PROGRESS REPORT IN

SEQUENCING AND BIOINFORMATIC ANALYSIS

2024

A Publication of the Department of Sequencing and Computational Biology, Institute of Viral and Emergent Pathogens Control and Research Irrua Specialist Teaching Hospital Irrua Edo State Nigeria

HIS EXCELLENCY

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EXECUTIVE **SUMMARY**

The Institute of Viral and Emergent Pathogens Control and Research (IVEPCR) at the Irrua Specialist Teaching Hospital (ISTH) embarked on bioinformatics and sequencing activities in April 2022. This initiative was made possible through the support of esteemed collaborators including the Bernhard Nocht Institute for Tropical Medicine (BNITM) in Hamburg, Germany; the Evolutionary and Computational Virology (ECV) group at the Catholic University of Leuven (KU Leuven) in Belgium; and the Laboratoire des Fièvres Hémorragiques Virales de Guinée (LFHVG) in Guinea. Together, we successfully established a state-of-the-art SARS-CoV-2 sequencing laboratory.

To enhance the sequencing capabilities at ISTH, six scientific staff members underwent comprehensive training in metagenomic sequencing throughout 2023. This training encompassed theoretical knowledge, practical benchwork, and bioinformatic analysis. Additionally, our staff participated in two intensive workshops at LFHVG in Conakry, Guinea. During the pre-implementation phase, we retrospectively sequenced four Lassa virus (LASV) positive samples collected between February and September 2022 from Edo and Kogi States, Nigeria. The genomic recovery of LASV ranged from 99.3% to 99.8% of the full genome. Phylogenetic analyses confirmed that these sequences belonged to lineage II of the Lassa virus, which is endemic to Nigeria, and indicated four independent virus transmission events.

To date, we have sequenced over 100 samples of the Lassa virus. The processing time for four samples, including laboratory procedures and data analysis, is approximately 10 to 14 days. The detected lineages have consistently remained II and IV, which aligns with the commonly reported lineages in Nigeria and the broader West African subregion.

For SARS-CoV-2, we have sequenced approximately 418 samples. The sequencing process for 20 samples, from laboratory work to data analysis, also takes about 10 to 14 days. Furthermore, we are expanding our sequencing efforts to include Monkeypox and other emerging viruses.

All our sequences have been submitted to the Global Initiative on Sharing All Influenza Data (GISAID). We are also planning to submit LASV sequences derived from metagenomic studies to GenBank.

Despite our advancements, we face significant challenges including inconsistent power supply, inadequate funding, and a need for more sophisticated equipment. The establishment of a dedicated computational biology laboratory is critical for overcoming these obstacles and further advancing our research capabilities.

We remain committed to enhancing our sequencing infrastructure and capabilities, thereby contributing to the global understanding and control of viral pathogens.

Prof. Reuben Eifediyi,
Chief Medical Director of ISTH Irrua Specialist Teaching Hospital (ISTH), Irrua, Edo State, Nigeria

INTRODUCTION

I am pleased to submit a report on the genomic sequencing activities at the Institute of Viral and Emergent Pathogens, Control and Research (IVEPCR), located within the Irrua Specialist Teaching Hospital (ISTH) in Edo State, Nigeria. Despite our journey beginning only two years ago, we have made remarkable strides in advancing our capabilities and understanding of viral pathogens.

This report coincides with the Nigeria Centre for Disease Control and Prevention's National Retreat aimed at developing a comprehensive National Genomic Surveillance Strategy. This strategy is pivotal for shaping an effective response to the dynamic landscape of infectious diseases in Nigeria. Furthermore, genomic surveillance is a key priority of the World Health Assembly. The launch of the World Health Organization's (WHO) "Global Genomic Surveillance Strategy" in April has set the framework to strengthen such capacities globally. In the field of viral infectious diseases, genomic surveillance offers a unique opportunity to timely identify, track, monitor, and characterize viral pathogens to improve public health decisions.

While efforts have been made during the COVID-19 pandemic to establish SARS-CoV-2-specific sequencing capacities in Africa, expanding these capabilities to encompass a broad range of other life-threatening viral pathogens is fundamental for preparedness and mitigation of infectious disease threats.

ISTH plays a crucial role in the containment and management of infectious diseases in Nigeria. The Institute of Viral and Emergent Pathogens, Control, and Research (IVEPCR), formerly known as the Institute of Lassa Fever Research and Control, has evolved to become a National Reference Centre for laboratory diagnosis, surveillance, case management, research, and capacity building. Our scope includes Lassa fever and other viral and emergent pathogens such as COVID-19, yellow fever, monkeypox, and Ebola. Integrating genomic surveillance into our hospital workflow will significantly enhance our ability to respond to infectious disease outbreaks with greater precision and efficacy.

Over the past two years, we have achieved significant breakthroughs in genomic sequencing, particularly for Lassa fever and COVID-19. These advancements have provided invaluable insights and expanded the knowledge base for viral diagnostics in Nigeria. Our efforts have not only improved local capabilities but also contributed to the global understanding of these pathogens.

I would like to express my deep appreciation for the unwavering support from our collaborators. The Bernhard Nocht Institute for Tropical Medicine has been instrumental in building the necessary human capacity and technological infrastructure within our institution. It is heartwarming to see our technical staff effectively utilizing this technology within our molecular laboratory network.

Additionally, I am grateful to the Federal Ministry of Health and the Nigeria Centre for Disease Control and Prevention for their support and the robust framework they provided. Their contributions have been crucial in achieving the milestones outlined in this report.

As we continue to enhance our genomic sequencing infrastructure and capabilities, we remain committed to advancing the field of viral pathogen research and contributing to the global efforts in disease control and prevention. Thank you for your attention to this report.

