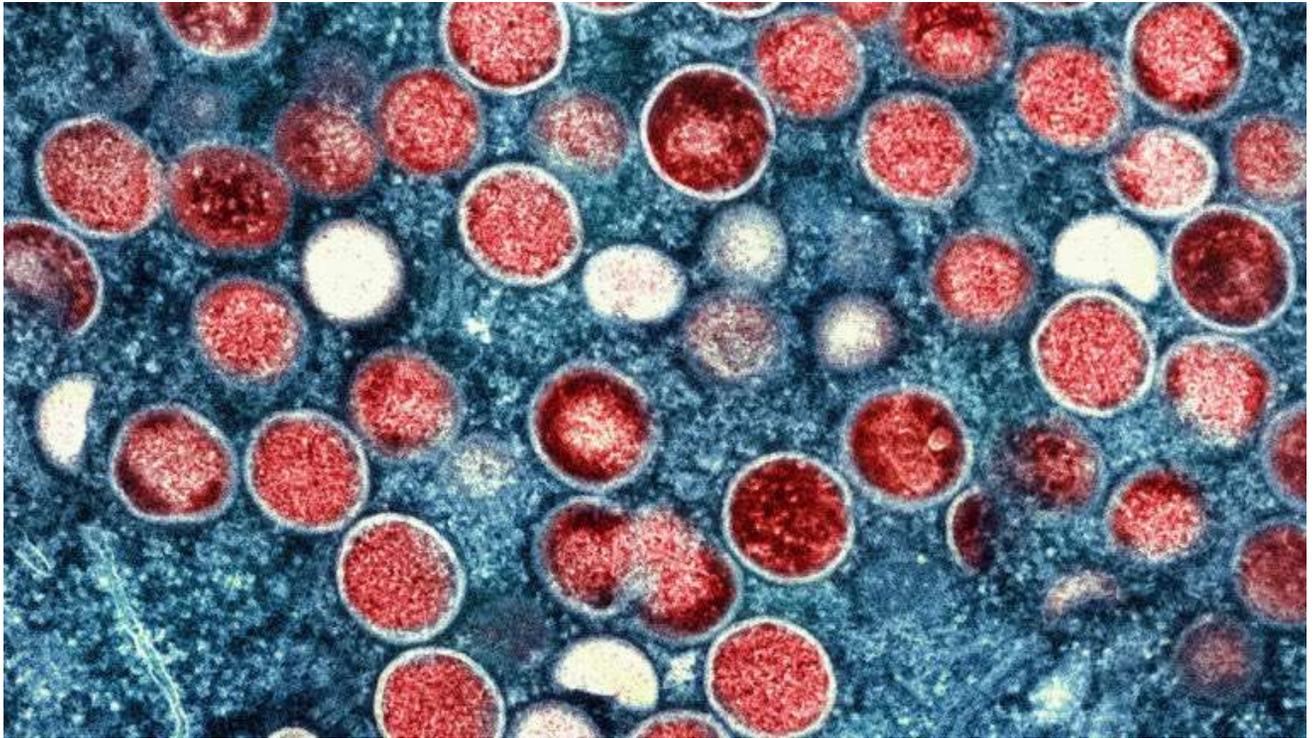


CERI & KRISP Newsletter

Volume 5, Number 6, June/July 2022



Introduction

Welcome to another edition of the CERI & KRISP Newsletter. What an eventful and action-packed period it has been! In this issue we feature our recent paper on the real-time tracking of the 2022 Monkeypox outbreak, the renaming of Monkeypox to remove geographic stigma and our continued research into the emergence of the BA.4 and BA.5 Omicron lineages and how they drove the 5th wave in South Africa.

We celebrate Prof. Tulio de Oliveira's nomination as one of Time Magazine's 100 most influential people in 2022, along with his previous PhD student, Dr Sikhulile Moyo! We also highlight a recent Lancet news article, which showcases how infectious disease science in Africa is leading the way globally.

Having a healthy work-life balance is key. We showcase and celebrate several of the achievements and adventures had by our team; from graduation ceremony's to exploring the Victoria Falls.

Highlights

News: Rename Monkeypox to remove geographic stigma, researchers says. Science.

Publication: Tracking the 2022 Monkeypox outbreak with epidemiological data in real-time. The Lancet Infectious Diseases.

Publication: Infectious diseases science in Africa takes a leading place in the world. The Lancet.

Awards: Time Magazine – The 100 most influential people of 2022

Announcement: SPARK South Africa – Call for new translational science projects now open!

