Building genomics Networks in **AFRICA**

Prof Tulio de Oliveira for the Network for Genomic Surveillance South Africa (NGS-SA) and the **Africa CDC Pathogen Genomics Initiative (PGI)**

























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Presentation



Network for Genomic Surveillance in South Africa



Africa CDC Pathogen Genomics Initiative (PGI) to expand surveillance to Africa.











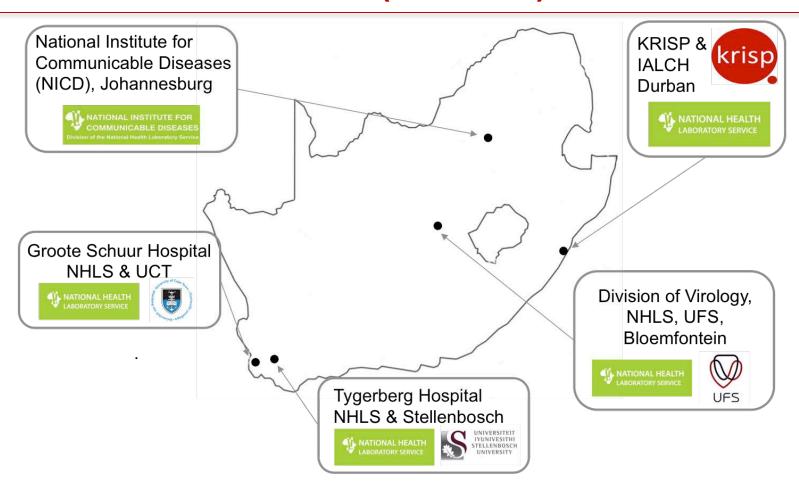








Network for Genomic Surveillance in South Africa (NGS-SA)





Supported by the DSI and the SA MRC Msomi N, Mlisana K, et al. Lancet Microbe 2020













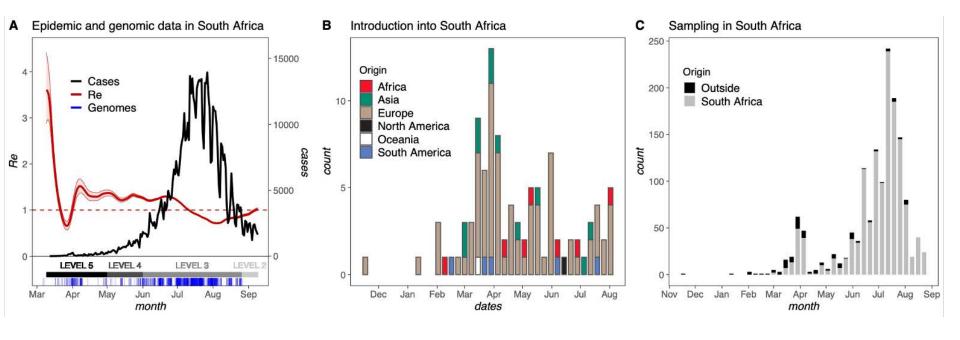






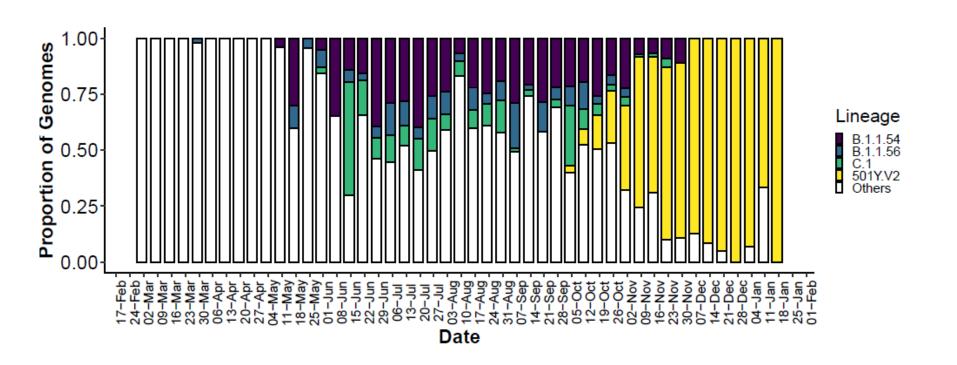


Introductions and local transmission of SARS-CoV-2 (first wave)





