SA’s first SARS-COV-2 genome sequence and analysis - REFLECTIONS

by Prof Alan Christoffels, DSI-NRF SARChI Chair in Bioinformatics and Health Genomics and Director of the South African National Bioinformatics Institute (SANBI), University of the Western Cape.

As additional sequencing data is generated locally and globally there will be opportunity to trace the evolution of this virus.

As citizens we applaud the speed with which the South African Government has responded to the COVID-19 pandemic. Our national response teams are ramping up the much-needed national control measures in response to COVID-19, including health screening, COVID-19 testing and associated contact tracing and provision for self-isolation of vulnerable communities.

Is there a place for a coordinated genomic response in all of this?

This question is particularly relevant in light of the recent sequencing and analysis of the first SARS-COV-2 genome by the National Institute for Communicable Diseases (NICD) in partnership with the South African DSI-NRF Research Chairs Initiative (SARChI) Chair in Bioinformatics and Health Genomics based at the South African National Bioinformatics Institute, University of the Western Cape.

The current COVID-19 pandemic comes on the back of outbreaks such as Ebola, Zika, Lassa Fever, Marburg Haemorrhagic Fever and Listeriosis to name a few. Global experience gleaned from these outbreaks reinforce the need for continuous surveillance, rapid diagnosis, real-time tracking of (emerging) infectious diseases and access to pathogen sequencing data. Collectively, such a disease surveillance platform can inform a public health response.

As of 10th April 2020, the Democratic Republic of Congo, Ghana, Nigeria, Senegal and South Africa have contributed SARS-COV-2 genomic data to the global collection of over 5000 SARS-COV-2 genomes currently stored in, and accessible from, the Global Initiative on Sharing All Influenza Data (GISAID database).

Pathogen sequencing data allows researchers to track disease transmission and the spread of the disease. The South African SARS-COV-2 data verified what we already know about the transmission origins of COVID-19, namely the spread of the virus in line with travel of South Africans abroad.

What does this mean for South Africa and more broadly for the African continent?

Successful use of pathogen sequencing data such as SARS-COV-2 towards an effective COVID-19 response, and more generally during an outbreak requires (1) access to laboratory expertise to extract virus material and high throughput sequencing capacity; (2) reproducible genomic analysis methods; (3) standardised protocols for data sharing; and (4) upholding ethics for research.

Access to laboratory expertise

The NICD has worked tirelessly to produce a virus isolate free of contamination with human genetic material. These experimental protocols and, in particular, refining these methods, can leverage from a network of like-minded scientists who have solved similar challenges or who grapple with the same technical challenges.

In a recent assessment of sequencing capacity in Africa, it is clear that the DRC, Ghana, Nigeria, Senegal and SA have the necessary in-country sequencing capability to generate sequencing data for SARS-COV-2. Leveraging or establishing this network of laboratory expertise would catalyse a coordinated pan-African response.

Reproducible genomic analysis methods

We should not allow the genomic analysis of >>>
As few as six single nucleotide polymorphisms were identified in the SA SARS-COV-2 sequence compared to the global collection.