Training: Microbiome Data Analysis & Modeling in R. Durban, 22-26 Aug 22. Applications open!

Feature: Life outside the laboratory – the adventures and achievements of our amazing team.



Events: Seminars and Events

Conference: SARS-CoV-2 Sequencing in Africa: Lessons form the 100 000 Genomes

Date: 10 June, 2022

Venue: Virtual

Prof. Tullio joined a scientific panel discussion for this prestigious conference, to mark the progress our continent has made in sequencing and genomic surveillance capabilities since the onset of the COVID-19 Pandemic in 2020, as well as the lessons learned for responding to future pandemics.

Seminar: Digital Health Computing, Information Systems and Machine Learning for Public Health

Date: 22 June, 2022 @ 11h30

Speaker: Prof. Douglas Pires

Venue: STIAS, Manor House Library, Wallenberg Centre, Stellenbosch or virtually*

Prof. Pires, Senior Lecturer in Digital Health at the University of Melbourne, travelled across the world to come and present at our scientific seminar series in June. He gave incredible insight into the use of AI to interpret genomic variants, and outlined the development of a web-based, universal framework to predict and assess the effects of mutations on proteins, vaccine design and the translation of these information systems to real-world issues, such as cancer risk, TB resistance and pandemic preparedness.



Upcoming

Seminar: Too many TB biomarkers for too many applications? What now?

Date: 13 July, 2022 @ 12h00

Speaker: Prof Gerhard Walzl

Venue: JN De Villiers Auditorium, Clinical Building, Tygerberg Campus or virtually*

Prof. Walzl is the head of the Division of Molecular Biology and Human Genetics at Stellenbosch University. His research focuses on the immunology of Mycobacterium tuberculosis (MTB) infection and in particular host biomarkers, including diagnostic markers, markers of TB treatment response and markers of protective immunity against MTB.



Nobel Symposium in Africa: Physics: Predictability in Science in the Age of AI

Date: 24 - 28 October 2022

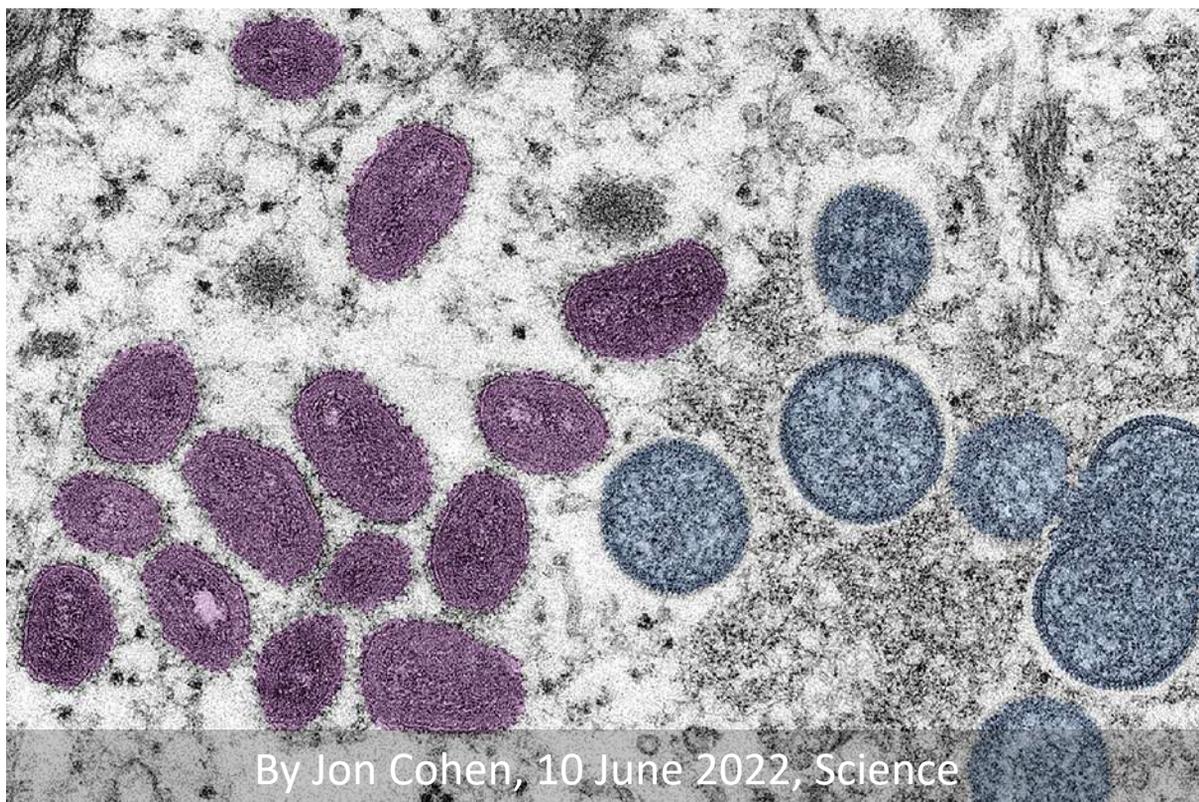
Speaker: Prof Tullio de Oliveira and Prof Francesco Petruccione

