Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

SARS-CoV-2 in low-income countries: the need for sustained genomic surveillance

See Articles page e933

The onset of the COVID-19 pandemic accelerated the implementation of genomic surveillance of its causal agent, SARS-CoV-2, on a global scale. As of April 6, 2023, there were more than 15 million SARS-CoV-2 genomic sequences deposited in the Global Initiative on Sharing Avian Influenza Data database and 6·8 million sequences in GenBank, the two largest virus sequence databases. Despite this unprecedented effort, a pronounced imbalance exists in the extent of SARS-CoV-2 genomic data from high-income and low-income countries.[1] African countries are especially underrepresented, accounting for less than 1% of the global SARS-CoV-2 sequences over the 3-year period of the pandemic (from March 6, 2020, to April 6, 2023), with sparce geographic representation across the continent.[2] Genomic surveillance in South Africa proved crucial in the early identification of the beta (B.1.351) and omicron (B.1.1.529) variants, which later spread across the globe.[3] Studies characterising the diversity of SARS-CoV-2 in Africa have filled important knowledge gaps in the local and global dynamics of the pandemic.[4]

In the *Lancet Global Health*, Francisco José Martínez-Martínez and colleagues[5] undertook a retrospective study to analyse the introductions of the beta and delta (B.1.617.2) variants of concern that circulated in Mozambique during 2021. With a comprehensive approach involving large-scale comparative analysis of the virus diversity in Mozambique and the most extensive collection of global virus sequences placed on a phylogenetic tree, they were able to identify closely related viruses from other geographical regions that potentially sourced the local virus population. Recognising the gap in genomic surveillance across the African continent, the authors further emphasise one of the main challenges of tracking the dynamics of the pandemic when inferring regional and local transmission events. They show that even when using a pandemic-scale analysis, introduction events remain that cannot be reliably assigned to a specific origin.

The molecular epidemiology findings by Martínez-Martínez and colleagues were obtained from analysing close to 700 SARS-CoV-2 genomes and showed that border closures during the beta and delta waves reduced the number of introductions from distant international locations but did not prevent the importation of the virus to Mozambique from neighbouring countries. From these data, the authors raise the question on the effectiveness of closing borders during public health emergencies and the justification of enforcing such measures with considerable social and economic implications. Many countries followed this approach, but the contribution of selective travel restrictions to reduce viral imports and decrease the burden on the health system, and the overall impact in the magnitude of the epidemic remains unknown and difficult to quantify. The long-standing debate of the effectiveness of border closures during a public health crisis involving infectious diseases[6,7] underscores the need for modeling and understanding the dissemination dynamics of respiratory pandemic viruses in an increasingly globalised world. The economic and social impact of sudden changes in international migration policies cannot be underestimated, making this a central issue to address to improve our preparedness for future pandemics.

The need to analyse and interpret the large amount of sequencing data in near real-time during the pandemic crisis has pushed the field of phylogenetics to develop novel methods that account for missing data, and that scale in a computationally efficient manner to very large data sets.[8,9] Since the emergence of early SARS-CoV-2 variants of interest and concern, we have witnessed repeatedly how the dissemination and establishment of new and distinct genetic lineages can negatively impact the efficacy of vaccination and robustness of population immunity.[10] Consequently, continued viral genomic surveillance to detect novel emerging variants in all corners of the world remains imperative. In many countries, routine viral sequencing for SARS-CoV-2 genomic surveillance and other seasonal and emerging pathogens has already decreased and the future of these efforts is uncertain. This issue increases the probability of being blindsided by cryptic circulation of unknown virus diversity, delaying the deployment of adequate countermeasures, should a novel and immune-evasive SARS-CoV-2 variant arise.

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