Dr. Joseph Okoeguale
Director of the Institute of Viral and Emergent Pathogens Control and Research (IVEPCR)

OFFICIAL REPORT N°01

IMPLEMENTATION of a SARS-CoV-2 SEQUENCING FACILITY AT ISTH: RELEASE of SARS-CoV-2 SEQUENCING RESULTS

Date: 22 APRIL 2022

SUMMARY

- Implementation of a SARS-CoV-2 sequencing laboratory at ISTH which is operational as of 21 April 2022 (Figure 1).
- During the pre-implementation phase, 20 SARS-CoV-2-positive samples collected between 27 December 2021 and 02 March 2022 have been sequenced (retrospective sequencing of samples, Table 1) and the results are shared in this report.
- SARS-CoV-2 genomic recovery ranged from 94.7 % to 99.3% of the full genome.
- Presence of the VOC 21K variant (Omicron or BA.1 or B.1.1.529) in the 20 samples
- collected:
    - Note that samples classify as sub-variants of Omicron (Table 1 and Figure 2).
- Sequences are planned to be soon submitted to GISAID (https://www.gisaid.org/)
- This new laboratory will be dedicated to monitor SARS-CoV-2 variant's circulation for the benefit of Nigeria.

BACKGROUND

- Sequencing results originate from a joint project between the following partner institutions and translated into support for COVID-19, namely:
    - Irrua specialist Teaching Hospital (ISTH), Institute for Lassa Fever Research and Control (ILFRC), Irrua, Edo State, Nigeria;
    - The Bernhard-Nocht Institute for Tropical Medicine (BNITM), Hamburg, Germany;
- The German Ministry of Health finances the development and implementation of SARS-CoV-2 real-time field sequencing at ISTH in the framework of the Global Health Protection Program (GHPP-CoronaGlobal).
- As part of this program, several trainings of laboratory staff have been ongoing since
- November 2021 to allow for this successful implementation and independent management.
- Sequencing (MinION technology, Oxford Nanopore), bioinformatic analyses, and production of consensus sequences are independently performed by ISTH-laboratory trained staff (Figure 1).

RESULTS

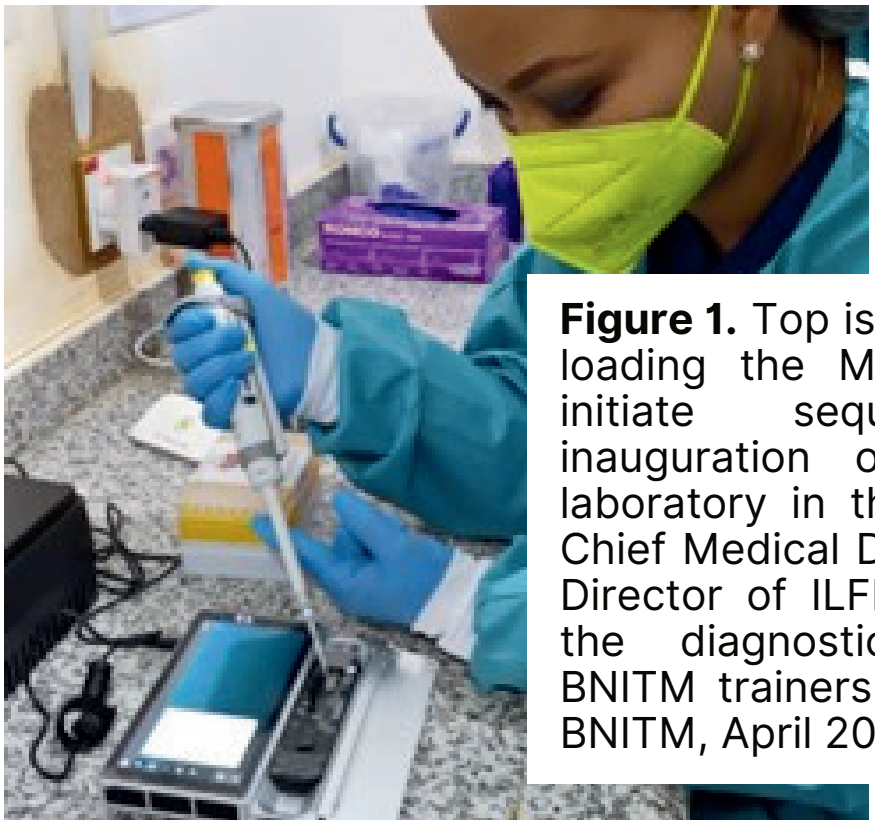


Figure 1. Top is the laboratory staff loading the MinION flow cell to initiate sequencing; Bottom inauguration of the sequencing laboratory in the presence of the Chief Medical Director of ISTH, the Director of ILFRC, the Director of the diagnostic laboratory and BNITM trainers. Copyright: ISTH & BNITM, April 2022.

ISTH-BNITM Clinical-Laboratory Research Review workshop 2022

ISTH GENOMIC PROJECT LEADS

- Prof R. A Eifediyi
- Prof S. A Okogbenin
- Dr Joseph Okoeguale
- Dr. Cyril Erameh
- Dr. Ehizojie Emua,
- Mrs. Rachael Omiunu,

TECHNICAL LEADS FROM BNITM

- Dr. Sophie Duraffour
- Dr. Giuditta Annibaldis

Table 1. Results of the 20 SARS-CoV-2 samples analyzed and collected between 27 December 2021 and 02 March 2022. The sequences denoting sub-variants of Omicron are highlighted in various colors. All samples have been de-identified to protect patient confidentiality.

