CERI & KRISP Newsletter

Volume 5, Number 8, August/September 2022

Introduction

Welcome to another edition of the CERI & KRISP Newsletter. This month we reflect on how much the world has changed over the last two years. It is still too early to declare the pandemic over, but it is time to begin thinking about what can be done better and how best to prepare for future threats to global health.

Pandemic preparedness, global collaboration, vaccine equality and the naming and renaming of pathogens; once only the concern of a select group of virus hunters, but now on the tongues and minds of us all.

Whilst our scientific research and surveillance efforts at CERI & KRISP remain under the global spotlight, our team remain committed to keeping South African and African scientists on the agenda through continued capacity building efforts and strategic collaborations

Highlights

News: **TIME – The Virus Hunters Trying to Prevent the Next Pandemic**

Feature: **Science – Pandemic preparedness in a changing world. Fostering global collaboration**

News: **New York Times – Why Experts Want to Rename Monkeypox**

Publication: **SARS-CoV-2 Genetic Diversity and Lineage Dynamics in Egypt during the first 18 months of the Pandemic**

Seminars: **Bad vibrations: Quantum tunneling and SARS-CoV-2 infections, Prof. Francesco Petruccione, 24th August @ 11h30 SAST**

Upcoming Workshop: Genomics Africa Fellowship**, 5-16 September 2022, Durban, South Africa**

CERI

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NEWS: The Virus Hunters Trying to Prevent the Next Pandemic

COVID-19 has turned out to be an ideal proving ground for this type of coalition. Partner labs in the coalition analyze the genetic sequences of thousands of virus samples collected from COVID-19 patients in their region.

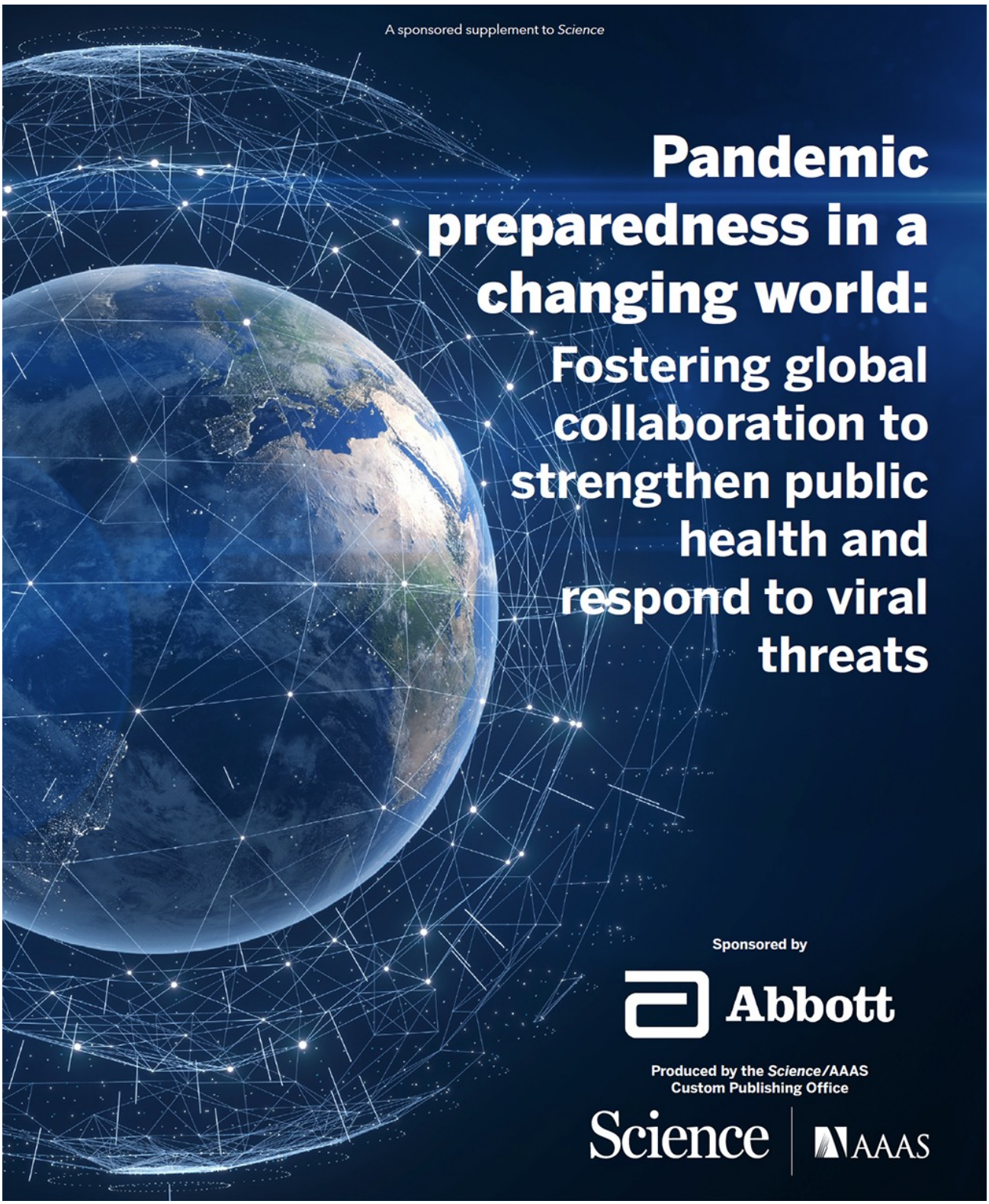
The only way to be truly prepared for the next pandemic is to make such coalitions the norm. Sustaining them between public health threats is among the best ways to defend against the next big one. “Public-private partnerships are essential for [disease] surveillance, testing, treatments, you name it,” says Dr. Eric Topol, director and founder of the Scripps Research Translational Institute. “We do better if those groups are working together.”