Distribution of SARS-CoV-2 lineages South Africa



Data from 3324 sequences from all 9 provinces, collected up to 19 Jan

Tegally, Wilkinson, Giovanetti, et al. Nature 2021 (in press)











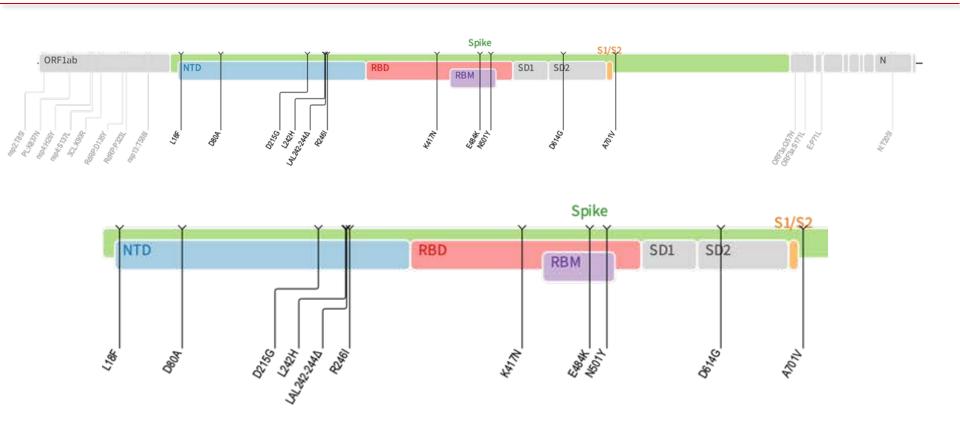








Genomic map of 501Y.V2 (B.1.351, 20H)



Three mutations in spike receptor-binding domain & cluster of mutations in N-terminal domain

Tegally, Wilkinson, Giovanetti, et al. Nature 2021 (in press)



















COMMENT | ONLINE FIRST

A genomics network established to respond rapidly to public health threats in South Africa

Nokukhanya Msomi 🏻 Koleka Mlisana 🖨 Tulio de Oliveira 🖾 🖻

on behalf of the Network for Genomic Surveillance in South Africa writing group † Show footnotes

Open Access Published: August 18, 2020 DOI: https://doi.org/10.1016/S2666-5247(20)30116-6

ALARMING COVID VARIANTS **GENOMIC SURVEILLANCE**

Efforts to track SARS-CoV-2 sequences have helped to identify worrying lineages - but researchers are blind to emerging mutations in some regions.

By David Cyranoski

lready, 2021 is shaping up to be the year of COVID-19 variants. In the past two months, scientists have identified in these regions. several fast-spreading viral variants hat have prompted government restrictions in many countries - and new

is patchy globally, particularly in the United

outbreak, and in many low- and middle-income countries. Scientists warn that worrying variants are probably spreading undetected

"Genomic epidemiology has come of age during this pandemic," says Oliver Pybus, who studies infectious-disease evolution at The pandemic has ushered in an era of transformed from a "theoretical backwater" genomic surveillance in which scientists are to a tool that helps drive public-health decitracking genomic changes to a virus at a speed sion-making quickly, he says. But to be as widespread, standardized and embedded in

States, which has the world's largest COVID-19 national pandemic-prevention programmes, scientists say.

Surveillance networks

The key to good surveillance is the sequencing and sharing of enough genomes to track mutations and variants of concern as they arise. In the past year, more than 360,000 SARS-CoV-2 lineages are being detected more frequently. the University of Oxford, UK. The field has genomes have been sequenced and stored on GISAID, a non-profit online database for sharing viral genomes, Geographical distribution of the sequences on GISAID is broad, and scale never seen before. But surveillance effective as possible, surveillance needs to be covering more than 140 countries. But most countries have uploaded only a small number

Nature | Vol 589 | 21 January 2021 | 337

wouldn't be useful, "I don't care for the term PHEIC," says Alexandra Phelan, a global-health lawyer at Georgetown University in Washington DC, "but I worry that if we get too into the words, we miss the point that countries need to act appropriately when there is a declaration."

