# CERI & KRISP Newsletter

Vol 5, Num 4
Apr/May 2022

**Centre for Epidemic Response and Innovation (CERI) & KwaZulu-Natal Research Innovation and Sequencing Platform (KRISP)**



## Introduction:

In this issue, we feature the recent research describing the **new BA.4 and BA.5 Omicron lineages in South Africa** and the massive collaborative effort that provides insights on the **evolving SARS-CoV-2 epidemic in Africa**.

We also highlight the New York Times article on how **South Africa's latest surge is a possible preview of the pandemic's next chapter**.

The upcoming **International Bioinformatics Workshop on Virus Evolution & Molecular Epidemiology** to be held in August 2022 in Panama City is also highlighted.

We are pleased to announce the availability of three **Postdoctoral positions** at CERI & KRISP and are excited to host Prof Rob Warren and Prof Moritz Kraemer at our upcoming **seminar series** for May.

## Highlights:

News: **South Africa's latest surge is a possible preview of the pandemic's next chapter.**

BA.4 and BA.5: **Continue Evolution of SARS-CoV-2 Omicron in South Africa: New BA.4 and BA.5 lineages**

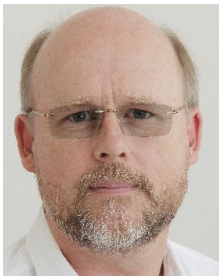
News: **How should the world respond to the next pandemic?**

Announcement: **Postdoctoral Positions in Molecular Epidemiology, Human and Pathogen Genomics and Bioinformatics at CERI & KRISP**

Seminar: **Using next generation sequencing methods to enhance understanding of the epidemiology and treatment of drug resistant TB, Prof Rob Warren, 11 May 2022**

Seminar: **Context-specific emergence and spread of SARS-CoV-2 lineage, Prof Moritz Kraemer, 25 May 2022**

# Events: **Seminars and Events at CERI & KRISP**



**Seminar: Using next generation sequencing methods to enhance understanding of the epidemiology and treatment of drug resistant TB**

**Speaker: Prof Rob Warren**

Director: South African Medical Research Council's Centre for Tuberculosis Research

**Date:** Wednesday, 11 May 2022

**Time:** 12:00 – 13:00

**Venue:** JN de Villiers auditorium, Stellenbosch Tygerberg Campus (in-person) & Zoom.

**Seminar: Context-specific emergence and spread of SARS-CoV-2 lineages**

**Speaker: Prof Moritz Kraemer**

Associate Professor of Computational and Genomic Epidemiology and Fellow at Reuben College at the University of Oxford

**Date:** Wednesday, 25 May 2022

**Time:** 11:30am – 12:30pm

**Venue:** STIAS, Manor House Library, Stellenbosch (in-person) & Zoom.

## 26th International Bioinformatics Workshop on Virus Evolution & Molecular Epidemiology (VEME), Aug 21- 26, 2022, Panama City

**The workshop comprises 6 full days of theoretical lectures, practical sessions, and keynote presentations.**

The VEME workshop faculty includes international leading researchers in virus evolution, molecular epidemiology, and bioinformatics. VEME has run for 26 years, and has became known as one of the best workshops in the world.

**Participants can select four modules:** Phylogenetic Inference, Evolutionary Hypothesis Testing, Next Generation Sequencing and From Trees to Public Health Policy.

The registration fee of US$ 700 covers attendance. In each 4-day module, participation is limited to 30 scientists and is dependent on a selection procedure based on the submitted abstract and statement of motivation.

**The abstract and application deadline is: 31st of May 2022**

Thanks to the financial support of the PAHO/WHO. **A selected number of Latin-American and African participants will receive a grant**. These grants will cover travel and registration fee.

Website: h**ttps://veme-fiocruzbr.ceri.africa**

Pan American Health Organization

Regional Office of the World Health Organization

# News: **South Africa's latest surge is a possible preview of the pandemic's next chapter**


By Alexandra E. Petri, New York Times, May 2, 2022

The spread of two newly discovered subvariants has doctors watching closely.

Coronavirus cases are surging again in South Africa, and public health experts are monitoring the situation, eager to know what's driving the spike, what it says about immunity from previous infections and what its implications are globally.

South Africa experienced a decline in cases after hitting an Omicron-fueled, pandemic peak in December. But in the past week, cases have tripled, positivity rates are up and hospitalizations have also increased, health officials said. The surge has the country facing a possible fifth wave.