So far, APDC members have contributed to identifying three major SARS-CoV-2 variants. In June and July 2020, as the coalition was being formed, hospitals in South Africa noticed a rapid uptick in patients admitted with COVID-19 that seemed out of proportion to previous trends. A research team at the Center for Epidemic Response and Innovation (CERI) at Stellenbosch University in South Africa —which was already collaborating with Abbott on tracking HIV—analyzed samples from patients at 200 clinics when they found the mutation that the WHO later designated as Beta.

“We found the exact same variant in samples from clinics that were hundreds of kilometers away, so we knew it was widespread and that we potentially had a new variant,” says Tulio de Oliveira, who leads CERI. Data from the South African hospitals suggested that younger people were the most affected, and that they were getting sicker than people who had been infected with the earlier version of the virus. De Oliveira immediately alerted global health authorities to the new variant, which allowed public health experts to prepare for a potential wave of patients who might need more intensive hospital care. Back in Chicago at Abbott’s headquarters, scientists quickly determined that, based on the variant sequences, the company’s existing PCR and recently authorized at-home rapid tests for SARS-CoV-2 could still detect the new variant.

Read full article: https://time.com/6202044/preparing-for-next-pandemic-virus-hunters/

FEATURE: Science Supplement – Pandemic Preparedness in a changing world



This publication provides a collection of important research, news, and editorial articles from Science leading up to and including the COVID-19 pandemic.

It also includes articles written by scientists—or "virus hunters"—in the Abbott Pandemic Defense Coalition.

CERI & KRISP had two featured publications in this Science supplement – **see overleaf…**