Nº	Sequencing identifier	Ct value (*cycle threshold*)	% consensus recovery*	Clade Nextstrain **	Pango lineage ***	WHO Label (VOC, VUI, or variant under monitoring)****
1	E0025	17.0	95.7%	21K (Omicron)	BA.1	VOC
2	E0026	19.5	99.1%	21K (Omicron)	BA.1.1	VOC
3	E0027	19.8	99.1%	21K (Omicron)	BA.1.1	VOC
4	E0028	18.5	99.3%	21K (Omicron)	BA.1.1	VOC
5	E0029	21.0	99.1%	21K (Omicron)	BA.1.1	VOC
6	E0030	18.8	99.3%	21K (Omicron)	BA.1.14	VOC
7	E0031	16.3	99.1%	21K (Omicron)	BA.1.1.14	VOC
8	E0033	17.0	99.3%	21K (Omicron)	BA.1.15	VOC
9	E0034	18.5	99.3%	21K (Omicron)	BA.1.1	VOC
10	E0035	18.9	94.7%	21K (Omicron)	BA.1.15	VOC
11	E0036	19.7	99.3%	21K (Omicron)	BA.1.1	VOC
12	E0037	19.3	97.3%	21K (Omicron)	BA.1.15	VOC
13	E0038	24.5	99.3%	21K (Omicron)	BA.1.1	VOC
14	E0039	24.9	99.3%	21K (Omicron)	BA.1.1	VOC
15	E0041	23.5	96.0%	21K (Omicron)	BA.1.15	VOC
16	E0042	24.1	96.0%	21K (Omicron)	BA.1.15	VOC
17	E0043	25.4	98.4%	21K (Omicron)	BA.1.1	VOC
18	E0044	22.4	97.5%	21K (Omicron)	BA.1.15	VOC
19	E0045	23.4	95.8%	21K (Omicron)	BA.1.15	VOC
20	E0046	21.1	98.7%	21K (Omicron)	BA.1.1	VOC

*The reference sequence used is "Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, completegenome" with accession number MN908947.3.
** Clade assignment was done using Nextstrain (https://clades.nextstrain.org/)

For another visualization of the results, the samples are shown in Figure 2 A-B. The 20 sequenced samples that match the 21K Omicron variant are all on the 21K Omicron clade (BA.1. or B.1.1.529 like), represented in orange on the phylogenetic tree, according to Nextclade and Pangolin.Sub-variants of the 21K are also shown (BA.1.1, BA.1.1.15, BA.1.14 and BA.1.1.14, Table 1).

Figure 2A.

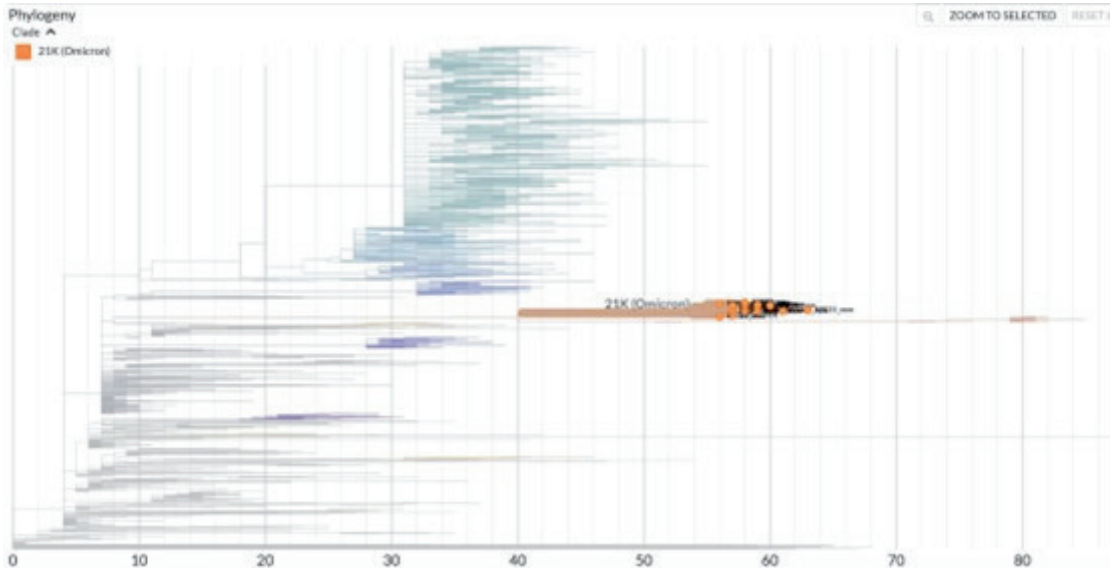


Figure 2B.

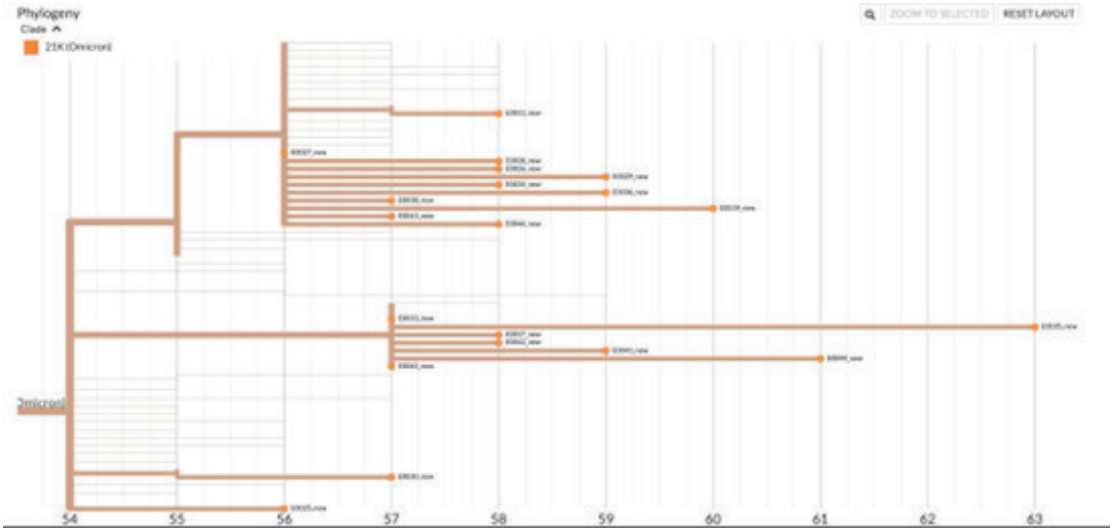


Figure 2: **Phylogenetic tree of the SARS-CoV-2 samples sequenced here. (A) Overall phylogenetic tree with all lineages. (B) Zoom on the Omicron clade with all samples sequenced here.** Phylogeny obtained via https://clades.nextstrain.org/; A dynamic nomenclature proposal for SARS-CoV-2 lineagesto assist genomicepidemiology, Rambaut A, Holmes EC, O'Toole Á, Hill V, McCrone JT, Ruis C, du Plessis L &Pybus OG (2020) Nature Microbiology DOI:10.1038/s41564-020-0770-5.