Global-health scholars question why a PHEIC for COVID-19 wasn't declared sooner. On 22 January 2020, Tedros convened a closed-door meeting of virologists, public-health researchers and certain government representatives - as the PHEIC process dictates. They decided that a warning wasn't warranted, but a week later, the committee flipped its position. The delay might have cost the world time to contain the virus.

Still, a one-week lag in declaring a global emergency isn't even the most concerning action that took place in the early days of the COVID-19 pandemic, critics say, When Tedros declared the PHEIC, he advised governments to move fast with public-health measures including tests and social distancing. He also asked them to resist bans on travel and trade because, historically, they had been of limited utility and are potentially harmful.

500 | Nature | Vol 589 | 28 January 2021

FAST-SPREADING COVID VARIANT CAN ELUDE **IMMUNE RESPONSES**

Early studies find that a variant of the virus identified in South Africa could compromise immunity.

By Ewen Callaway

vidence is growing that some coronavirus variants could evade immune responses triggered by vaccines and previous infections. Researchers are trying to make sense of a tsunami of laboratory studies released last week that raise concerns about some emerging variants and

"Some of the data I've seen have really scared me," says Daniel Altmann, an immunologist at Imperial College London, who worries that

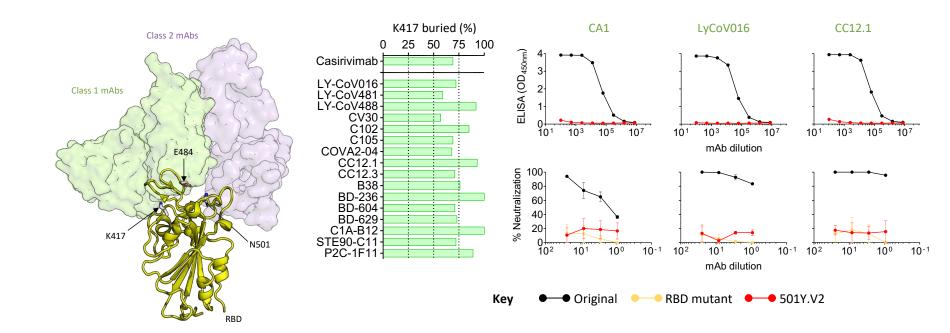
some of the results could portend a reduction in the effectiveness of COVID-19 vaccines.

But the picture is murky, Altmann and other scientists emphasize. The studies which examined the blood of small numbers of people who had recovered from COVID-19 or received a vaccine - probed only their antibodies' capacity to 'neutralize' variants in laboratory tests, and not the wider effects of other components of their immune response.

Neither do the studies indicate whether the changes in antibody activity make any difference to the real-world effectiveness of

UKZN INSPIRING GREATNESS

Triple RBD mutant and 501Y.V2 resistant to "class 1" mAbs



Wibmer et al, 2021 (Nature Medicine in review)











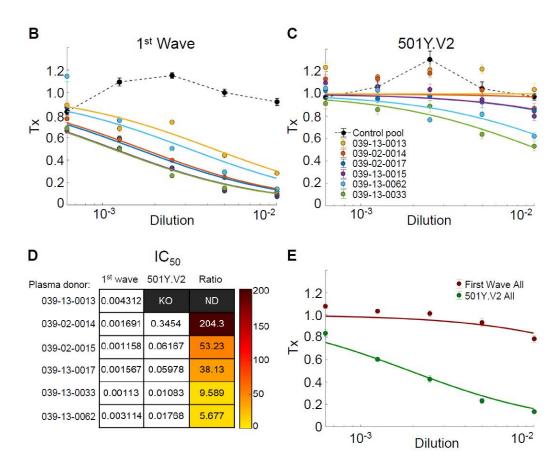


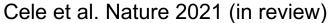






Loss of neutralization with 501Y.V2 (Live Virus)























Sensitivity of 501Y.V2 to plasma from ChAdOx vaccinees

PSVN: Penny Moore LVN: Alex Sigal Vaccinated Vaccinated RBD-only B.1.351 Original 256-Veutralization titre (IC₅₀) 3000-64-16-400 4-Original RBD-only B.1.351 B.1.1 B.1.351 Placebo Placebo Original RBD-only B.1.351 256-Veutralization titre (IC₅₀) 3000 64-16-400 4-B.1.1 B.1.351 Original RBD-only B.1.351 Titre >400 50-399 <50

















Madhi NEJM 2021 (in review)



Los Angeles Times

Sharp split on Trump trial

UC poll finds wide divisions in California about ex-president's role in Capitol riot.