PUBLICATION: A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa

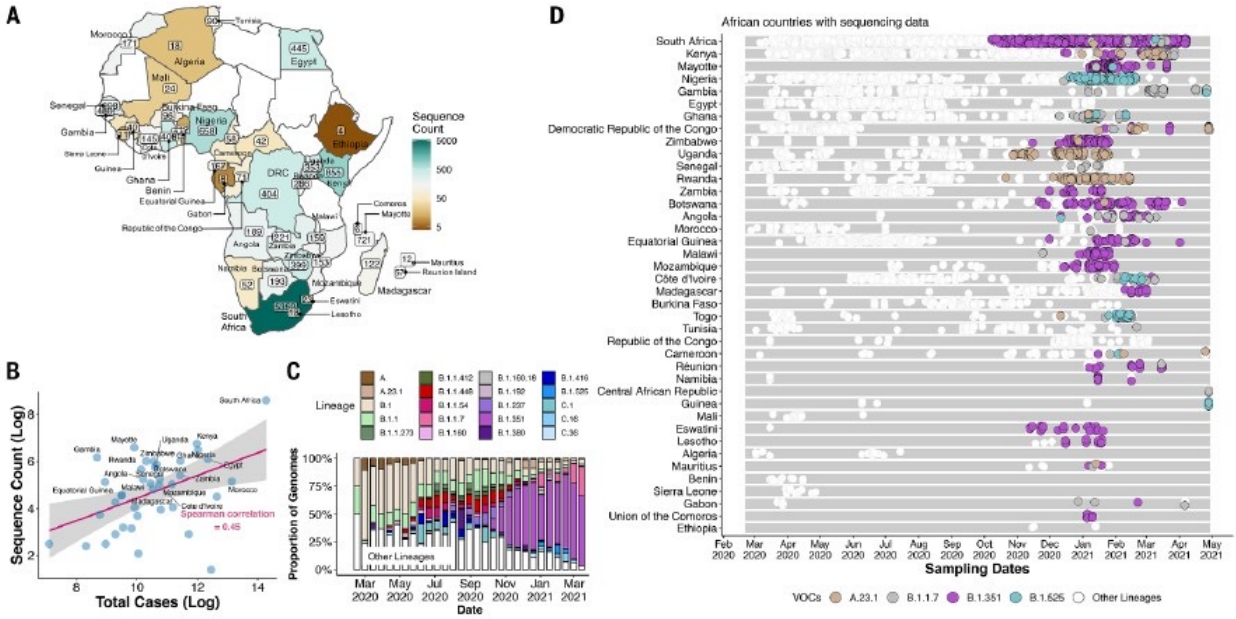


Fig. 1. SARS-CoV-2 sequences in Africa. (**A**) Map of the African continent with the number of SARS-CoV-2 sequences reflected in GISAID as of 5 May 2021. (**B**) Regression plot of the number of viral sequences vs. the number of reported COVID-19 cases in various African countries as of 5 May 2021. Countries with >500 sequences are labeled. (**C**) Progressive distribution of the top 20 PANGO lineages on the African continent. (**D**) Temporal sampling of SARS-CoV-2 sequences in African countries (ordered by total number of sequences) through time with VOCs of note highlighted and annotated according to their PANGO lineage assignment.

The progression of the SARS-CoV-2 pandemic in Africa has so far been heterogeneous and the full impact is not yet well understood.

Here, we describe the genomic epidemiology using a dataset of 8746 genomes from 33 African countries and two overseas territories. We show that the epidemics in most countries were initiated by importations predominantly from Europe, which diminished following the early introduction of international travel restrictions.

As the pandemic progressed, ongoing transmission in many countries and increasing mobility led to the emergence and spread within the continent of many variants of concern and interest, such as B.1.351, B.1.525, A.23.1 and C.1.1.

Although distorted by low sampling numbers and blind spots, the findings highlight that Africa must not be left behind in the global pandemic response, otherwise it could become a source for new variants.

Severe acute respiratory syndrome-related coronavirus 2(SARS-CoV-2) emerged in late 2019 in Wuhan, China (*1*, *2*). Since then, the virus has spread to all corners of the world, causing almost 150 million cases of coronavirus disease 2019 (COVID-19) and over three million deaths by the end of April 2021. Throughout the pandemic, it has been noted that Africa accounts for a relatively low proportion of reported cases and deaths – by the end of April 2021, there had been ~4.5 million cases and ~120000 deaths on the continent, corresponding to less than 4% of the global burden.

However, emerging data from seroprevalence surveys and autopsy studies in some African countries suggests that the true number of infections and deaths may be several fold higher than reported (*3*, *4*).

Link to full publication:
https://www.krisp.org.za/publications.php?pubid=362

Building genomic sequencing capacity in Africa to respond to the SARS-CoV-2 pandemic

Tulio de Oliveira[1,2,3,4*], Eduan Wilkinson[1], Cheryl Baxter[1,3], Houriiyah Tegally[1], Jennifer Giandhari[2], Yeshnee Naidoo[1], Sureshnee Pillay[2]

Genomics surveillance aims to transform public health interventions by monitoring genetic changes that impact pathogenicity, diagnostics, therapeutics, and vaccines. Monitoring the genetic changes in SARS-CoV-2 has played an important role in shaping the scientific response to the pandemic and allowed the identification of several variants of interest (VOI) and five variants of concern (VOC) to date. Although Africa accounts for only about 2.5% and 4.1% of the world's reported COVID-19 cases and deaths, respectively (*1*, *2*), two of the VOC were identified by scientists from South Africa. Here, we reflect on some of the investments and capacity development initiatives that have resulted in an exponential growth in genomic sequencing capabilities across the continent over the past 2 years.

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Early in the SARS-CoV-2 pandemic, genomic surveillance was available in just a few African countries with only 5,245 SARS-CoV-2 genome sequences being made publicly available in 2020 (*3*). In 2020 and 2021, significant investments in equipment and training were made to extend the geographic coverage of sequencing within many laboratories in Africa, thus increasing surveillance capacity on the continent. These investments resulted in an exponential increase in the number of SARS-CoV-2 genome sequences produced (Figure 1). Interestingly, it took 375 days to produce the first 10,000 SARS-CoV-2 genomes, 87 days to produce the next 10,000, and just 24 days to produce the most recent 10,000 genomes. To date, almost 100,000 SARS-CoV-2 genome sequences from Africa have been shared, and 54 African countries are now contributing to SARS-CoV-2 genome sequencing.