**Venue: STIAS Wallenberg Research Centre
STIAS, Stellenbosch**



This is the first Nobel Symposium in Africa. In the first symposium, Prof Tullio de Oliveira is giving a keynote speech. This is the second Nobel Symposium that Prof. de Oliveira is presenting CERI and KRISP outstanding contribution to science. A not to be missed event!

NEWS: New versions of Omicron are masters of Immune Evasion



The name “hMPXV A.1” may not roll off the tongue, but a prominent, international group of researchers contends that something like it should emerge from an overhaul of the current naming system for monkeypox and its so-called West African and Congo Basin strains.

“In the context of the current global outbreak, continued reference to, and nomenclature of this virus being African is not only inaccurate but is also discriminatory and stigmatizing,” write 29 co-authors from 11 countries in a preprint posted on virological.org today. They further note that the strain now circulating in people outside Africa is probably distinct from the virus in animals—and they “urge a speedy decision and adoption of a new name.”

The call echoes previous debates over the names of other diseases and pathogens, including a recent one that led to the current nomenclature for SARS-CoV-2 variants, with Greek letters replacing geographical names like the Wuhan or South African strain. Similarly, the preprint authors want a **“practical and neutral system of nomenclature”** used for monkeypox.

“Very, very delighted to see this,” tweeted Neil Stone, an infectious disease specialist at University College London Hospitals, in response to the preprint.

The current monkeypox outbreak—the first to ever occur on multiple continents outside of Africa—has spread to more than 1500 people in 47 countries. Years ago, researchers divided monkeypox viruses into West African and Congo Basin “clades,” or branches, which have unique genomic signatures and cause disease of different severity. Viruses sequenced in the current outbreak broadly match those in the typically milder West African clade.

But some researchers argue the human strains now being seen around the world actually form a third clade, and those viruses may also have different transmission characteristics. **“It’s quite clear that this virus is related in a very different way”** to previously sequenced strains, says Tulio de Oliveira, an evolutionary biologist at the University of KwaZulu-Natal and Stellenbosch University who is last author of the preprint.

Read full article:

<https://www.science.org/content/article/rename-monkeypox-remove-geographic-stigma-researchers-say>

Read Virological.org post:

<https://virological.org/t/urgent-need-for-a-non-discriminatory-and-non-stigmatizing-nomenclature-for-monkeypox-virus/853>

PUBLICATION: Tracking the 2022 Monkeypox outbreak with epidemiological data in real-time. The Lancet ID 2022.

Monkeypox virus was first documented in humans in the 1970s and outbreaks have been reported in many countries, with most cases restricted to endemic areas.

In early May, 2022, monkeypox cases were reported in the UK, Spain, and elsewhere in Europe. The pattern of geographical dispersal was much larger compared with past outbreaks that were more localised and occurred often in under-resourced communities.

The size of the outbreak clusters is growing each day, as is the geographical spread across Europe and North America. Within the first week of the initial report, 24 countries reported suspected and confirmed cases of monkeypox virus, some of which had known travel links to the UK, Spain, Canada, and western Europe.