Trump was a major contributor to the insurrection.
Only 19% of California Republicans favor a Senate conviction of Trump, compared with 25% of the state? Democratis, according to the poil released Monday by UC Berckely's Institute of Contributor Contri

have their own internal divi-tions over the former presi-dent, with a significant mi-nority-viewing him as at least partially culpable and re-jecting him as a continuing leader for their party. Similar divides show up in polls nationwide and in

Divide in GOP hits California lawmakers

BY MELANIE MASON

Nearly a month after ob-jecting to electoral votes cast for President Biden. Rep. Mike Garcia wanted to clear the air. In a lecal newspaper, the Santa Clarita Republican and former Nayr fighter-jet pilot denounced the blow-back on social media that back on social media that kralito, or even worse. Roughly 150 miles to the north, Rep. David Valadao also had some explaining to



THE MAGNIFICENT SEVENTH

Legacy of Tuskegee: Distrust

Recalling syphilis study, Black Alabamians wary of vaccine





S. Africa's vaccination plans upended

TUSKEGEE Ala - Omar Nea

ften thinks back on the calculated be-rayal of hundreds of Black men and low it still shapes so much about this ural Alabama community.

He remembers the mechanic who ent from house to house fixing cars not the sharecropper who lived off a arrow dirt road. He thinks too of his

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Variant-proof vaccines invest now for the next pandemic

COVID's evolution signals the importance of rational vaccine design based on broadly neutralizing antibodies.





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A participant in the South African trial of the AstraZeneca-University of Oxford COVID-19 vaccine has blood drawn before receiving her second dose. AP PHOTO/JEROME DELAY

South Africa suspends use of AstraZeneca's COVID-19 vaccine after it fails to clearly stop virus variant

By Jon Cohen | Feb. 8, 2021, 2:15 PM

BUSINESS INSIDE: Biden inherits ambiguous regulations for driver-assist technology, A10









Will Biden push for electric cars?

COVID deepens Mexico's despair

VACAVILLE, Calif. - I











Conclusion I:

- Genomic surveillance is a critical component of the epidemic response – exemplified by early detection, characterization and tracking of this new 501Y.V2 variant within and outside South Africa
- We detected a new lineage with multiple mutations at key sites in spike protein which decrease neutralization of antibodies.
- Variant decrease efficacy of certain vaccines.

















Accelerating SARS-CoV-2 Sequencing in Africa





COMMENT | ONLINE FIRST

Accelerating genomics-based surveillance for COVID-19 response in Africa

Sofonias K Tessema • Seth C Inzaule • Alan Christoffels • Yenew Kebede • Tulio de Oliveira • Ahmed E Ogwell Ouma Christian T Happi • John N Nkengasong 🖾 • Show less

Open Access Published: August 18, 2020 DOI: https://doi.org/10.1016/S2666-5247(20)30117-8

Africa's \$100-million Pathogen Genomics Initiative

On Oct 12, 2020, the Africa Centres for Disease Control and Prevention (CDC) secured US\$100 million for pathogen genomics research and development through a partnership, the Africa Pathogen Genomics Initiative (PGI), expected to transform disease surveillance on the continent and is now preparing to start running programmes in 2021.

Africa PGI is a 4-year collaboration between the Africa CDC Institute of Pathogen Genomics, US CDC, the Bill & Melinda Gates Foundation, software giant Microsoft, genomics sequencing technology company Illumina, and UK- of high-impact applications, and the integration of pathogen genomics into the existing disease surveillance system are required, he said.

