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)
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)

National Institute for Communicable Diseases (NICD), Johannesburg

Groote Schuur Hospital
NHLS & UCT

KRISP & IALCH
Durban

Division of Virology,
NHLS, UFS,
Bloemfontein

Tygerberg Hospital
NHLS & Stellenbosch

Supported by the DSI and the SA MRC
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

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

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

ALARMING COVID VARIANTS SHOW KEY ROLE OF 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

Already, 2021 is shaping up to be the year of COVID-19 variants. In the past two months, scientists have identified several fast-spreading viral variants that have prompted government restrictions in many countries—and new lineages are being detected more frequently.

The pandemic has ushered in an era of genomic surveillance in which scientists are tracking genomic changes to a virus at a speed and scale never seen before. But surveillance is patchy globally, particularly in the United States, which has the world’s largest COVID-19 outbreak, and in many low- and middle-income countries. Scientists warn that worrying variants are probably spreading undetected in these regions.

“Genomic epidemiology has come of age during this pandemic,” says Oliver Pybus, who studies infectious disease evolution at the University of Oxford, UK. The field has transformed from a “theoretical backwater” to a tool that helps drive public health decision-making quickly, he says. But to be as effective as possible, surveillance needs to be widespread, standardized and embedded in 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 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, covering more than 140 countries. But most countries have uploaded only a small number wouldn’t be useful. “I don’t care for the term PHEIC,” says Alexandra Philani, a global health lawyer at Georgetown University in Washington DC. “I just worry that if we get too into the weeds, 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 gap 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 testing and social distancing. He also asked them to resist bans on travel and trade.

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

Evidence 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 mutations.

“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 emphasise. 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
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)

Cele et al. Nature 2021 (in review)
Sensitivity of 501Y.V2 to plasma from ChAdOx vaccinees

PSVN: Penny Moore
LVN: Alex Sigal

Neutralization titre (IC₅₀)

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Madhi NEJM 2021 (in review)
**Los Angeles Times**

**Sharp split on Trump trial**
UC poll finds wide division in California about re-convening Senate trial
By Dion Limas

**Variant-proof vaccines – invest now for the next pandemic**

**Science**

**Variant-proof vaccines – invest now for the next pandemic**

COVID’s evolution signals the importance of rational vaccine design. An investment now could save many lives.

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

**Variant-proof vaccines – invest now for the next pandemic**

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

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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
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

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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-
ACCELERATING SARS-COV-2 SEQUENCING IN AFRICA

Operationalization of the network

Leverage on existing capacity

Coordination

Specialized Genomics and Bioinformatics Centers (SGBC)

Regional COVID-19 Sequencing Laboratories

National COVID-19 Sequencing Laboratories

ACEGID
Nigeria

SANBI
South Africa

KRISP
South Africa

INRB
DRC

CIRMF
Gabon

UVRI
Ugana

KEMRI
Kenya

NICD
South Africa

IPD
Senegal

NMIMR
Ghana

Nigeria
CDC

Morocco

Senegal

The Gambia

Mali

Burkina Faso

Guinea

C. Ivoire

G. Bissau

Niger

Cabo, Verde

Ghana

Benin

Liberia

Sierra Leone

Togo

DR Congo

Cameroon

CAR

Chad

Rep. of the Congo

Gabon

STP

Eq. Guinea

Uganda

Rwanda

S. Sudan

Tanzania

Burundi

Kenya

Djibouti

Eritrea

Ethiopia

Somalia

S. Africa

Angola

Botswana

Eswatini

Lesotho

Malawi

Mozambique

Namibia

Zambia

Zimbabwe

Comoros

Mauritius

Seychelles

Madagascar

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)

501Y.V2 (B.1.351)  
Introduced from South Africa  
at least 12 times

At least 3 localized  
transmission clusters

8 or 9 mutations in Spike  
L18F, D80A, D215G, K417N,  
E484K, N501Y, D614G, A701V
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
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 Lessells¹,², Yunus Moosa², Inbal Gazy¹, Maryam Fish¹, Lavanya Singh¹, Khulekani Sedwell Khanyile¹, Vagner Fonseca¹,³,⁴, Marta Giovanetti⁴, Luiz Carols Alcantara³,⁴, Tulio de Oliveira¹,⁵,⁶,
¹KwaZulu-Natal Research Innovation and Sequencing Platform (KRISP), School of Laboratory Medicine & Medical Sciences, University of KwaZulu-Natal, Durban, South Africa;
²Infectious Diseases Department, Nelson R Mandela School of Medicine, University of KwaZulu-Natal, Durban, South Africa;
³Laboratorio de Genetica Celular e Molecular, ICB, Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, Brazil;
⁴Laboratório de Flavivírus, Instituto Oswaldo Cruz Fiocruz, Rio de Janeiro, Brazil;
⁵Centre for Aids Programme of Research in South Africa (CAPRISA), Durban, South Africa;
⁶Department of Global Health, University of Washington, Seattle, Washington, USA

dx.doi.org/10.17504/protocols.io.bhjgj4jw
Assembly Automation – Illumina, S5Ion and Nanopore

(A) Run assembly on the server

(B) BaseSpace
   - Upload Sequencing Data to the Cloud

(C) Submission to GISAID and SRA
   - Lineage assignment

(D) Fastqs/ metadata

(E) Fastq files, consensus and assembly report

(F) Nextclade

(G) Genome Detective

(I) Illumina, S5Ion and Nanopore
Data is only analyzed when in GISAID!

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.

GISAID data Submitters and Curators ensure real-time data sharing of hCoV-19 remains reliable, to enable rapid progress in the understanding of the new COVID-19 disease and in the research and development of candidate medical countermeasures.

EpiCoV Data Curation Team

Aengus Stewart
The Francis Crick Institute, London

Shella 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/BCSI-R-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  Emmanuel James San

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

TO REGISTER VISIT: https://bit.ly/2Okfoqy

Organized by: In partnership with:

Weekly Seminar Series
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Glaudina Loots

**SA MRC**
Glenda Gray