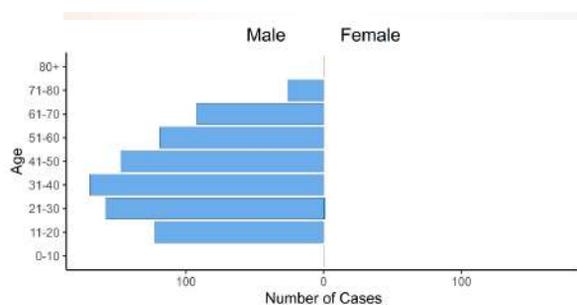
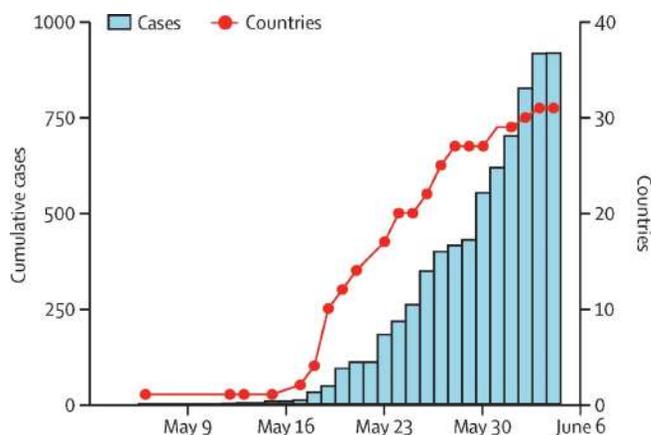
As of June 5, 2022, there have been 920 confirmed and 70 suspected cases. Of 64 confirmed cases with known travel history, 32 were associated with travel from Europe, three from west Africa, two from Canada, and one from Australia. For 26 cases, travel history locations remain unknown.

WHO convened a meeting of experts and technical advisory groups on May 20, 2022, to investigate the causes of the outbreak and have released updated guidance on surveillance, case investigation, and contact tracing.

The reason for the outbreak having a broader geographical reach is being investigated by the international and national public health community and the research community, contributing to a finer scale understanding of the outbreak dynamics. However, cessation of smallpox vaccination programmes, encroachment of humans into forested areas, and growing international mobility seem to be playing important roles in the epidemiology of monkeypox virus outbreaks.

To support global response efforts, our team created an open-access [database](#) and visualisation to [track the occurrence of cases](#) in different countries. In addition, where available, we added information on age (aggregated into age ranges, with a minimum range of 5 years), gender, dates of symptom onset and laboratory confirmation, symptoms, locations (aggregated to the state level), travel history, and additional metadata defined by WHO.

Data is compiled from verified sources, including reports from governments and public health organisations and news media reporting of health official statements.



As verified information and official statements are published, we document secondary sources and update the metadata in the dataset. An on-call schedule for curators that runs 24 h a day, 7 days a week was established to ensure data are updated in near real-time. Each case is seen and discussed by at least two curators before being made available via our [Global.health GitHub repository](#), and pushed to the map visualisation at least four times per day.

During the early stages of outbreaks, obtaining reliable, synthesised data on the characteristics of cases is a challenge, especially at a global scale. Our work attempts to harmonise information across countries and provide additional data to support the epidemiological understanding of the origins and transmission dynamics of this outbreak.

Ideally, these data are paired with virus genomic data and integrated directly with countries' epidemiological line-list data. In our repository, we are also working with colleagues and the WHO Hub for Pandemic and Epidemic Intelligence to define a contact data schema allowing countries and researchers to estimate and re-estimate key epidemiological parameters.

Link to full paper:

<https://ceri.org.za/publication/?token=396>

NEWS: Time Magazine – The 100 most influential people of 2022



By John Nkengasong, Time Magazine, 2022

Scientists in Africa have been monitoring and sequencing pathogens since long before the pandemic.

The world benefited from this network when scientists including Sikhulile Moyo, laboratory director for the Botswana-Harvard HIV Reference Laboratory, and Tulio de Oliveira, director of South Africa's Centre for Epidemic Response and Innovation, [identified and reported the emergence of the Omicron variant](#) last November.

It was a transformational moment and a shift in paradigm—one that for me symbolized that excellence in science can originate in Africa.

The international response to news of this discovery—which included travel bans imposed on African countries by other nations—was complex. It made me reflect on what global cooperation and solidarity must look like when we fight a common threat like [COVID-19](#).

Every generation has people who inspire subsequent generations. Sikhulile and Tulio have the potential to be that for people who will work in public health and [genomics](#). We have not seen the end of their contributions.

Nkengasong is the director of the Africa Centres for Disease Control and Prevention.