Africa PGI is building a pan-African disease surveillance and laboratory network based on pathogen genomic sequencing to identify and inform research and public health responses to COVID-19 as well as other epidemic threats and endemic diseases such as AIDS, tuberculosis, malaria, cholera, and other infectious diseases. "Africa is one continent beaten by many pathogens and pandemics", Tulio de Oliveira, director of the KwaZulu-Natal

An African-owned data library and real-time data-sharing platform will be established to support the laboratory network, in alignment with different African Union member states' regulations.

At the initiative's onset, 72% of Africa's genome sequencing capacity is concentrated in four countries: South Africa has 50 institutions, Kenya 20, Nigeria ten, and Morocco five. According to Africa CDC, about 83% of these are in non-public health institutions. A few African countries have a single, privately owned, genomic sequencing institution.



For more on Africa PGI see https://africacdc.org/download/ africa-pathogen-genomicsinitiative-factsheet/

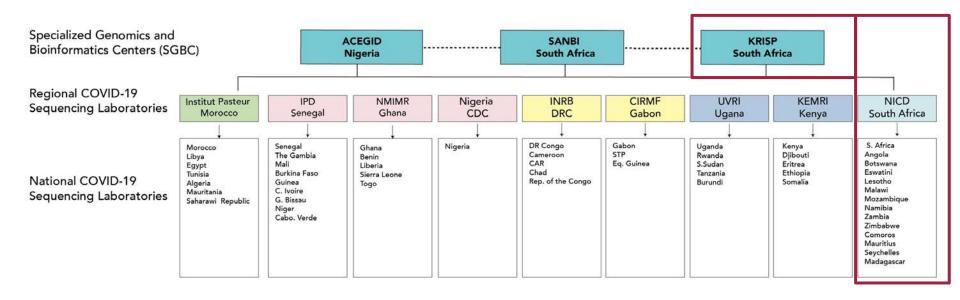
For more on **Network for Genomic Surveillance** see **Comment** Lancet Microbe 2020; 1: e299–30

ACCELERATING SARS-COV-2 SEQUENCING IN AFRICA

Coordination

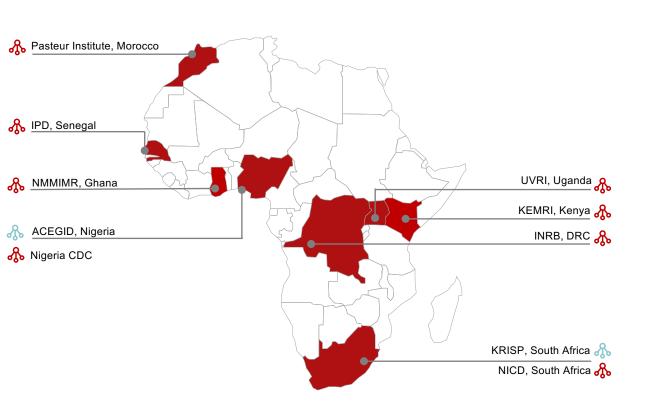
Operationalization of the network

Leverage on existing capacity



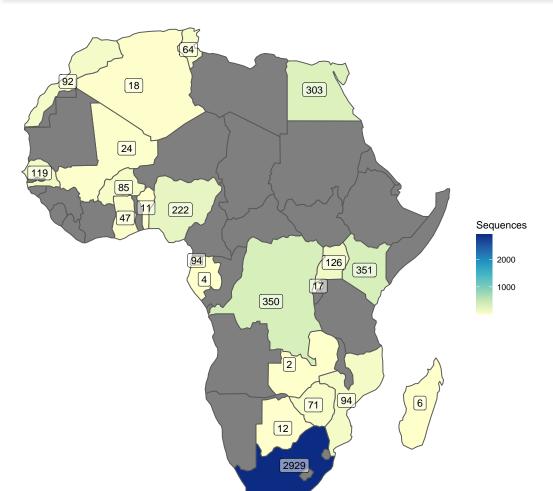
Access to sequencing facility

ACCELERATING SARS-COV-2 SEQUENCING IN AFRICA



- 1. Mobilize resources and leverage on existing capacity
- 2. Start simple and establish routine surveillance
- 3. Support sample collection and shipment logistics
- 4. Support sequencing reagents, equipment upgrades, and personnel
- 5. Support data analysis, sharing, and interpretation

Sampling and sequencing



Due to various reasons not all African sequences are sufficient for analyses (i.e. to short, clustered SNPs or high number of SNPs). These needs to be removed prior to phylogenetic analyses.