In 2020, the World Health Organization (WHO) and the Africa Centres for Disease Control and Prevention (Africa CDC)

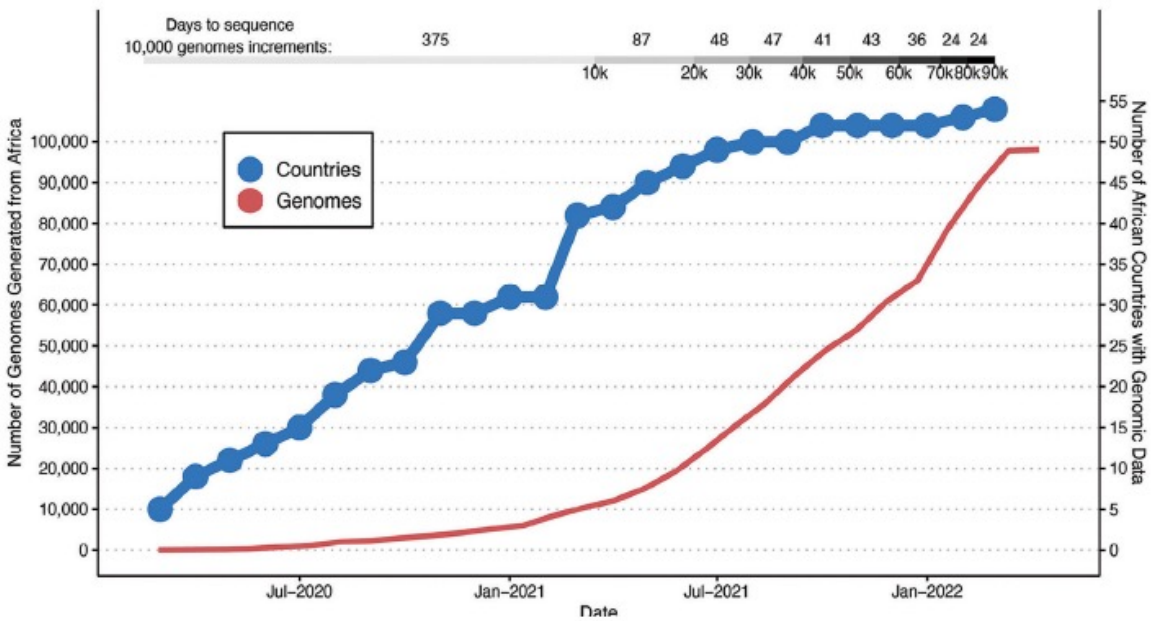


FIGURE 1. Increase in the number of SARS-CoV-2 sequences (solid red line) and African countries (blue circles) contributing genomic sequences to the Global Initiative on Sharing All Influenza Data (GISAID) between January 2020 and March 2022. Note that countries contributing to genomic sequences include 52 African countries and two overseas territories (Reunion and Mayotte).

Access full Science supplement here:
https://www.science.org/content/resource/pandemic-preparedness-changing-world-fostering-global-collaboration

Download the full publication from our website:
https://ceri.org.za/publication/?token=406

PROFILE: Tulio de Oliveira: collaborating to boost science in Africa

By Udani Samarasekera, The Lancet, 6th August, 2022

Bioinformatician Tulio de Oliveira's philosophy has been to do "science not for journal publications or the academic career but science that can go back to the community and to the managing physicians and nurses of patients", he says.

In South Africa, as founder and Director of the KwaZulu-Natal Research Innovation and Sequencing Platform (KRISP) at the University of KwaZulu-Natal (UKZN) in Durban and the Centre for Epidemic Response and Innovation (CERI) at Stellenbosch University, his work focuses on genomic surveillance and analysis in the COVID-19 pandemic and for viral and bacterial epidemics, including HIV and tuberculosis in South Africa and arboviruses in Brazil.

A leader of African science in the COVID-19 pandemic, he established the Network for Genomic Surveillance in South Africa in 2020, and his team was the first to identify the beta (B.1.351) and omicron (B.1.1.529) variants of SARS-CoV-2. But he points out he is "much more interested in the response than the science per se".

After the beta variant was discovered, de Oliveira co-founded the COVID Variant Consortium in South Africa, which now involves 500 scientists who confer each week and "allows South Africa not only to do genomic surveillance but as we identify a variant…we also have a live virus outgrown and we can very quickly estimate vaccine effectiveness against the variant and the change in neutralisation and clinical severity", he says.

Training health professionals is also crucial. After de Oliveira and infectious disease expert and collaborator Richard Lessells investigated a large COVID-19 outbreak in a hospital in South Africa early in the pandemic, they "trained over 5000 medical doctors and nurses between March and August, 2020" on approaches to avoid hospital outbreaks, he recalls. Now at KRISP and CERI, he says, "we probably spend half of our time and 20–30% of our budgets to give feedback to clinicians and do training".