Report done at ISTH, Irrua, on 22 April 2022

Dr. Cyril Erameh, Director of ILFRC

Prof. Sylvanus Okogbenin, Chief Medical Directorof ISTH

OFFICIAL REPORT N°02

IMPLEMENTATION of a SARS-CoV-2 SEQUENCING FACILITY at ISTH: RELEASE of SARS-CoV-2 SEQUENCING RESULTS

Date: 14 JUNE 2022

SUMMARY

- 23 SARS-CoV-2-positive samples collected between 22 December 2021 and 09
- January 2022 have been sequenced (retrospective sequencing of samples, Table 1) and the results are shared in this report.
- SARS-CoV-2 genomic recovery ranged from 94.5 % to 99.3% of the full genome.
- Presence of the VOC 21K variant (Omicron or BA.1 or B.1.1.529) in the 23 samples collected:
  - Note that samples classify as sub-variants of Omicron (Table 1 and Figure 2).
- Sequences are planned to be soon submitted to GISAID (https://www.gisaid.org/)

BACKGROUND

- Sequencing results originate from a joint project between the following partner institutions and translated into support for COVID-19, namely:
  - Irrua specialist Teaching Hospital (ISTH), Institute for Lassa Fever Research and Control (ILFRC), Irrua, Edo State, Nigeria;
  - The Bernhard-Nocht Institute for Tropical Medicine (BNITM), Hamburg, Germany;
- The German Ministry of Health finances the development and implementation of SARS-CoV-2 real-time field sequencing at ISTH in the framework of the Global Health Protection Program (GHPP-CoronaGlobal).
- As part of this program, several trainings of laboratory staff have been ongoing since November 2021 to allow for this successful implementation and independent management.
- Sequencing MinION technology, Oxford Nanopore), bioinformatic analyses, and production of consensus sequences are independently performed by ISTH-laboratory trained staff.

RESULTS

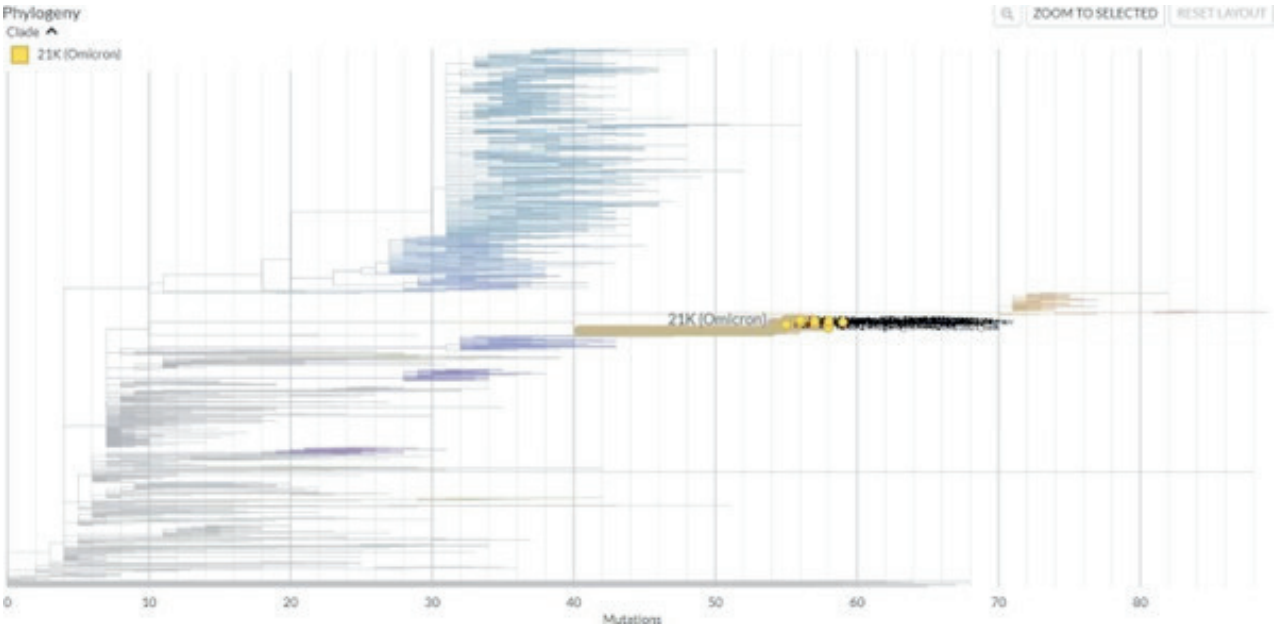
Table 1. Results of the 23 SARS-CoV-2 samples collected between 24 December 2021 and 09 January 2022. The sequences denoting sub-variants of Omicron are highlighted in various colors. All samples have been de-identified to protect patient confidentiality.