Article link:

<https://time.com/collection/100-most-influential-people-2022/6177832/sikhulile-moyo-tulio-de-oliveira/>

See all the nominees:

<https://time.com/collection/100-most-influential-people-2022/>

Other notable responses:

Business Insider Africa

<https://africa.businessinsider.com/local/leaders/all-the-africans-featured-on-time-magazines-most-influential-people-of-2022-list/sbm9lvf>

News24

<https://www.news24.com/news24/southafrica/news/st-ellenbosch-university-scientists-on-prestigious-time-magazine-list-of-100-most-influential-people-20220524>

Daily Maverick

<https://www.dailymaverick.co.za/article/2022-06-15-tulio-de-oliveira-scientists-in-africa-should-be-recognised-not-punished-for-scientific-discovery/>

PUBLICATION: Infectious diseases science in Africa takes a leading place in the world. The Lancet 2022.



By Tulio de Oliveira, The Lancet, 2022

During the COVID-19 pandemic, the lives of many loved ones and colleagues have been lost. Despite the terrible toll of COVID-19, in South Africa scientists have worked relentlessly to produce some of the science that has driven the global COVID-19 response. But researchers faced challenges, notably the international travel ban that was placed on South Africa for much of the pandemic and deeply affected the local economy.

Some researchers in South Africa received death threats and, at some point, even needed armed guards in front of our laboratories. Against all the odds, we persevered and are a leading country in SARS-CoV-2 genomics surveillance.

Praise and recognition of scientists in Africa is not common on the global stage; typically, researchers in Africa have to produce at least twice as much to get less than half the respect of researchers from high-income countries (HICs). For example, the discovery of Ebola virus in 1976 was credited to European scientists, when much of the work had been done in Africa by African scientists.

This kind of scientific discrimination against researchers from low-income and middle-income countries (LMICs) is widespread.

It is time to enter a new global phase where researchers in Africa and other LMICs are recognised and not punished for their scientific discoveries.

Scientists in Africa and other LMICs have key contributions to make in advancing global health, especially in areas such as epidemic response and infectious diseases. It is time to invest more in science in LMICs if the world is to be better prepared to deal with future epidemics and pandemics.

HICs, which have discriminated against the work of scientists in Africa for centuries, are only now starting to recognise the leading role they have had during this pandemic.

On May 23, 2022, I presented at the Nobel Symposium of Medicine in Sweden, where 26 global scientists reflected on the scientific advances made during the COVID-19 pandemic.

Full article link:

[https://www.thelancet.com/journals/lancet/article/PIIS0140-6736\(22\)00977-1/fulltext](https://www.thelancet.com/journals/lancet/article/PIIS0140-6736(22)00977-1/fulltext)

PUBLICATION: Emergence of SARS-CoV-2 Omicron lineages BA.4 and BA.5 in South Africa. Nature Medicine 2022.

Three lineages (BA.1, BA.2 and BA.3) of the SARS-CoV-2 Omicron variant of concern predominantly drove South Africa's fourth COVID-19 wave.

We have now identified two new lineages, BA.4 and BA.5, responsible for a fifth wave of infections. The spike proteins of BA.4 and BA.5 are identical, and comparable to BA.2 except for the addition of 69-70del (present in the Alpha variant and the BA.1 lineage), L452R (present in the Delta variant), F486V and the wild type amino acid at Q493.