Read full article:
https://www.thelancet.com/journals/lancet/article/PIIS0140-6736(22)01426-X/fulltext

NEWS: Why Experts Want to Rename Monkeypox

By Andrew Jacobs, New York Times, August 23rd, 2022

Are monkeys spreading monkeypox to humans? Researchers say the answer is no. But recently in Brazil, the unfounded fear that monkeys transmit the virus to people has spurred an outbreak of violence against marmosets and capuchin monkeys, leading to the death of at least seven animals, according to Brazilian officials.

The stoning and poisoning of wild primates in Brazil is an especially lurid example of how an inaptly named disease can have real-world implications.

Just as the so-called Spanish Flu of 1918 wasn't born on the Iberian Peninsula, the spread of monkeypox has little to do with monkeys. In fact scientists say that rodents are the most likely animal reservoir for the virus, which is a cousin of smallpox that made its first recorded leap to humans decades ago in the Democratic Republic of Congo. But in 1958, when Danish scientists first identified the virus in a colony of lab monkeys, they decided to bestow the naming honor on their captive primates.

In the three months since the first cases of monkeypox were reported in Europe and the United States, public health experts have been urging the World Health Organization to come up with new nomenclature that might help to clear up any confusion and reduce the shame and stigmatization associated with a disease that has been spreading largely among men who have sex with men.

'Names matter, and so does scientific accuracy, especially for pathogens and epidemics that we are trying to control,' said Tulio de Oliveira, a bioinformatician at Stellenbosch University in South Africa who has been among those pushing the W.H.O.

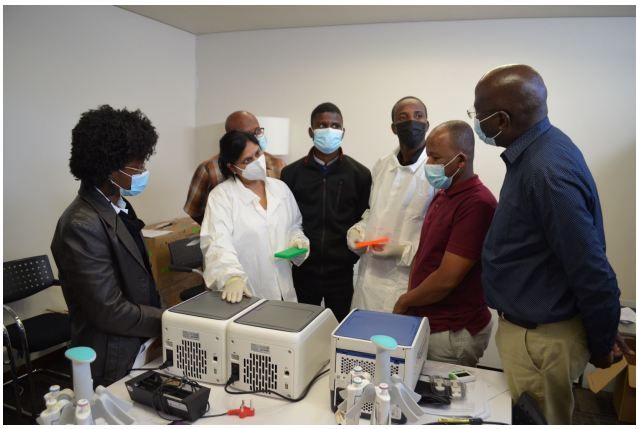
In June, Dr. de Oliveira and more than two dozen other scientists from across the African continent published an open letter urging the organization to move quickly. Failure to do so, they warned, risked hamstringing efforts to contain the disease.

Read full article:
https://ceri.org.za/news/?token=589

CAPACITY BUILDING: Genomics Africa Fellowships

Genomics Africa fellowship program is extended to Latin America:
The Africa Genomics Fellowship is a program funded by the Rockefeller Foundation and we have already hosted over 100 scientists at CERI, KRISP, ACEGID, and ILRI. We have expanded this program in South Africa with CERI and KRISP with the The Abbott Pandemic Defense Coalition to also host fellows from other regions in the world.

We are happy to announce that we will be receiving 6 fellows from Latin America for the hands-on NGS training on Oxford Nanopore Technologies (ONT) and Illumina sequencing. The Latin American fellows will be trained together with African fellows at the state-of-the-art KRISP labs at UKZN, 4-16 Sept 2022.



We are also working on the expansion of this training and fellowship program to south and east Asia, so the Global South can work together to expand capacity in genomics and bioinformatics. Please visit the Genomics.Africa website to get to know all of our fellows and new opportunities for fellowships.

Website link:
https://www.genomics.africa

PUBLICATION: SARS-CoV-2 Genetic Diversity and Lineage Dynamics in Egypt during the First 18 Months of the Pandemic

Abstract: COVID-19 was first diagnosed in Egypt on 14 February 2020. By the end of November 2021, over 333,840 cases and 18,832 deaths had been reported. As part of the national genomic surveillance, 1027 SARS-CoV-2 near whole-genomes were generated and published by the end of July 2021.

Here we describe the genomic epidemiology of SARS-CoV-2 in Egypt over this period using a subset of 976 high-quality Egyptian genomes analyzed together with a representative set of global sequences within a phylogenetic framework. A single lineage, C.36, introduced early in the pandemic was responsible for most of the cases in Egypt.