N°	Sequencing identifier	Ct value (*cycle* threshold)	% consensus recovery *	Clade Nextstrain **	Pango lineage ***	WHO Label (VOC, VUI, or variant under monitoring) ****
1	E0147	23.4	99,4	21K (Omicron)	BA.1.1	VOC
2	E0148	20.2	99,4	21K (Omicron)	BA.1.1	VOC
3	E0149	17.0	99,4	21K (Omicron)	BA.1.1	VOC
4	E0150	21.9	99,4	21K (Omicron)	BA.1.1	VOC
5	E0151	18.9	99,4	21K (Omicron)	BA.1.15	VOC
6	E0152	20.4	99,4	21K (Omicron)	BA.1.1	VOC
7	E0153	20.8	99,4	21K (Omicron)	BA.1.15	VOC
8	E0154	20.8	99,4	21K (Omicron)	BA.1.1	VOC
9	E0156	19.4	99,4	21K (Omicron)	BA.1.1	VOC
10	E0157	20.1	99,4	21K (Omicron)	BA.1.1	VOC
11	E0158	22.3	99,2	21K (Omicron)	BA.1.17	VOC
	E0160	17.4	99,4	21K (Omicron)	BA.1.1	VOC
13	E0162	22.6	99,4	21K (Omicron)	BA.1.1	VOC
14	E0164	17.8	99,4	21K (Omicron)	BA.1.1	VOC
15	E0166	22.8	99,4	21K (Omicron)	BA.1.1	VOC

*The reference sequence used is "Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, completegenome" with accession number MN908947.3.
** Clade assignment was done using Nextstrain (https://clades.nextstrain.org/)
*** Pangolin COVID-19 LineageAssigner for the Phylogenetic Assignment of Named Global Outbreak LINeages is used (https://pangolin.cog-uk.io/).
****The genomicdefinition of variantsunder investigation (VUI) or variantsof interest (VOC) is based on PHE technical reports and analysis tools automatically assigns these genomic definitions to the obtained sequences.

For another visualization of the results, the samples are shown in **Figure 1 A-B.** The 20 sequenced samples that match the 21K Omicron variant are all on the 21K Omicron clade (BA.1. or B.1.1.529 like), represented in orange on the phylogenetic tree, according to Nextclade and Pangolin. Sub-variants of the 21K are also shown **(BA.1.1, BA.1.1.15 and BA.1.1.17, Table 1).**

Figure 1A.



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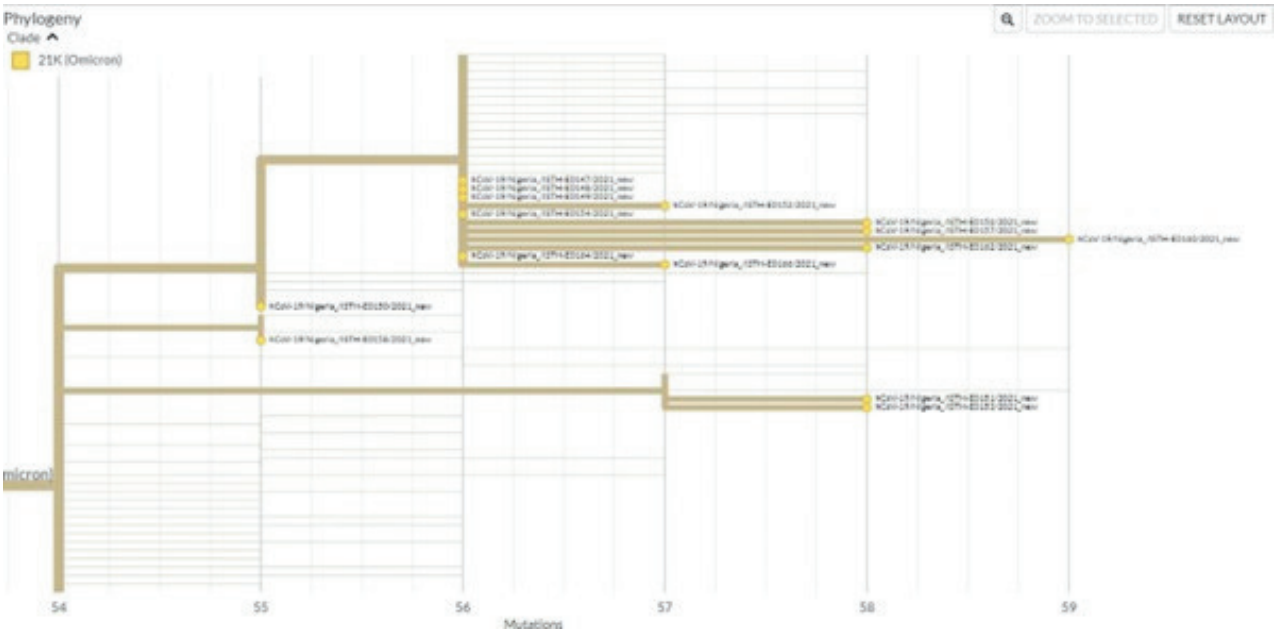

Figure 1: Phylogenetic tree of the SARS-CoV-2 samples sequenced here. (A) Overall phylogenetic tree with all lineages. (B) Zoom on the Omicron clade with all samples sequenced here. Phylogeny obtained via https://clades.nextstrain.org/; A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology, Rambaut A, Holmes EC, O'Toole Á, Hill V, McCrone JT, Ruis C, du Plessis L &Pybus OG (2020) Nature Microbiology DOI:10.1038/s41564-020-0770-5

TECHNICAL POINT AND PARTNERS

The MinION technology (Oxford Nanopore) is used for this program. A direct coronavirus amplification approach is performed following the ONT Midnight protocol in combination with the analysis shared by epi2me/wf-artic. The work presented in this report comes from a collaborative project of ISTH and BNITM in the coronavirus response

Report done at ISTH, Irrua, on 14 June 2022

Dr. Cyril Erameh, Director of ILFRC

Prof. Sylvanus Okogbenin, Chief Medical Directorof ISTH

OFFICIAL REPORT N°03

SARS-CoV-2 SEQUENCING FACILITY at ISTH: RELEASE of SARS-CoV-2 SEQUENCING RESULTS

Date: 30 June 2022

SUMMARY

- Retrospective sequencing of 15 SARS-CoV-2-positive samples collected between 8 and 13 December 2021 (Table 1) and the results are shared in this report.
- SARS-CoV-2 genomic recovery ranged from 99.2 % to 99.4% of the full genome.
- Presence of the VOC 21K variant (Omicron or BA.1 or B.1.1.529) in the 15 samples: o Note that samples classify as sub-variants of Omicron (Table 1 and Figure 1).
- Sequences have been submitted to GISAID (https://www.gisaid.org/)
- Since its opening, the ISTH sequencing laboratory reported a total of 58 SARS-CoV-2 sequences on GISAID