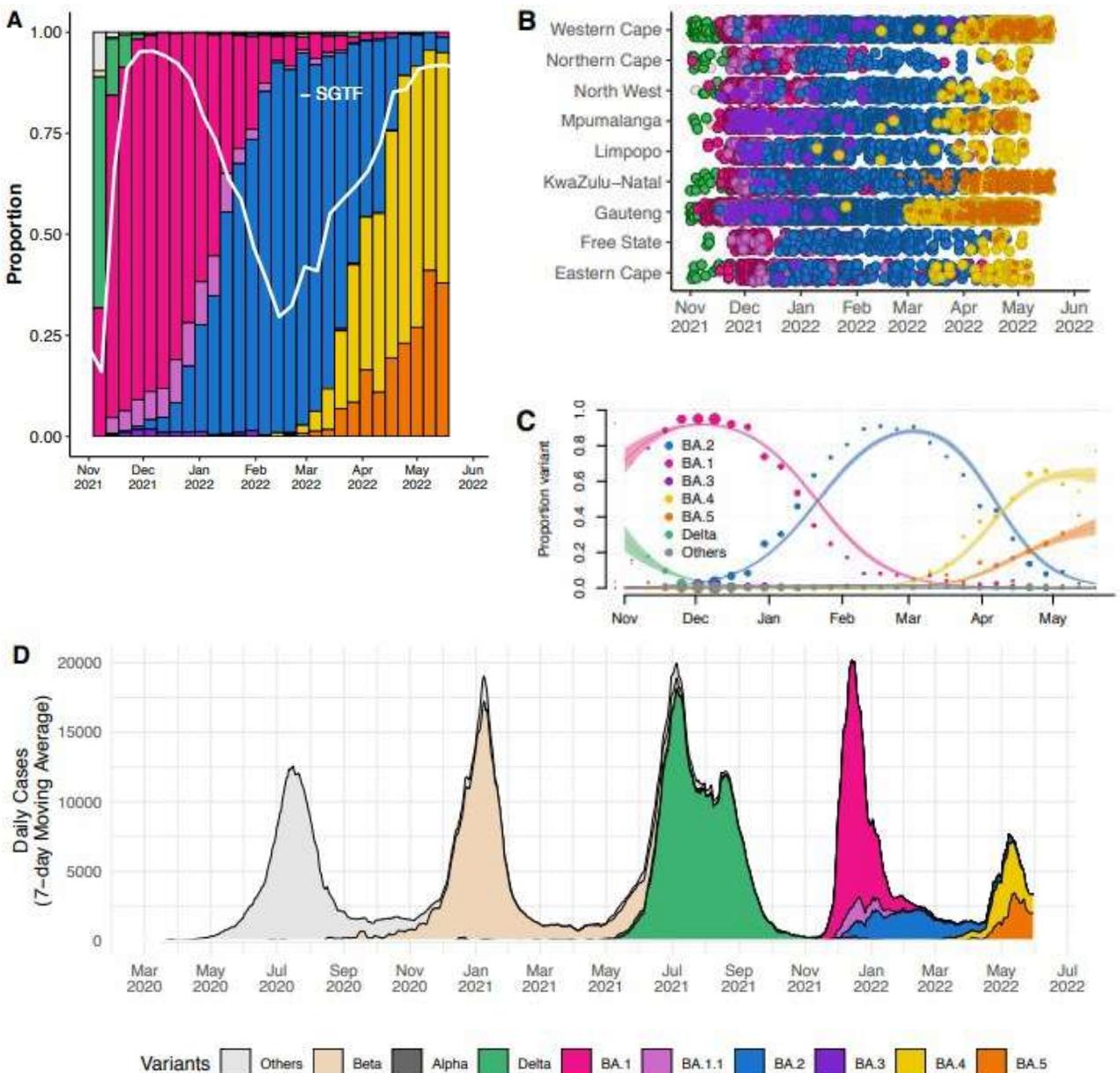
The two lineages only differ outside of the spike region.

The 69-70 deletion in spike allows these lineages to be identified by the proxy marker of S-gene target failure, on the background of variants not possessing this feature.

BA.4 and BA.5 have rapidly replaced BA.2, reaching more than 50% of sequenced cases in South Africa by the first week of April 2022.

Link to full paper:

<https://ceri.org.za/publication/?token=398>



OPPORTUNITY ALERT:

SPARK South Africa's Call for Translational Science Projects

SPARK TRANSLATIONAL SCIENCE INNOVATIONS IN SOUTH AFRICA

**Does your research have potential
to be transferred to the market?**

**Are you sitting on a potential new technology
addressing current or new needs of the market?**

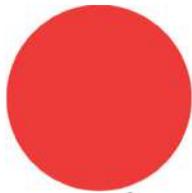
**SPARK SOUTH AFRICA has opened a call
to support promising research discoveries transfer
from the bench to the market or to the community!**

**Apply for the project grant and receive
mentorship from experts and professionals in the field.**

**More info: biodurban.org
Deadline for application: **31 July 2022 at 18:00****



UKZN INSPIRING GREATNESS

CAPACITY BUILDING:

Workshop: Exploratory Data Analysis and Modelling in R with Microbiome Applications

22-26 August 2022

Nelson R. Mandela School of Medicine, University of KwaZulu-Natal

Registration Deadline: 7 August, 2022**No course fee- must bring laptop**

This intensive, hands-on workshop will use microbiome data as a backdrop to learn R. The workshop will feature morning & afternoon sessions taught by expert faculty and technical assistants. All participants will acquire fundamental computational skills, bioinformatics best practices, exploratory data analysis, and modeling techniques.