The spike is linked to BA.4 And BA.5, two subvariants that are part of the Omicron family.

Tulio de Oliveira, director of South Africa's KwaZulu-Natal Research and Innovation Sequencing Platform, said that BA.4 and BA.5 demonstrate how the virus is evolving differently as global immunity increases.

**"What we are seeing now, or at least maybe the first signs, is not completely new variants emerging, but current variants are starting to create lineages of themselves,"** Dr. de Oliveira said. Since its initial identification in South Africa and Botswana last November, Omicron has produced several subvariants.

Emerging data show that in unvaccinated people, BA.4 and BA.5 evades natural defenses produced from an infection with the BA.1, which sent case counts skyrocketing in South Africa last winter, Dr. de Oliveira said. The result is symptomatic infections with the new subvariants.

"That is the reason why it is starting to fuel a wave in South Africa," Dr. de Oliveira said.

Scientists are still studying whether this new wave creates milder or more severe illness, and it is unclear if the two subvariants could surge elsewhere in the world.

Read full article:
**https://www.nytimes.com/2022/05/02/world/africa/south-africa-surge-variants.html**

# Publication: **Continue Evolution of SARS-CoV-2 Omicron in South Africa: New BA.4 and BA.5 lineages**

South Africa's fourth COVID-19 wave was driven predominantly by three lineages (BA.1, BA.2 and BA.3) of the SARS-CoV-2 Omicron variant of concern. We have now identified two new lineages, BA.4 and BA.5.

The spike proteins of BA.4 and BA.5 are identical, and comparable to BA.2 except for the addition of 69-70del, L452R, F486V and the wild type amino acid at Q493. The 69-70 deletion in spike allows these lineages to be identified by the proxy marker of S-gene target failure with the TaqPath™ COVID-19 qPCR assay.

BA.4 and BA.5 have rapidly replaced BA.2, reaching more than 50% of sequenced cases in South Africa from the first week of April 2022 onwards. Using a multinomial logistic regression model, we estimate growth advantages for BA.4 and BA.5 of 0.08 (95% CI: 0.07 - 0.09) and 0.12 (95% CI: 0.09 - 0.15) per day respectively over BA.2 in South Africa.

The most recent common ancestor of BA.4 and BA.5 is estimated to have originated in mid-November 2021 (HPD 29 September 2021 to 6 December (Fig. 1A), coinciding with the emergence of the other lineages, for example BA.2 in early November 2021 (HPD: 9 October 2021 to 29 November 2021).


*Fig. 1B: Phylogeography*

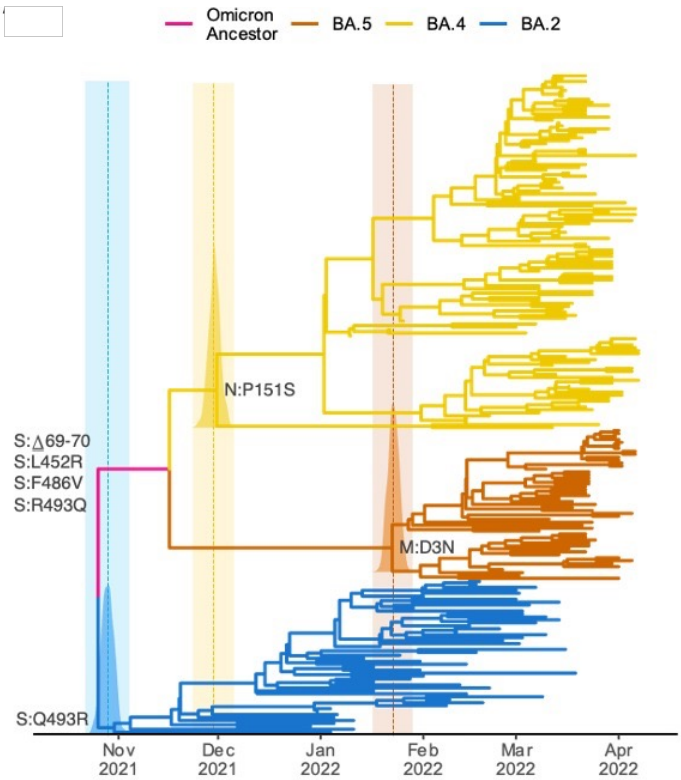



*Fig. 1A: Phylogenetics*

Phylogeographic analysis suggests early dispersal of BA.4 from Limpopo to Gauteng, with later spread to other provinces (Fig. 1B); and early dispersal of BA.5 from Gauteng to KwaZulu-Natal, with more limited onward spread to other provinces.