Furthermore, to remain dominant in the face of mounting immunity from previous infections and vaccinations, this lineage acquired several mutations known to confer an adaptive advantage.

These results highlight the value of continuous genomic surveillance in regions where VOCs are not predominant and the need for enforcement of public health measures to prevent expansion of the existing lineages.

Link to full publication:
https://ceri.org.za/publication/?token=407

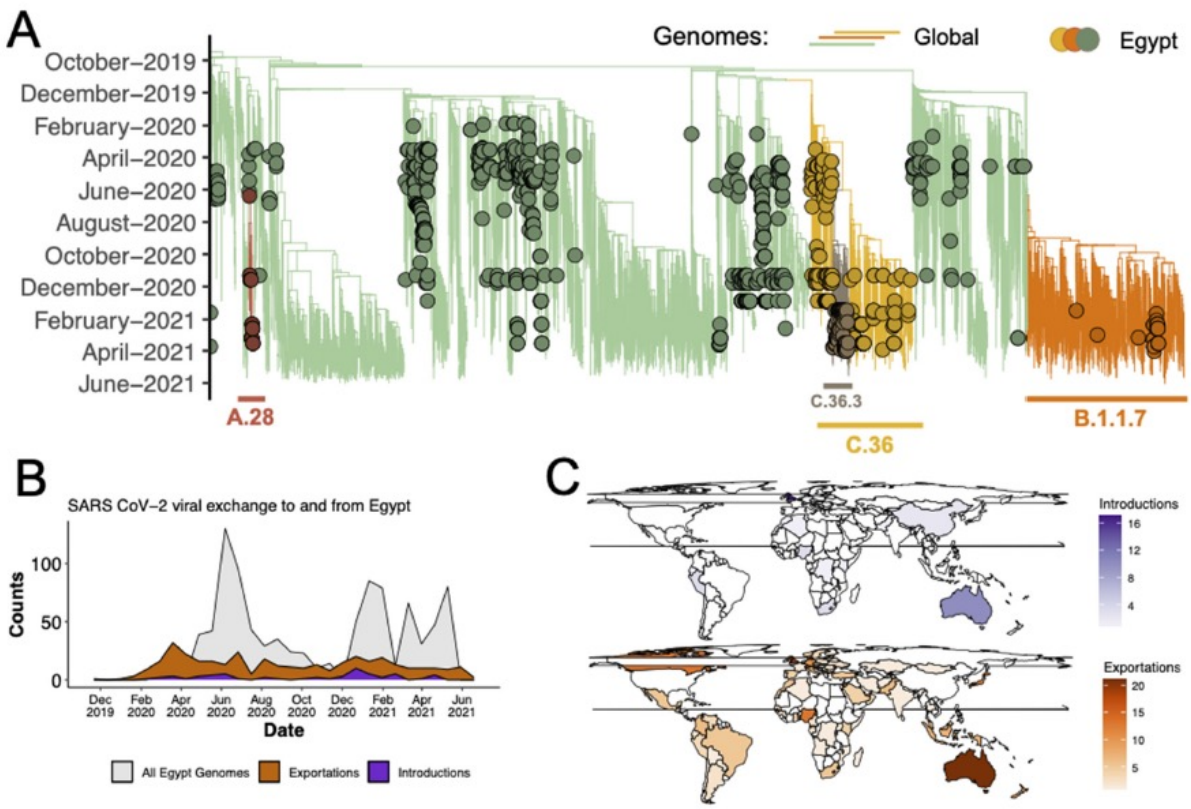


Figure 2. Phylogenetic reconstruction of the SARS-CoV-2 epidemic in Egypt. (A) Time-resolved maximum clade credibility phylogeny of the major lineages circulating in Egypt. (B) Area plot showing viral import-export as proportions of the sampled genomes. (C) Inferred locations of imports into and exports of SARS-CoV-2 out of Egypt. Sampling for molecular and genomic analyses across Egypt were sporadic across 2020 and 2021. Although genomic sequencing only detected C.36/C.36.3 in Cairo (GISAID Metadata), qPCR assays were able to detect these lineages in various other locations (Figure 3B) at a high proportion of the total numbers of samples tested with the qPCR assay (Figure 3A).

nature microbiology

ANALYSIS

https://doi.org/10.1038/s41564-022-01191-z

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OPEN

Genomic epidemiology of the SARS-CoV-2 epidemic in Brazil

The high numbers of COVID-19 cases and deaths in Brazil have made Latin America an epicentre of the pandemic. SARS-CoV-2 established sustained transmission in Brazil early in the pandemic, but important gaps remain in our understanding of virus transmission dynamics at a national scale. We use 17,135 near-complete genomes sampled from 27 Brazilian states and bordering country Paraguay. From March to November 2020, we detected co-circulation of multiple viral lineages that were linked to multiple importations (predominantly from Europe). After November 2020, we detected large, local transmission clusters within the country. In the absence of effective restriction measures, the epidemic progressed, and in January 2021 there was emergence and onward spread, both within and abroad, of variants of concern and variants under monitoring, including Gamma (P.1) and Zeta (P.2). We also characterized a genomic overview of the epidemic in Paraguay and detected evidence of importation of SARS-CoV-2 ancestor lineages and variants of concern from Brazil. Our findings show that genomic surveillance in Brazil enabled assessment of the real-time spread of emerging SARS-CoV-2 variants.