BACKGROUND

- Sequencing results originate from a joint project between the following partner institutions and translated into support for COVID-19, namely: o Irrua specialist Teaching Hospital (ISTH), Institute for Lassa Fever Research and Control (ILFRC), Irrua, Edo State, Nigeria; o The Bernhard-Nocht Institute for Tropical Medicine (BNITM), Hamburg, Germany;
- The German Ministry of Health finances the development and implementation of SARS-CoV-2 real-time field sequencing at ISTH in the framework of the Global Health Protection Program (GHPP-CoronaGlobal).
- As part of this program, several trainings of laboratory staff have been ongoing since November 2021 to allow for this successful implementation and independent management.
- Sequencing (MinION technology, Oxford Nanopore), bioinformatic analyses, and production of consensus sequences are independently performed by ISTH-laboratory trained staff.

RESULTS

Table 1. Results of the 15 SARS-CoV-2 samples analyzed and collected between 8 and 13 December 2021. The sequences denoting sub-variants of Omicron are highlighted in various colors. All samples have been de-identified to protect patient confidentiality Results

N°	Sequencing identifier	Ct value (*cycle* threshold)	% consensus recovery *	Clade Nextstrain **	Pango lineage ***	WHO Label (VOC, VUI, or variant under monitoring) ****
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*The reference sequence used is "Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, completegenome" with accession number MN908947.3.
** Clade assignment was done using Nextstrain (https://clades.nextstrain.org/)
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Figure 1A.

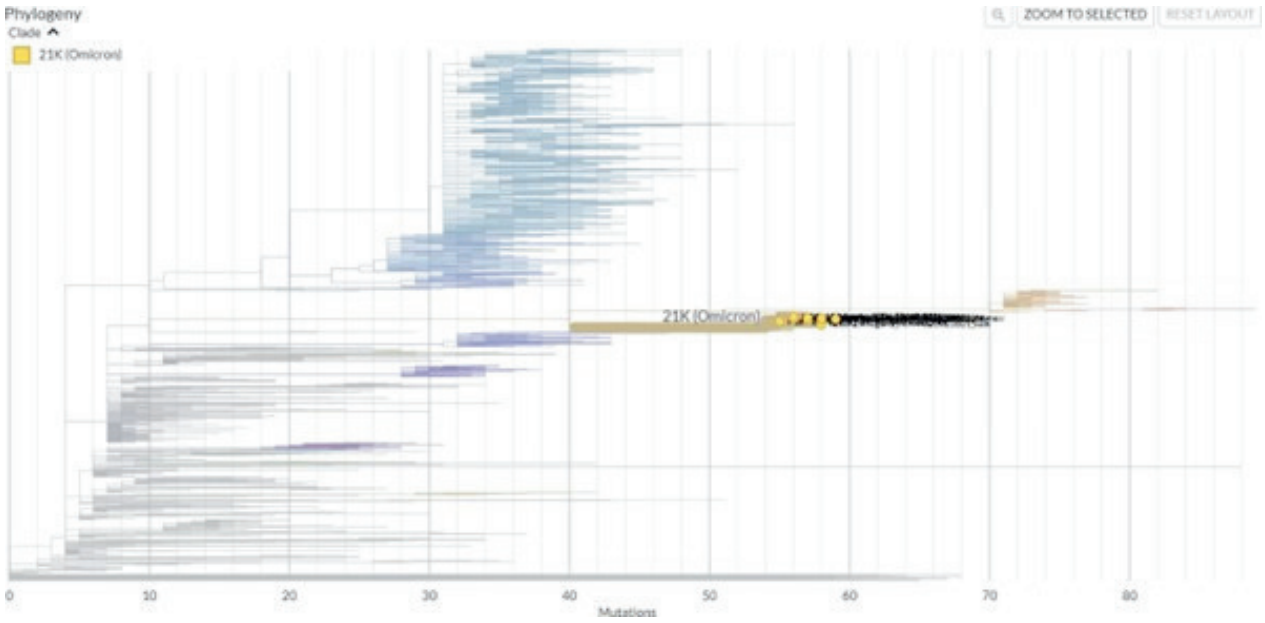


Figure 1B.