Workshop Organizers

Joseph Elsherbini, PhD
Harvard Medical School

Scott Handley, PhD
Washington University in St. Louis

Tulio de Oliveira, PhD
University of KwaZulu-Natal

Douglas Kwon, MD PhD
Harvard Medical School



When and Where:

22-26 August, 2022

AHRI Seminar Rooms 1&2

Nelson Mandela School of Medicine

719 Umbilo Road, Durban, South Africa

Topics

- UNIX computing
- Introduction to R
- Library prep of human microbiome samples
- Processing raw microbiome data
- Connecting sequencing data and metadata through exploratory data analysis

Registration:

- <https://forms.gle/ZKSzzvRif25V1T2k8>
- Email:
2022MicroDataDurban@kwonlab.org

CAPACITY BUILDING:

NGS-BRICS

Viral Sequencing & Phylogenetics Workshop

STELLENBOSCH SOUTH AFRICA & VIRTUALLY

2022

The BRICS' Network for Genome Surveillance (NGS-BRICS) was established in 2021 and generates and investigates sequence data of viral pathogens of public health importance, such as for COVID-19. In the interest of increasing bioinformatic and experimental expertise within BRICS countries.

The NGS-BRICS is hosting a workshop on SARS-CoV-2 genome sequencing, assembly, and phylogenetic analyses. The workshop will take place 26th-30th September 2022, 9AM-12PM GMT, and will be presented virtually. It is aimed at BRICS scientists, individuals in the field of academia, or representatives working in public health laboratories.

The Workshop is aimed at anyone working in a BRICS country in the field of academia or in a public health laboratory.

The workshop which will take place 26th-30th of September 2022 (9AM-12PM GMT), Applications closes on 1st of August 2022 at 12AM GMT.

Interested candidates can apply using the following link: <https://tinyurl.com/yn4fcx7y>.

FEATURE: Life outside the Laboratory

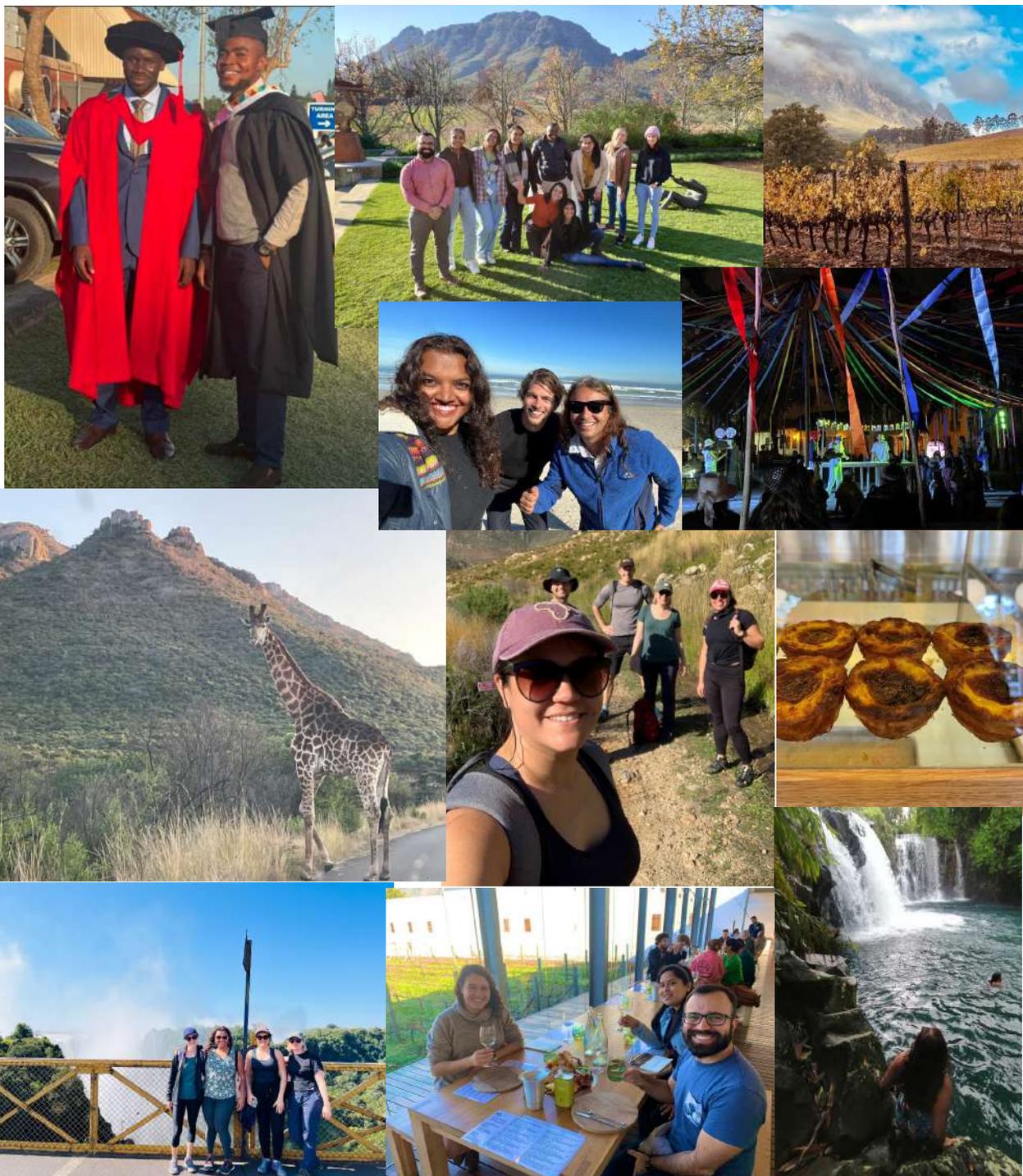
Finding the right work-life balance is so important to ones productivity, mental health and general enjoyment of life. Our CERI & KRISP team members are encouraged to put this method into practice all the time!