It remains unclear how large an effect this shift in the distribution of different Omicron lineages will have on the epidemic in South Africa and elsewhere in the world. Although the incidence of reported cases and the proportions of positive qPCR and antigen tests were relatively low (5-10%) through to early April 2022, these indicators began to rise from mid-April 2022.

Link to full paper: Tegally et al. Continued Emergence and Evolution of Omicron in South Africa: New BA.4 and BA.5 lineages. https://ceri.org.za/publication/?token=392

# Publication: **The evolving SARS-CoV-2 epidemic in Africa: Insights from rapidly expanding genomic surveillance.**

Investment in Africa over the past year with regards to SARS-CoV-2 genotyping has led to a massive increase in the number of sequences, exceeding 100,000 genomes generated to track the pandemic on the continent. This analysis show an increase in the number of African countries able to sequence within their own borders, coupled with a decrease in sequencing turnaround time (Fig 1A). Findings from this genomic surveillance underscores the heterogeneous nature of the pandemic but repeated dissemination of SARS-CoV-2 variants within the continent are observed.

Ancestral state reconstruction analysis reveals patterns of dissemination of variants of concern (VOCs) and shows that most viral transfers occured between African countries and followed distinct regional patterns for each VOC (Fig 1B).

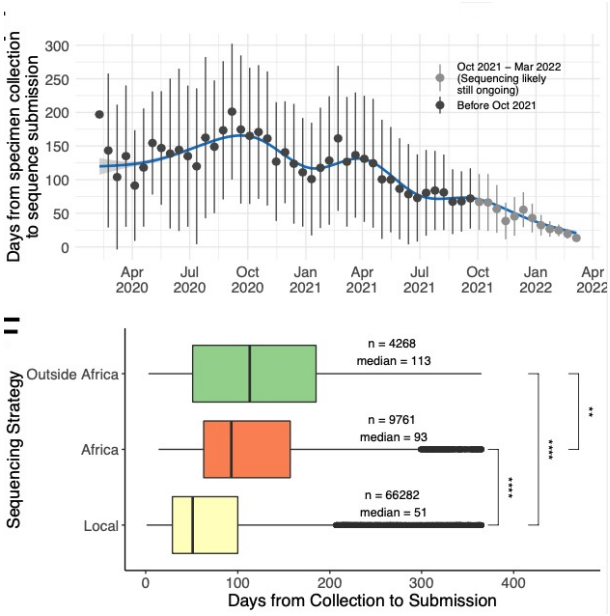



*Fig. 1A: Sequencing turn-around times*

Sustained investment for genomic surveillance in Africa is needed as the virus continues to evolve, particularly in the low vaccination landscape. These investments are very crucial for preparedness and response for future pathogen outbreaks.

Link to full paper: Tegally et al. [The evolving SARS-CoV-2 epidemic in Africa: Insights from rapidly expanding genomic surveillance (medrxiv.org)]

