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Insights from Zimbabwe's SARS-CoV-2 genomic surveillance

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Understanding the genomic epidemiology of SARS-CoV-2 is essential in developing effective public health policy and control programmes. The Article by Tapfumanei Mashe and colleagues[1] published in *The Lancet Global Health* is a valuable contribution to the scientific literature to inform the COVID-19 response in southern Africa. The current problems in the COVID-19 response in many African countries are largely due to a scarcity of scientific evidence to guide response strategies, thus, this Article is not only relevant but timely and complements the efforts from other African countries to understand the evolution of the virus in this part of the world.[2] Earlier, when Africa had only reported a few cases, experts had warned that African countries were ill prepared to confront the COVID-19 pandemic.[3] It is clear that although case numbers have been lower than in other world regions,[4] the pandemic has certainly created public health and socioeconomic challenges, in part, due to insufficient evidence to support public health policies. Moreover, if the pandemic is not controlled in Africa, vaccination efforts could be profoundly affected with the potential emergence of vaccine escape variants in the region.

Mashe and colleagues show that human movement is a key driver shaping SARS-CoV-2 transmission dynamics.[1] Zimbabwe was one of the first countries in southern Africa to impose a nationwide lockdown banning air and local interprovincial travel.[5] Quarantine and testing for travellers from high-risk countries was mandated. However, substantial inward and outward movement from the country through informal borders and limited SARS-CoV-2 testing capacity could have usurped the effect of the lockdown.[6,7] Effective control of future resurgences using human movement restriction strategies would need better enforcement strategies, which include public engagement and awareness and social support for susceptible individuals.

Although Mashe and colleagues outline important findings on the molecular epidemiology of the COVID-19 pandemic in Zimbabwe, the sample size was relatively low (only 156 [1·9%] of 8099 positive samples were successfully genotyped). Additionally, the sample was not representative of the whole country as more than 100 of the 156 sample genotypes were collected in the first 3 months of the study when the pandemic was concentrated in the Harare and Bulawayo provinces. There is smaller representation of the period when local transmission had slightly increased during July to October, 2020. Despite these shortfalls, the study provides important insights as most of the samples were sequenced from almost all travellers in the earlier days of the pandemic. The study findings are important in designing COVID-19 prevention and control policies in light of potential resurgences from new emerging virus variants. Enhancing surveillance through periodic genomic sequencing capacity cannot be overemphasised, especially as variants of concern continue to emerge.[8]

The emergence of SARS-CoV-2 variants pose a serious threat to national vaccination programmes due to potential shifts in herd immunity thresholds. Frequent travel from South Africa as a result of close economic ties between the two countries presents a great risk of importing variants. The usefulness of genomic surveillance studies like the one discussed here as a tool to prevent the emergence and spread of emerging variants would depend on the intensity with which the findings are incorporated into policies by national public health programmes. As with most other parts of the world, the success of genomic surveillance in Zimbabwe, and African countries in general, would require intensification of COVID-19 testing, substantial increments in the proportions of positive samples being sequenced, and persistent analyses of these sequences for concerning signals of new emerging variants. Without periodic sequencing, emerging variants pose a major threat to containing COVID-19 transmission.

Although the Article by Mashe and colleagues provides a substantial contribution to the literature, some key questions remain unanswered. For instance, the study misses key epidemiological analyses (eg, clinical disease spectrum) to detect any shifts from the ancestral wild-type. This assessment would be useful in improving understanding of circulating variants and the effectiveness of the ongoing vaccination efforts. Follow-up research that collects and analyses these key epidemiological data in a nationwide representative sample could better inform COVID-19 response strategies. Granular analysis at the regional level including gender, age group, disease severity, and

clinical outcomes including mortality would be highly informative.

As of Sept 20, 2021, approximately 30% of Zimbabwe's population has received at least one dose of a COVID-19 vaccine, one of the highest vaccination rates in Africa.[9] The country's COVID-19 response will benefit from research in genomic surveillance of positive cases among fully vaccinated individuals to determine effectiveness against variants of concern or interest capable of infecting vaccinated individuals.

Some experts have expressed concern over the emerging evidence that individuals with weakened immune systems due to HIV might be prone to prolonged infection and increased likelihood of SARS-CoV-2 mutations. It is important to note that although Zimbabwe is one of the very few countries to have met the UNAIDS target of having at least 73% of people with HIV with viral load suppression, it is neighbour to South Africa, which has a substantially weaker HIV response with one of the largest numbers of people with HIV without viral load suppression in the world.[10] Under this epidemiological context, local genomic surveillance among people with HIV could be informative.

We declare no competing interests.

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