At the end of 2019, a respiratory pathogen designated the Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) emerged in the city of Wuhan, China. Since its identification, the virus has spread rapidly around the world, causing the Coronavirus disease 2019 (COVID-19) pandemic (declared on 11 March 2020), with infected patients overwhelming many healthcare systems[1]. By mid-February 2022, more than 415 million cases of COVID-19 with more than 5.84 million associated deaths, had been reported globally[2]. Brazil is the epicentre of the COVID-19 epidemic in the Americas, with more than 21.2 million cases and a death toll of 591,000 reported cases (September 2021). Brazil is one of the countries hit hardest by COVID-19[3]. Crucially, a lack of genome sequence data from Brazil has limited our ability to fully understand transmission dynamics at the national scale.

We present a phylogenetic and phylogeographic analysis of genomic data from 27 Brazilian states and one neighbouring country, Paraguay, collected up to September 2021. We evaluate the genomic epidemiology of SARS-CoV-2 in Brazil, including the emergence and spread of key viral variants of concern (VOCs; for example, Gamma) and variants under monitoring (VUMs; for example, Zeta), to assess how their emergence may have contributed to a more severe second wave in the country.

Results

COVID-19 transmission dynamics in Brazil. The first confirmed infection of SARS-CoV-2 in Brazil was on 26 February 2020 in the State of São Paulo (SP), in a traveller returning from Italy (Fig. 1a). On 17 March 2020, the first COVID-19-related death, a 61-year-old male, was reported in the same state[4,5]. Four days later, all Brazilian states reported at least one confirmed case of COVID-19 and the Brazilian Ministry of Health (BRMoH) declared an outbreak of large-scale community transmission of the virus[6]. By 10 April 2020, the virus had already reached remote locations, such as the Yanomami indigenous community located in the state of Roraima in northern Brazil[6] (Fig. 1a).

After the World Health Organization (WHO) declared the outbreak of SARS-CoV-2 as a public health emergency of international concern on 30 January 2020, the Brazilian government introduced restriction measures to mitigate viral spread (Fig. 1a)[7]. The primary measure involved social isolation, followed by the closure of schools, universities and non-essential businesses[8]. Additional measures included the mandatory use of personal protective masks[9], the cancellation of events expected to attract large numbers of people and tourists, and opening only of services considered as essential such as markets and pharmacies[8,10]. However, while the epidemic was growing, restriction measures were progressively eased to mitigate negative impacts on the economy. Notably, even during periods of restriction, travel between Brazilian states largely remained possible, enabling SARS-CoV-2 transmission throughout the country[11]. Travel was probably linked to the emergence of more contagious viral lineages, such as VOC Gamma (lineage P.1) and VUM Zeta (lineage P.2). Notably, these variants may have contributed to a second wave that was more severe in terms of infections and deaths than the first wave (Fig. 1b)[11,12–14].

The COVID-19 death toll in Brazil rose steadily after March 2021. It reached a daily total of 4,250 deaths on April 2021, the highest number of daily fatalities from COVID-19 worldwide (Fig. 1b). Signs of collapse of the health system were reported in numerous cities around the country. The situation worsened after multiple VOCs and VUMs emerged during a slow vaccination campaign[15]. Vaccination in Brazil began on 17 January 2021, when the Instituto Butantan imported the first 6 million doses of CoronaVac (a whole-virus inactivated vaccine) from Sinovac Biotech (Fig. 1a)[16,17]. As of 16 February 2022, approximately 71.8% of the Brazilian population had been vaccinated with the first dose of any of the vaccines available (CoronaVac, AstraZeneca, Pfizer and Janssen), but only 22% were fully vaccinated (with a single dose of Janssen or two doses of any other vaccine)[18].

By analysing the total number of COVID-19 notified cases to the end of September 2021, we observed that the Brazilian region with the highest population density (Southeast) also contained the highest number of the cases registered in the country, with the state of São Paulo documenting the largest number of cases ($n = 4,369,410$) in that period (Fig. 1c). However, when we considered the incidence rate (number of reported cases per population) by state, we found that the Midwest, the least populated region in Brazil, had the highest incidence rate, with 13,604.23 cases per 100,000 inhabitants[1].

