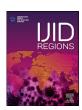


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Perspective

Inadequate SARS-CoV-2 Genetic Sequencing capacity in Zimbabwe: A call to urgently address this key gap to control current and future waves



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ABSTRACT

Zimbabwe continues to confront the COVID-19 pandemic; there is an urgent need for the rapid scale-up of genomic surveillance efforts. In this piece, we express concern on the limited capacity for SARS-CoV-2 genomic surveillance in Zimbabwe due to limited skillsets and laboratory infrastructural deficiencies. We call for an urgent need for funding from the government of Zimbabwe to set up a robust genomic surveillance program to detect SARS-CoV-2 variants of concern in Zimbabwe and guide public health responses accordingly.

Perspective

Severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2) that causes coronavirus disease-2019 (COVID-19) emerged in Wuhan, China in late 2019 (Wang, C., Horby, P. W., Hayden, F. G., & Gao, G. F., 2020). The virus has caused more than 191,000,000 million cases and 4,100,000 million deaths worldwide as of 18 July 2021 (Worldometer, 2021). The first case of COVID-19 in Zimbabwe was reported on 21 March 2020 (Dzobo, M., Chitungo, I., & Dzinamarira, T., 2020); more than 83, 000 cases and 2,600 deaths have been reported as of 18 July 2021 (Worldometer, 2021). Zimbabwe has now entered a third wave of the pandemic largely attributed to a more virulent and transmissible delta variant (B.1.617.2) which has caused a surge in infections and deaths in the African region (Tony Blair Institute of Global Change, 2021). The third wave in Zimbabwe began on the 12th of June as circuit lockdowns were imposed on hotspot districts in Mashonaland West province (MoHCC, 2021a). The third wave has seen Zimbabwe experiencing a surge in cases and deaths. For instance, at the time of writing, the number of COVID-19 cases recorded during the third wave (43,769) represents 52% of the total (83, 619 COVID-19) cases recorded in Zimbabwe since the outbreak begun (MoHCC, 2021a).

COVID-19 prevention in Zimbabwe has been multi-sectoral and the diagnostic laboratory has played a very important role. At present, 128 private laboratories, 26 government laboratories and 3 research laboratories are authorised to conduct SARS-CoV-2 testing and issue results (MoHCC, 2021). Of all the laboratories performing SARS-CoV-2 diagnostic PCR testing in Zimbabwe, the National Microbiology Reference

Laboratory (NMRL) is the only laboratory performing sequencing of the virus for the country's ten provinces. When compared to other countries like Nigeria (NCDC, 2021) and South Africa (Moorthy, Restrepo, Preziosi & Swaminathan, 2020) that have the government and private laboratories working together to conduct sequencing, Zimbabwe's capacity is low. The NMRL is still building capacity for the SAS-CoV-2 virus sequencing. At present, there are two nanopore sequencers (a portable sequencing platform with a throughput of 96 samples per run) received from Africa CDC and the Quadram Institute. NMRL currently relies on the shipment of samples to the Quadram Institute and the Kwazulu-Natal Research Innovation and Sequencing Platform for sequencing to meet the testing needs. There is a need to increase sequencing capacity in Zimbabwe to monitor ongoing SARS-CoV-2 evolution and detection of new SARS-CoV-2 variants to better inform public health responses. This letter highlights the current state of SARS-CoV-2 genomic surveillance and proffers solutions that have the potential to increase genomic surveillance of human pathogens in Zimbabwe.

SARS-CoV-2 genome sequencing of samples from patients answer two important questions about the virus: 1) how the virus is mutating into variants and 2) distribution of different clades of SARS-CoV-2 among geographical regions, shedding light on the diversity of strains. Of particular interest are the mutations affecting the spike protein that influences how infectious the virus is, how severe the infection may become, and how well current vaccines protect against the virus. Genomic surveillance can therefore inform and complement strategies to reduce the burden of COVID-19 by providing valuable insights that could inform policy decisions about mitigation strategies for

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targeted interventions (WHO, 2021a). As of June 25, 2021, there have been four SARS-CoV-2 variants of concern (VOCs) that have emerged and undergone transmission around the world. A variant becomes a concern when it exhibits features of increased infectivity and/or transmissibility (WHO, 2021b).

What efforts have been made for sequencing in Zimbabwe?

The emergence of new, more contagious SARS-CoV-2 variants has underscored the need to step up genomic surveillance efforts to better control the pandemic (Habibzadeh, P., Mofatteh, M., Silawi, M., Ghavami, S., & Faghihi, M. A., 2021). Currently, SARS-CoV-2 sequencing is taking place at the NMRL, the leading government referral laboratory. Funding and training from the African Centre for Disease Control and Prevention (Africa CDC) and Quadram Biosciences Institute (QIB, United Kingdom) has boosted SARS-CoV-2 sequencing in Zimbabwe. A report of the first data on SARS-CoV-2 sequencing in Zimbabwe revealed that the B.1.351 VOC, originally identified in South Africa was present in 74 (69%) of 107 sequenced cases in December 2020, and 99 (95%) of 104 sequenced cases in January 2021 (Mashe, T., Takawira, F. T., Gumbo, H., Juru, A., Nyagupe, C., Maeka, K. K., et al., 2021). As of 18 July 2021, Zimbabwe has submitted a total of 558 SARS-CoV-2 sequences to the GISAID database. The percentage number of cases sequenced and shared to date is 0.667 (GISAID, 2021). However, Zimbabwe has not submitted any sequences in the last 90 days (GISAID, 2021); considering the country is at its peak of COVID-19 infections, more effort needs to be directed towards sequencing to identify variants circulating within the population.

What other measures can be employed to improve capacity and ramp up sequencing capacity?

Despite the efforts of the Zimbabwean government and its partners, the current state of pathogen genomic surveillance needs improvement to enable surveillance of current and future epidemics.

- 1 The current efforts by the government of Zimbabwe are laudable; however, there is a need for strong political will and commitment to funding research and supporting genomics as an important tool for disease surveillance and monitoring of outbreaks. For instance, the Innovation Hub and High-Performance Computing centre at the University of Zimbabwe could act as a referral center for genomics and bioinformatics respectively.
- 2 During the Ebola Virus disease outbreak of 2014 in West Africa, genomic surveillance capacity was increased by decentralising the application of portable field-based technologies like the Oxford Nanopore Technology-MinION sequencer which are cheaper than high throughput sequencing platforms like Next-seq and Hi-Seq (Hoenen, T., Groseth, A., Rosenke, K., Fischer, R. J., Hoenen, A., Judson, S. D. et al, 2016). Zimbabwe could invest in such technologies to decentralise surveillance, detection, tracking and monitoring of outbreaks.
- 3 To build local capacity in genomic surveillance, local research and academic institutions could seek collaborations with genomics hubs of excellence in the region. For example, Africa CDC established regional genome sequencing networks (Africa CDC, 2020) from which Zimbabwe can benefit. This can facilitate the training of Zimbabwean biomedical scientists in sequencing technologies and bioinformatic analysis.

Conclusion

There is limited capacity for SARS-CoV-2 genomic surveillance in Zimbabwe due to limited skillsets and laboratory infrastructural deficiencies. There is an urgent need for funding from the government of Zimbabwe to set up a robust genomic surveillance program to detect SARS-CoV-2 VOCs in Zimbabwe and guide public health responses accordingly. Additionally, partnerships between local public health laboratories, private laboratories, and academia should be strengthened to ensure a coordinated approach to genomic surveillance.

Conflict of Interest

None to declare

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Ethical Approval

Not applicable

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