May and June were very eventful months, filled with graduation ceremonies, prestigious nominations, adventures in new countries, visits from overseas experts and the enjoyment of all the wonders our beloved South Africa has to offer: berg, beach and bush!

Below are a series of pictures shared by our team over the last few months to give you a glimpse of what they have been up to outside of the laboratory and away from their computer screens!

All these serve as a reminder of how lucky we are to have such a great team around us and to be able to work in such a rewarding and fun work environment.

We look forward to the next chapter ahead!



CERI & Krisp Papers



Continued Emergence and Evolution of Omicron in South Africa: New BA.4 and BA.5 lineages. Tegally H, Moir M, Everatt J, Giovanetti M, Scheepers C, Wilkinson E, Subramoney K, Moyo S, Amoako D, Althaus C, et al, **Nature Medicine** (2022), MEDRXIV-2022-274406v1-deOliveira



Omicron infection engenders Delta antibody immunity in vaccinated persons
Khadija Khan, Farina Karim, Sandile Cele, Kajal Reedoy, James Emmanuel San, Gila Lustig, Houriiyah Tegally, Yuval Rosenberg, et al. **Nature** (2022), doi: 10.1038/s41586-022-04830-x



Emergence and phenotypic characterization of the global SARS-CoV-2 C.1.2 lineage. Scheepers C, Everatt J, Amoako DG, Tegally H, Wibmer CK, Mnguni A, Ismail A, Mahlangu B, Lambson BE, Martin DP, et al **Nature Communications** (2022), 13(1):1976. doi: 10.1038/s41467-022-29579-9.



Urgent need for a non-discriminatory and non-stigmatizing nomenclature for monkeypox virus
Christian Happi, Ifedayo Adetifa, Placide Mbala, Richard Njouom, Emmanuel Nakoune, Anise Happi, Nnaemeka Ndodo, Oyeronke Ayansola, Gerald Mboowa, Trevor Bedford, et al, **Virological** (2022), doi:https://virological.org/t/urgent-need-for-a-non-discriminatory-and-non-stigmatizing-nomenclature-for-monkeypox-virus/853



Selection analysis identifies clusters of unusual mutational changes in Omicron lineage BA.1 that likely impact Spike function.
Martin DP, Lytras S, Lucaci AG, Maier W, Grüning B, Shank SD, Weaver S, MacLean OA, Orton RJ, Lemey P, et al. **Mol Biol Evol.** (2022), doi: 10.1093/molbev/msac061.

For more information please contact:

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Websites: www.ceri.org.za & www.krisp.org.za

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science & innovation
Department:
Science and Innovation
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The
ROCKEFELLER
FOUNDATION



Disclaimer: CERI at SU and KRISP at UKZN wishes to express its gratitude to the following funders for their generous support for the production of this report: The Rockefeller Foundation, the Technology Innovation Agency (TIA) of the Department of Science and Innovation (DSI), South African Medical Research Council (SAMRC), European Commission (EC) and the National Institute of Health. The newsletter is published as open access under a Creative Commons ShareAlike 30 Unported (CC BY-SA 30) license (<http://creativecommons.org/licenses/by-sa/30/>) and is available in printed format as well as electronically as PDF, Web-format, etc The contents of this report and the opinions expressed herein are solely the responsibility of the authors and do not necessarily represent the official views or policies of any of the funders.