with distinct mutational profiles (8, 9). Within this context, Bruno et al. examined SARS-CoV-2 genomic surveillance across four Andean countries using 16,867 sequences collected between 2020 and 2024. In that study, the authors showed the temporal progression of major lineages, from early variants (19A/19B) to Gamma, Delta, Lambda, Mu, and later the dominance of Omicron and its sub-lineages, including JN.1. Computational analysis revealed a consistent pattern of viral evolution across countries, emphasizing rapid transnational spread within the region. These findings emphasize the importance of coordinated regional genomic surveillance to track viral evolution and enhance readiness for public health responses (10).

Wastewater-based epidemiology and environmental surveillance

Wastewater-based surveillance has become a critical approach for tracking community-level SARS-CoV-2 transmission in a timely and non-invasive manner and has been extensively investigated since the beginning of the COVID-19 pandemic (11, 12). In this Research Topic, Mustapha et al. analyzed national data from Denmark, the Netherlands, and the United States (2022–2024) and found a strong correlation between SARS-CoV-2 wastewater levels and COVID-19 hospitalization rates. They demonstrated that wastewater virus levels preceded hospitalizations by about a week and could accurately predict short-term trends.

Consistent with these results, Silva-Magaña et al. investigated wastewater-based epidemiology in Mexico City and observed a 6–8-day temporal lag between SARS-CoV-2 RNA levels in wastewater and reported COVID-19 cases. Together, these studies emphasize the utility of wastewater surveillance as a promising tool for predicting healthcare needs and guiding public health decision-making.

Clinical characteristics, disease severity, and patient outcomes

Understanding the clinical features and factors influencing disease severity is crucial for improving patient management and outcomes in COVID-19 (13, 14). Chen et al. analyzed 158 hospitalized COVID-19 patients from Fujian Province, China, during the early pandemic period to characterize clinical presentation, management, and outcomes. Most patients presented with mild to moderate disease, with fever and cough being the most common symptoms, while severe cases showed significant laboratory abnormalities. Older age, elevated white blood cell count, and increased D-dimer levels were identified as key risk factors for disease severity.

In another interesting study, Morales-Jadán et al. investigated coinfections and superinfections in 24 critically ill COVID-19 patients in an intensive care unit (ICU) in Ecuador, reporting a high prevalence of secondary infections (70.8%), predominantly hospital-acquired. The most common pathogens included *Klebsiella pneumoniae*, *Staphylococcus aureus*, and *Enterococcus faecalis*, with bloodstream infections being the most frequent complication. These results highlight the significant role of microbial co-infections in severe COVID-19 cases and emphasize the need for improved microbiological monitoring in COVID-19 patients.

Beyond the acute phase of the disease, Graf et al. analyzed 22,571 hospitalized COVID-19 patients in Austria and found that baseline medication load was strongly associated with long-term mortality and rehospitalization. Polypharmacy and the use of specific drug classes, including antipsychotics and antiepileptics, were linked to a higher risk of death. These results emphasize the significance of baseline health status and medication use in predicting long-term outcomes after COVID-19 hospitalization.

Immunity, seroprevalence, and host factors

The immune response to SARS-CoV-2 infection and its differences across populations remain key to understanding COVID-19 outcomes (7). Through these lines, Dassaye et al. assessed SARS-CoV-2 seroprevalence among 645 participants, including schoolchildren, parents, and teachers in a semi-rural setting in South Africa. They found high levels of seropositivity across all groups, despite a low proportion of self-reported prior infections. These findings suggest widespread exposure to SARS-CoV-2, likely driven by repeated waves of infection and a high prevalence of asymptomatic cases.

Building on population-level evidence of widespread exposure, Lizarazo-Taborda et al. investigated the role of host biological factors in shaping COVID-19 outcomes by analyzing hormonal receptor expression and immune responses across demographic groups of unvaccinated individuals diagnosed with COVID-19 (e.g., premenopausal women, postmenopausal women, and men). The authors identified distinct patterns of estrogen receptor and Angiotensin-Converting Enzyme 2 (ACE2) expression, along with differential cytokine profiles, especially in premenopausal women.

In another very interesting study, Zheng et al. further explored the dynamics of post-infection immunity by analyzing serum antibody levels from 2,521 individuals in China and identifying demographic and behavioral factors associated with immune responses. They observed a general decline in IgG levels over time, highlighting the transient nature of humoral immunity and the importance of sustained immunization strategies to maintain population-level protection.

Vaccination, behavior, and public health interventions

The rapid deployment of COVID-19 vaccines has led to a significant decrease in worldwide deaths, saving millions of lives during the first year of implementation (15). However, while vaccines are among the most effective strategies for reducing the burden of infectious diseases, vaccine hesitancy was considered a significant challenge throughout the COVID-19 pandemic (16). To address this question, Sardinha et al. conducted a systematic review and meta-analysis to estimate COVID-19 vaccine hesitancy in Brazil, reporting an overall prevalence of 13.3%. Hesitancy was higher among parents of children and adolescents and was influenced by factors like misinformation, lack of knowledge, and sociodemographic features.

Expanding on these findings, Luo et al. examined how access and trust influence vaccine uptake in a U.S. population. In an analysis of 255 individuals, they found that proximity to vaccination sites significantly increased vaccination rates, while greater distance reduced uptake. As shown in these and other studies, vaccine hesitancy continues to be a significant challenge that needs to be tackled urgently. Clearly, there is no single solution to this societal challenge, but it will require commitment and coordinated efforts from scientists, global health authorities, and society to enhance trust in vaccines and science.

Data science and risk assessment

Data science and risk assessment are critical for navigating both the epidemiological and information landscapes of the COVID-19 pandemic (17). In this context, Michalak et al. examined how COVID-19 risk is estimated across 101 countries, highlighting limitations in current approaches that underutilize testing data as a quantitative input. In that study, the authors demonstrated that probabilistic metrics, such as local infection probability, more effectively captured spatial transmission patterns than traditional indicators, highlighting the importance of incorporating testing data into risk assessment frameworks to enhance the accuracy of epidemic monitoring.

Concluding remarks and final considerations

The COVID-19 pandemic emerged with an unprecedented impact on global public health. Much has been done, and much has been learned from the efforts undertaken in recent years. The pandemic highlighted the resilience of the global community, particularly scientists, health professionals, and public health authorities, as well as many others who confronted this threat head-on. Importantly, much was achieved despite limited resources, especially in low- and middle-income countries (LMICs) (18).

Although the pandemic has mostly been controlled and SARS-CoV-2 continues to circulate globally, with cases emerging over time, these efforts must not stop. Continued vigilance and sustained monitoring remain essential. Equally important, the knowledge gained during the COVID-19 pandemic will be invaluable for addressing future public health crises of similar magnitude.

Author contributions

SS: Methodology, Supervision, Investigation, Data curation, Formal Analysis, Conceptualization, Validation, Writing – original draft, Project administration, Writing – review & editing, Visualization. LK: Conceptualization, Validation, Project administration, Supervision, Data curation, Writing – review & editing, Investigation, Writing – original draft, Visualization, Formal Analysis. RC: Formal Analysis, Validation, Project administration, Data curation, Supervision, Conceptualization, Visualization, Writing – review & editing, Investigation, Writing – original draft. ZQ: Conceptualization, Investigation, Validation, Writing – review & editing, Formal Analysis, Supervision, Visualization, Data curation, Project administration, Writing – original draft.

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Conflict of interest

The author(s) declared that this work was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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The author(s) declared that Generative AI was not used in the creation of this manuscript.

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