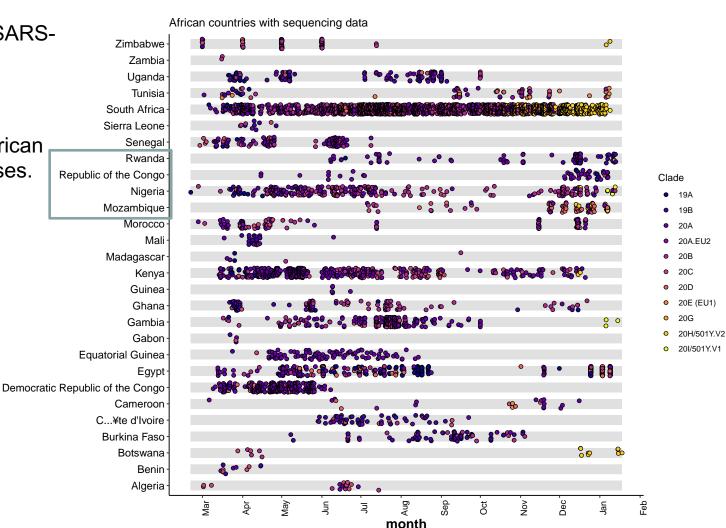
Done in NextClade

https://clades.nextstrain.org

Sampling and sequencing

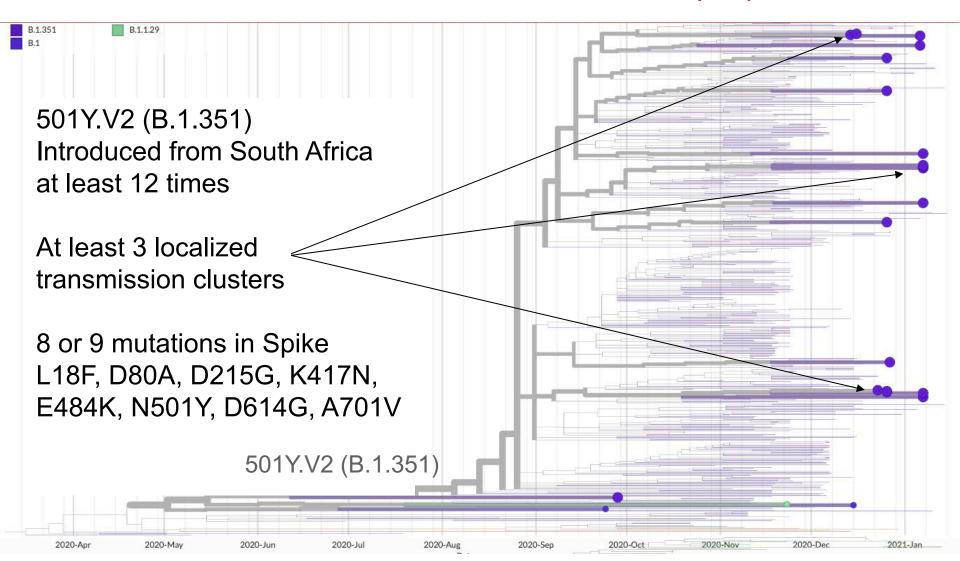
Genomic data from SARS-CoV-2 sequencing in Africa.

5438 good quality African sequences for analyses.



501Y.V2 in Mozambique

Data from Instituto Nacional de Saúde (INS)





















ACCELERATING SARS-COV-2 SEQUENCING IN AFRICA

Current challenges

- 1. Lack of standardized sampling framework tailored to the African setting (what to sequence?)
- 2. Market and custom issues on the timely availability of reagents
- 3. Material Transfer Agreements and import permits
- 4. Standardized data analysis, sharing, and reporting frameworks

め protocols.io



Jun 17, 2020



5= Run

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S Illumina Nextera DNA Flex library construction and sequencing for SARS-CoV-2: Adapting COVID-19 ARTIC protocol ▼