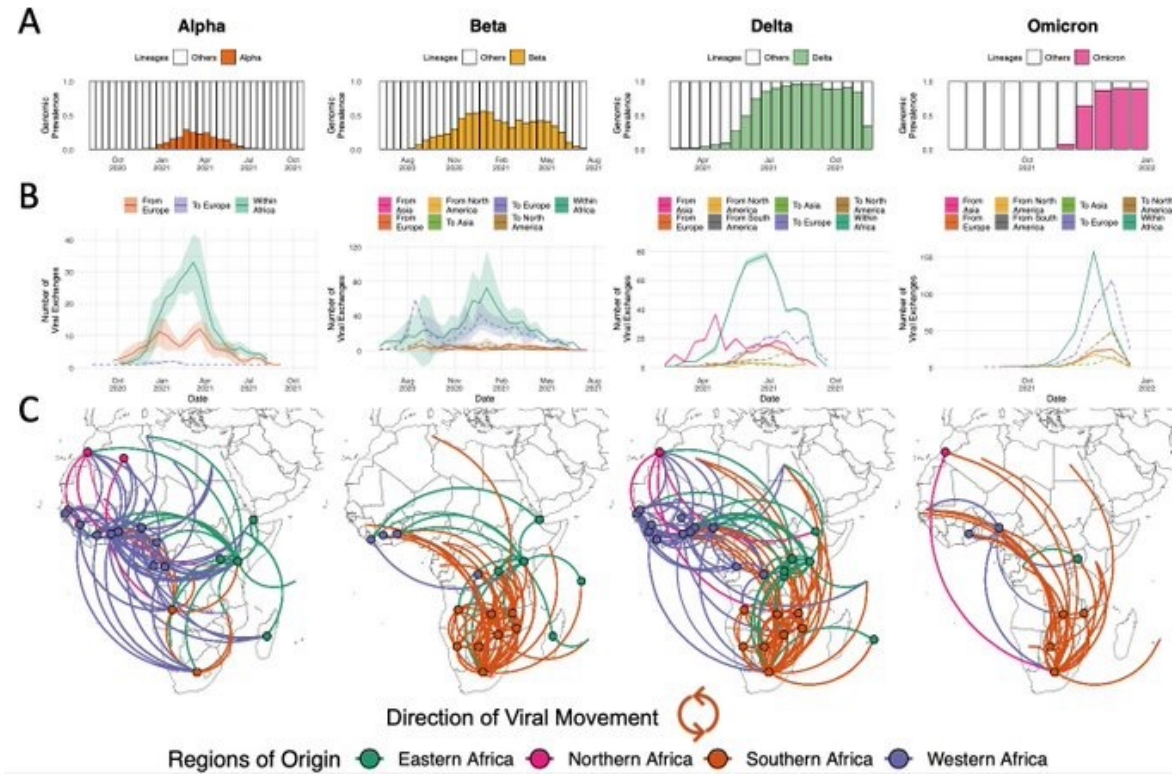
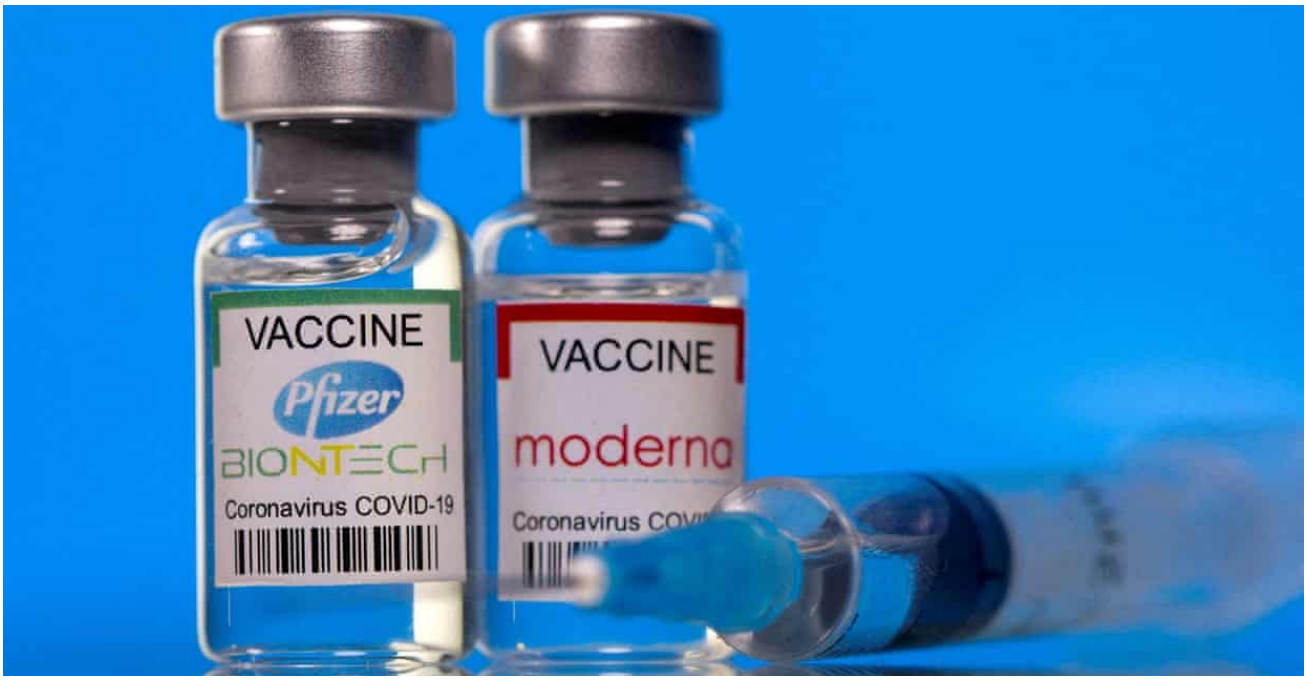