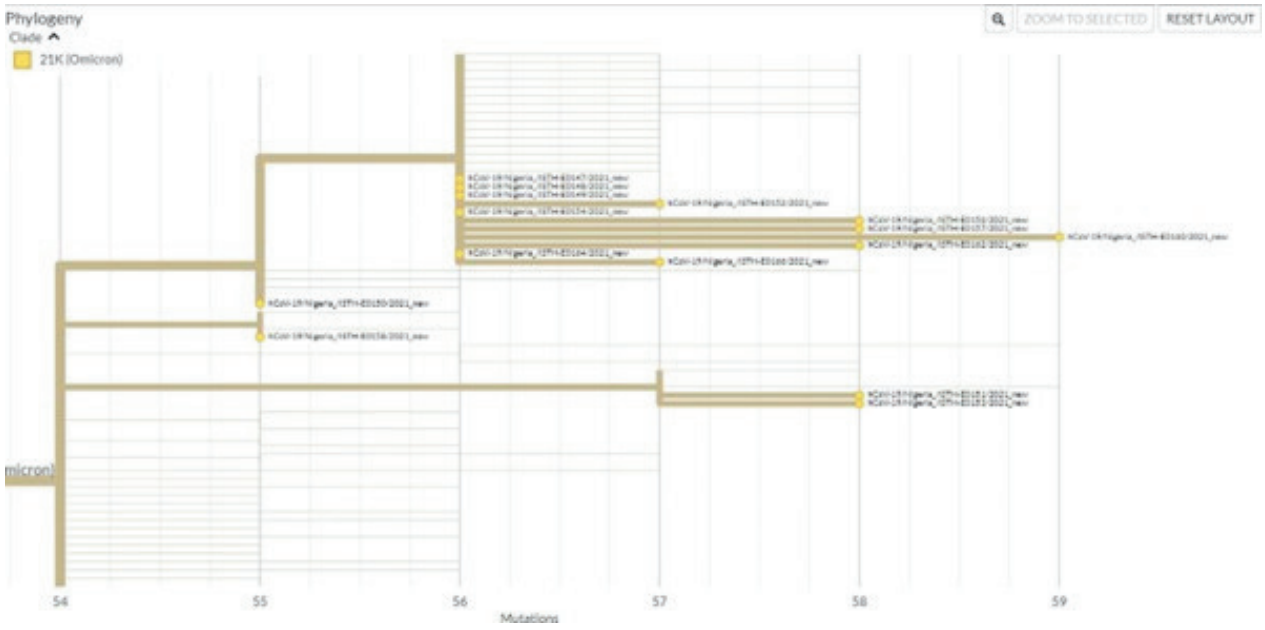


Figure 1: Phylogenetic tree of the SARS-CoV-2 samples sequenced here. (A) Overall phylogenetic tree with all lineages. (B) Zoom on the Omicron clade with all samples sequenced here. Phylogeny obtained via https://clades.nextstrain.org/; A dynamic nomenclature proposalfor SARS-CoV-2 lineagesto assist genomicepidemiology, Rambaut A, Holmes EC, O'Toole Á, Hill V, McCrone JT, Ruis C, du Plessis L &Pybus OG (2020) Nature Microbiology DOI:10.1038/s41564-020-0770-5.

TECHNICAL POINT AND PARTNERS

The MinION technology (Oxford Nanopore) is used for this program. A direct coronavirus amplification approach is performed following the ONT Midnight protocolin combination with the analysis shared by epi2me/wf-artic. The work presented in this report comes from a collaborative project of ISTH and BNITM in the coronavirus response.

Report done at ISTH, Irrua, on 30 June 2022

Dr. Cyril Erameh, Director of ILFRC

Prof. Sylvanus Okogbenin, Chief Medical Directorof ISTH

OFFICIAL REPORT N°04

ISTH sequencing facility
SARS-CoV-2 sequencing results: detection of Omicron BQ.1.12 variant

Date: 3 December 2022

SUMMARY

- Retrospective sequencing of 60 SARS-CoV-2-positive samples collected between 27 June and 26 September 2022 (Table 1)
- SARS-CoV-2 genomic recovery ranged from 93.5 % to 99.3% of the full genome.
- Presence of the variants of concern (VOC) 22A, 22B and 22E variants in the 60 samples
  Table 1 and Figure 1):
  - Sequences classify as sub-variants of Omicron
  - Finding of relevance: identification of 6 variants BQ.1.12 from samples collected between 20 and 23 August 2022 and of another 3 variants BQ.1.12 from samples collected between 05 and 24 September 2022, all with full genome recovery ranging from 95.9% to 99.2%. The variant BQ.1.12 derives from the parent lineage Omicron 22E which is also known as BQ.1. As of today 3 December 2022, the earliest reported date of BQ.1.12 detection in worldwide repository is 29 August 2022 and this variant has not yet been reported to circulate in Africa (attention: see note 1 below) whereas it has been in Europe, Asia, North and South America, and Oceania (Figure 2). Our finding indicates that BQ.1.12 was circulating in Nigeria on 20 August 2022 which is earlier than the current earliest reported date for this variant.
- Refer to the following links enabling the monitoring of variant detection and circulation worldwide:
  - https://cov-lineages.org/lineage.html?lineage=BQ.1.12 (accessed 3 December 2022)
  - https://outbreak.info/situation-reports?xmin=2022-06-03&xmax=2022-12-03&pango=BQ.1.12 (accessed 3 December 2022)
  - Attention and important not about bias: there may be a bias linked to the prevalence data presented in online reports: “SARS-CoV-2 (hCoV-19) sequencing is not a random sample of mutations. As a result, this report does not indicate the true prevalence of the undefined but rather our best estimate now”, for more information see https://outbreak.info/situation-reports/caveats
- Note 1: the E-clinic & Diagnostics Laboratory, National Reference Laboratory, Nigeria Centre for Disease Control, Gaduwa, Abuja, Nigeria has also reported the likely detection of BQ.1.12 from a sample collected on 04 August 2022 (hCoV-19/Nigeria/NCDC-NR-GL-006458/2022 or EPI_ISL_15544317.pdf) but due to low sequence coverage (stretch of NNNs representing 20.57% of overall sequence) it has not considered/included in official database/worldwide analysis.

- All sequences have been uploaded to GISAID (https://www.gisaid.org/)
- Since its opening in April 2022, the ISTH sequencing laboratory intensively participate to Nigeria and worldwide monitoring of variants and has reported 200 SARS-CoV-2 sequences which have all been deposited on GISAID.

RESULTS

Table 1. Results of the 60 SARS-CoV-2 samples analyzed and collected between 27 June and 26 September 2022. The sequences denoting different clades of Omicron are highlighted in various colors (blue indicates BQ.1.12). All samples have been de-identified to protect patient confidentiality.