SARS-CoV-2 genomic data. A total of 3,866 near-full genome sequences from SARS-CoV-2 RT–qPCR positive samples were obtained as part of this study. SARS-CoV-2 sequencing spanned

A full list of authors and affiliations appears at the end of the paper.

Link to full publication:
https://ceri.org.za/publication/?token=408

Events: Seminars and Events at CERI & KRISP

Workshop: **Exploratory Data Analysis and Modelling in R with Microbiome Applications**
Date: **22-26 August, 2022**
Venue: **Nelson R. Mandela School of Medicine, UKZN, Durban, South Africa**
Application Deadline: **7 August, 2022**

***No course fee, must bring own laptop**

Seminar: **Bad vibrations: Quantum tunneling and SARS-CoV-2 infections**
Date: **24 August, 2022**
Speaker: **Prof. Francesco Petruccione**
Venue: **STIAS, Stellenbosch University or virtually**

Francesco Petruccione is a Professor of Quantum Computing at Stellenbosch University, a fractionalProfessor at the University of KwaZulu-Natal (UKZN) and the interim Director of the National Institute for Theoretical and Computational Sciences.

Upcoming

Workshop: **Genomics Africa Workshop: 2 week short term fellowships with hands-on NGS sequencing**
Date: **5 – 16 September, 2022**
Venue: **KRISP at UKZN, Durban, South Africa**

A fellowship program funded by the Rockefeller Foundation and the Abbott Pandemic Defense Coalition.

NGS-BRICS 2022
Viral Sequencing & Phylogenetics Workshop
STELLENBOSCH SOUTH AFRICA & VIRTUALLY

Workshop: **Viral Sequencing and Phylogenetics Workshop**
Date: **26-30 September, 2022**
Venue: **Virtual presentations**

The NGS-BRICS is hosting a workshop on SARS-CoV-2 genome sequencing, assembly, and phylogenetic analyses.

It is aimed at BRICS scientists, individuals in the field of academia, or representatives working in public health laboratories.

CERI & KRISP Papers

OPEN ACCESS

Urgent need for a non-discriminatory and non-stigmatizing nomenclature for monkeypox virus. Happi C, Adetifa I, Mbala P, Njouom R, Nakoune E, Happi A, Ndodo N, Ayansola O, Mboowa G, Bedford T, Neher RA, Roemer C, Hodcroft E, Tegally H, O'Toole Á, Rambaut A, Pybus O, Kraemer MUG, Wilkinson E, Isidro J, Borges V, Pinto M, Gomes JP, Freitas L, Resende PC, Lee RTC, Maurer-Stroh S, Baxter C, Lessells R, Ogwell AE, Kebede Y, Tessema SK, de Oliveira T, **PLoS Biology** (2022), doi: 10.1371/journal.pbio.3001769.:.

Genomic epidemiology of the SARS-CoV-2 epidemic in Brazil. Giovanetti M, Slavov SN, Fonseca V, Wilkinson E, Tegally H, Patané JSL, Viala VL, San EJ, Rodrigues ES, Santos EV, Aburjaile F, Xavier J, Fritsch H, Adelino TER, Pereira F, Leal A, Iani FCM, de Carvalho Pereira G, Navegantes W, do Carmo Said RF, Campelo de A E Melo CF, Almiron M, Lourenço J, de Oliveira T, Holmes EC, Haddad R, Sampaio SC, Elias MC, Kashima S, Junior de Alcantara LC, Covas DT, et al. **Nature Microbiology** (2022), doi: 10.1038/s41564-022-01191-z:.

SARS-CoV-2 Genetic Diversity and Lineage Dynamics in Egypt during the First 18 Months of the Pandemic. Roshdy WH, Khalifa MK, San JE, Tegally H, Wilkinson E, Showky SM, Darren P, Moir M, Naguib AEN, Gomaa MR, Fahim MAEH, Mohsen AGR, Hassany M, Lessells R, Al-Karmalawy AA, EL-Shesheny R, Kandeil AM, Ali MA, de Oliveira T, **Viruses** (2022), https://www.mdpi.com/1999-4915/14/9/1878:.

Building genomic sequencing capacity in Africa to respond to the SARS-CoV-2 pandemic. de Oliveira T, Wilkinson E, Baxter C, Tegally H, Giandhari J, Naidoo Y, Pillay S, **Science** (2022), https://www.science.org/content/resource/pandemic-preparedness-changing-world-fostering-global-collaboration. 2022:.

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NIH

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