Sureshnee Pillay¹, Jennifer Giandhari¹, Houriiyah Tegally¹, Eduan Wilkinson¹, Benjamin Chimukangara¹, Richard Lessells^{1,2}, Yunus Moosa², Inbal Gazy¹, Maryam Fish¹, Lavanya Singh¹, Khulekani Sedwell Khanyile¹, Vagner Fonseca^{1,3,4}, Marta Giovanetti⁴, Luiz Carols Alcantara^{3,4}, Tulio de Oliveira^{1,5,6},

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2 Works for me

dx.doi.org/10.17504/protocols.io.bhjgj4jw

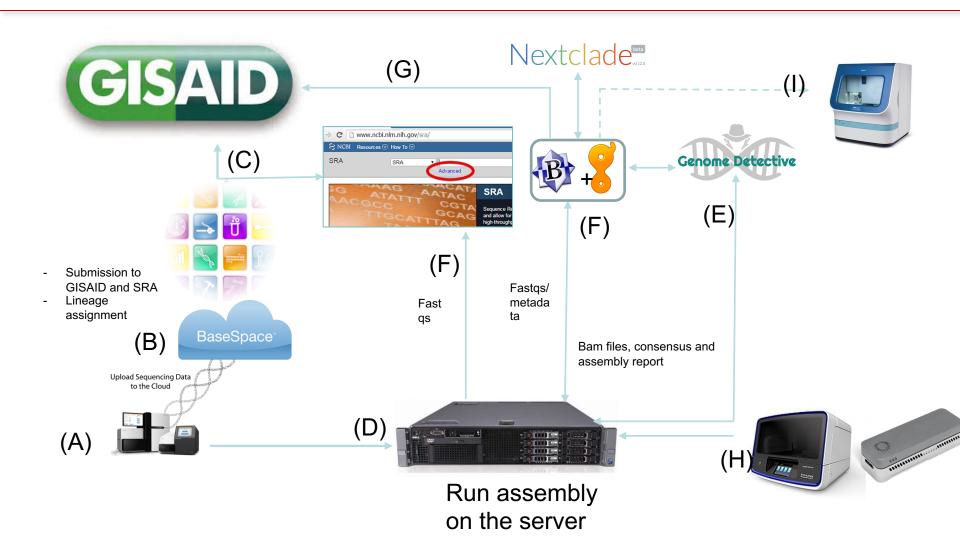
Coronavirus Method Development Community KRISP



Jennifer Giandhari



Assembly Automation – Illumina, S5Ion and Nanopore

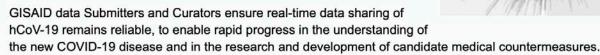


Data is only analyzed when in GISAID!

In Focus

41,000 viral genomic sequences of hCoV-19 shared with unprecedented speed via GISAID

Since the start of the COVID-19 outbreak and the identification of the pandemic virus, laboratories around the world are generating viral genome sequence data with unprecedented speed, enabling real-time progress in the understanding of the new disease and in the research and development of candidate medical countermeasures. Sequence data are essential to design and evaluate diagnostic tests, to track and trace the ongoing outbreak, and to identify potential intervention options. Listen to PRI's Elana Gordon.





EpiCoV Data Curation Team



Aengus Stewart

The Francis Crick Institute, London

Sheila Ons

Universidad Nacional de La Plata, Buenos Aires

Thomas Bigot

CNRS & Institut Pasteur, Paris

Daniel See Rui En

Bioinformatics Institute Singapore A*Star

Recent hCoV-19 data submissions

hCoV-19/Russia/CRIE162784/2020

hCoV-19/Bangladesh/BCSIR-NILMRC 050/2020

hCoV-19/Singapore/323/2020

hCoV-19/England/SHEF-D3464/2020

hCoV-19/USA/WA-UW-10138/2020

Number of hCoV-19 genomic sequences: 41,735

Webinar Series on COVID-19 Genomic Surveillance in Africa /Technical Session/

SARS-CoV-2 whole genome sequencing and quality control



Dr. Jennifer Giandhari



Sureshnee Pillay



Houriiyah Tegally



James San



Wednesday, 05 August 2020 2:00PM - 3:00PM East Africa Time

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Weekly Seminar Series

Acknowledgements

KRISP at UKZN:

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Glenda Gray