*Fig. 1B: Patterns of dissemination of VOCs in and out and within the continent*

# News: **How should the world respond to the next pandemic?**




By Laura Spinney, The Guardian

As the WHO mulls when to call the Covid pandemic over, attention is turning to the future. Last November, having alerted the world to the new and highly transmissible Omicron variant of the Sars-CoV-2 virus, South Africa-based scientist Tulio de Oliveira saw that country hit with travel bans.

Already smarting at what he saw as wealthier nations' hoarding of vaccines, antiviral drugs and test reagents, his frustration spilled over. **'If the world keeps punishing Africa for the discovery of Omicron and 'global health scientists'** keep taking the data, who will share early data again?' he tweeted.

Two years into this pandemic, as the World Health Organization (WHO) mulls the tricky question of when to call it over and some countries, including the UK, pre-empt that decision, the world's attention is turning to the future.

**How do we improve our response to the next pandemic?**

There are two main challenges: improving the surveillance of pathogens; and ensuring vaccine equity.

And as De Oliveira intimated, these are linked. Not only morally, but for the first time in pandemic history, legally.

**Do we need a pandemic treaty?**

It used to be that living organisms, including pathogens, were considered humanity's common heritage, and sharing them for scientific purposes happened informally. That changed with the UN's 1992 convention on biological diversity (CBD), which states that countries have sovereign rights over genetic resources found on their territory.

Link to complete article:
**https://www.theguardian.com/world/2022/mar/18/how-should-world-respond-to-next-pandemic-covid**

# Postdoctoral Positions (x3) at CERI & KRISP: Molecular Epidemiology, Human and Pathogen Genomics and Bioinformatics

We are seeking to appoint three post-doctoral fellows with great potential and ambition to become leading scientists. These positions will work with some of the best genomics and bioinformatics scientists in the world. We aim to identify both pathogen and human genomic variation that are associated with the transmission and virulence of pathogens and the development of diseases.

The fellows will have access to data generated at the largest and most automated genomic facility in Africa and will analyse and/or code software for high-throughput genomic data generated in Illumina Novaseq6000s, Nextseq2000s, Oxford Nanopore Technologies (ONT) GRIDIons and Genexus sequencers. CERI and KRISP have access to novel sequencing and diagnostic technologies in collaboration with industry. **Our vision is to be a leader of the fast moving field of genomics data generation and analysis to save lives in real-time.**

**The fellows will be able to select the location of the positions**, which can be based in any of our three state-of-the-art campuses: CERI Data at Stellenbosch, CERI Genomics at Tygerberg Stellenbosch Campus in Cape Town or at KRISP at UKZN in Durban

**Hosts:** Prof Tulio de Oliveira, Dr. Eduan Wilkinson, Dr. Richard Lessells, Dr. Jennifer Giandhari and Dr. Cheryl Baxter, CERI at Stellenbosch University and KRISP at UKZN**.**

**Minimum requirements for positions:**

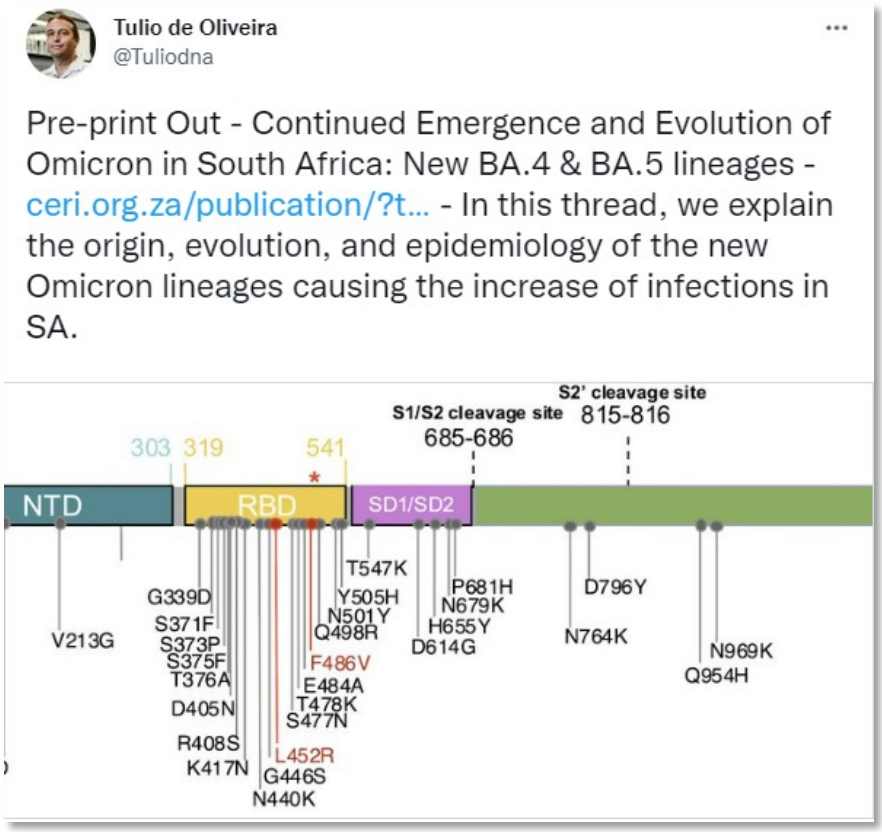
- Genomics and/or bioinformatics experience at PhD and/or MSc level.
- Experience in publishing in top international peer reviewed journal.
- Advanced data analysis expertise (e.g. R, Phyton, JAVA or other statistical or programming language).
- Experience working with the analysis of viral, bacterial and/or human genomes.

**Closing date: 1 June 2022**

**Application process:** Send a letter of application, accompanied by a CV, a motivation letter and contact details of two referees, to:

Mrs Zethu Luthuli, luthuliz@sun.ac.za

# Twitter Science: **The new way to quickly communicate Science**




**Twitter real-time updates:**

**CERI at Stellenbosch**
@ceri_news

**KRISP at UKZN**
@krisp_news

**Houryiah Tegally**
@houzhou

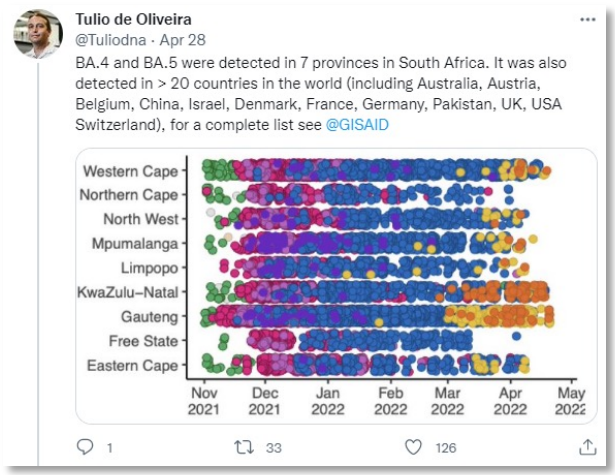
**Eduan Wilkinson**
@EduanWilkinson

**Richard Lessells**
@rjlessells

**Tulio de Oliveira**
@tuliodna

**Stellenbosch University**
@StellenboschUni

**University of KwaZulu-Natal**
@UKZN





# CERI & KRISP Papers

OPEN ACCESS

**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, **medRxiv** (2022), MEDRXIV-2022-274406v1-deOliveira

**Effectiveness of the Ad26.COV2.S vaccine in health-care workers in South Africa (the Sisonke study): results from a single-arm, open-label, phase 3B, implementation study.**
Bekker LG, Garrett N, Goga A, Fairall L, Reddy T, Yende-Zuma N, Kassanjee R, Collie S, Sanne I, Boulle A, et al. **Lancet** (2022), 399(10330):1141-1153. doi: 10.1016/S0140-6736(22)00007-1:

**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 Commununications** (2022), 13(1):1976. doi: 10.1038/s41467-022-29579-9:.

**Replacement of the Gamma by the Delta variant in Brazil: Impact of lineage displacement on the ongoing pandemic.**
Giovanetti M, Fonseca V, Wilkinson E, Tegally H, San EJ, Althaus CL, Xavier J, Nanev Slavov S, Viala VL, Ranieri Jerônimo et al, **Virus Evolution** (2022), doi: 10.1093/ve/veac024:.

**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:.**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