N°	Sequencing identifier	Ct value (*cycle* threshold)	% consensus recovery*	Clade Nextstrain**	Pango lineage ***	Label (VOC, VUI, or variant under monitoring) ****
1	E0289	20.7	98.9	22B (Omicron)	BE.1.1.1	VOC
2	E0290	23.5	99.0	22B (Omicron)	BA.5	VOC
3	E0291	23.1	97.1	22B (Omicron)	BE.1.1	VOC
4	E0292	20.5	98.9	22B (Omicron)	BE.1.1	VOC
5	E0293	23.7	98.9	22B (Omicron)	BE.1.1.1	VOC
6	E0294	21.6	97.4	22B (Omicron)	BE.1.1.1	VOC
7	E0295	20.7	98.9	22A (Omicron)	BA.4.1	VOC
8	E0297	20.4	98.6	22B (Omicron)	BE.1.1.1	VOC
9	E0298	26.1	95.7	22B (Omicron)	BE.1.1	VOC
10	E0299	24.6	97.9	22B (Omicron)	BE.1.1.1	VOC
11	E0300	22.5	97.9	22B (Omicron)	BE.1.1.1	VOC
12	E0301	22.2	98.3	22B (Omicron)	BE.1.1.1	VOC
13	E0302	23.2	97.4	22B (Omicron)	BE.1.1.1	VOC
14	E0303	21.2	98.8	22B (Omicron)	BE.1.1	VOC
15	E0304	22.2	97.1	22B (Omicron)	BE.1.1.1	VOC
16	E0305	22.9	97.4	22B (Omicron)	BA.5	VOC
17	E0306	20.3	97.7	22B (Omicron)	BE.1.1	VOC
18	E0307	20.8	98.5	22B (Omicron)	BE.1.1.1	VOC
20	E0309	21.7	96.9	22B (Omicron)	BE.1.1.1	VOC
21	E0310	22.3	95.7	22B (Omicron)	BE.1.1.1	VOC
22	E0355	24.3	96.6	22B (Omicron)	BE.1.1.1	VOC
23	E0356	20.06	97.9	22B (Omicron)	BE.1.1.1	VOC
24	E0361	22.46	93.5	22B (Omicron)	BE.1.1.1	VOC
25	E0362	23.58	95.6	22B (Omicron)	BE.1.1.1	VOC
26	E0363	20.44	97.2	22E (Omicron)	BQ.1.12	VOC
27	E0364	24.28	95.6	22E (Omicron)	BQ.1	VOC
28	E0365	22.26	95.6	22E (Omicron)	BQ.1	VOC
29	E0366	21.06	95.9	22E (Omicron)	BQ.1.12	VOC
30	E0367	24.22	96.9	22E (Omicron)	BQ.1.12	VOC
31	E0368	21.63	95.6	22B (Omicron)	BE.1.1.1	VOC
32	E0369	22.38	94.6	22B (Omicron)	BE.1.1.1	VOC
33	E0370	24	95.6	22B (Omicron)	BE.1.1	VOC
34	E0371	22.77	96.3	22B (Omicron)	BE.1.1.1	VOC
35	E0372	22.97	95.6	22B (Omicron)	BE.1.1	VOC
36	E0373	23.85	95.6	22A (Omicron)	BA.4.1	VOC

Table 1 continues:

N°	Sequencing identifier	Ct value (cycle threshold)	% consensus recovery*	Clade Nextstrain**	Pango lineage ***	Label (VOC, VUI, or variant under monitoring) ****
37	E0374	19.58	97.3	22B (Omicron)	BE.1.1	VOC
38	E0375	22.56	95.6	22B (Omicron)	BE.1.1.1	VOC
39	E0376	19.05	96.6	22B (Omicron)	BE.1.1.1	VOC
40	E0377	22.65	97.3	22E (Omicron)	BQ.1	VOC
41	E0379	20.18	97.2	22E (Omicron)	BQ.1	VOC
42	E0380	20.62	98.4	22E (Omicron)	BQ.1	VOC
43	E0381	22.4	96.9	22E (Omicron)	BQ.1.3	VOC
44	E0385	25.99	97.3	22B (Omicron)	BE.1.1.1	VOC
45	E0386	24.29	99.2	22E (Omicron)	BQ.1.12	VOC
46	E0387	24.36	98.5	22B (Omicron)	BE.1.1.1	VOC
47	E0388	24.5	99.1	22B (Omicron)	BE.1.1.1	VOC
48	E0391	24.49	98.7	22E (Omicron)	BQ.1.25	VOC
49	E0392	25.75	97.5	22B (Omicron)	BE.1.1	VOC
50	E0393	27.38	95.6	22B (Omicron)	BE.1.1.1	VOC
51	E0394	26.61	98.3	22E (Omicron)	BQ.1	VOC
52	E0395	25.57	99.2	22B (Omicron)	BE.1.1	VOC
53	E0396	25.7	98.9	22E (Omicron)	BQ.1.12	VOC
52	E0395	25.57	99.2	22B (Omicron)	BE.1.1	VOC
53	E0396	25.7	98.9	22E (Omicron)	BQ.1.12	VOC
54	E0397	25	99.2	22E (Omicron)	BQ.1.12	VOC
55	E0399	25.72	99.3	22E (Omicron)	BQ.1.1	VOC
56	E0401	18.47	99.2	22B (Omicron)	BE.1.1	VOC
57	E0402	18.56	99.2	22E (Omicron)	BQ.1.12	VOC
58	E0403	17.69	99.2	22E (Omicron)	BQ.1.12	VOC
59	E0404	16.44	99.2	22E (Omicron)	BQ.1	VOC
60	E0406	18	99.2	22E (Omicron)	BQ.1.12	VOC

The reference sequenceused is "Severe acute respiratory syndromecoronavirus 2 isolateWuhan-Hu-1, complet egenome" with accession number MN908947.3. **Clade assignment was done using Nextstrain (https://clades.nextstrain.org/). * Pangolin COVID-19 Lineage Assigner for the Phylogenetic Assignment of Named Global Outbreak LINeages is used (https://pangolin.cog-uk.io/). ****The genomic definition of variants under investigation (VUI) or variants of concern (VOC) is based on PHE technical reports and analysis tools automatically assigns these genomic definitions to the obtained sequences.*

PHYLOGENY

For another visualization of the results, the samples are shown in Figure 1A-C. The 60 sequenced samples that matchthe 22A, 22B or 22E Omicron variantare represented in yellow, orangeand red on the phylogenetic tree, according to Nextclade and Pangolin.

Figure 1: Phylogenetic tree highlighting the diversity of the SARS-CoV-2 samples sequenced here. (A) Overallphylogenetic tree with all lineages. (B) Zoom on the Omicronlineage with all samples sequenced here as 22A, 22B and 22E1. (C) Focus on the 22E lineage and particularly on the BQ1.12 sequences reported in this report.

Figure 1A.

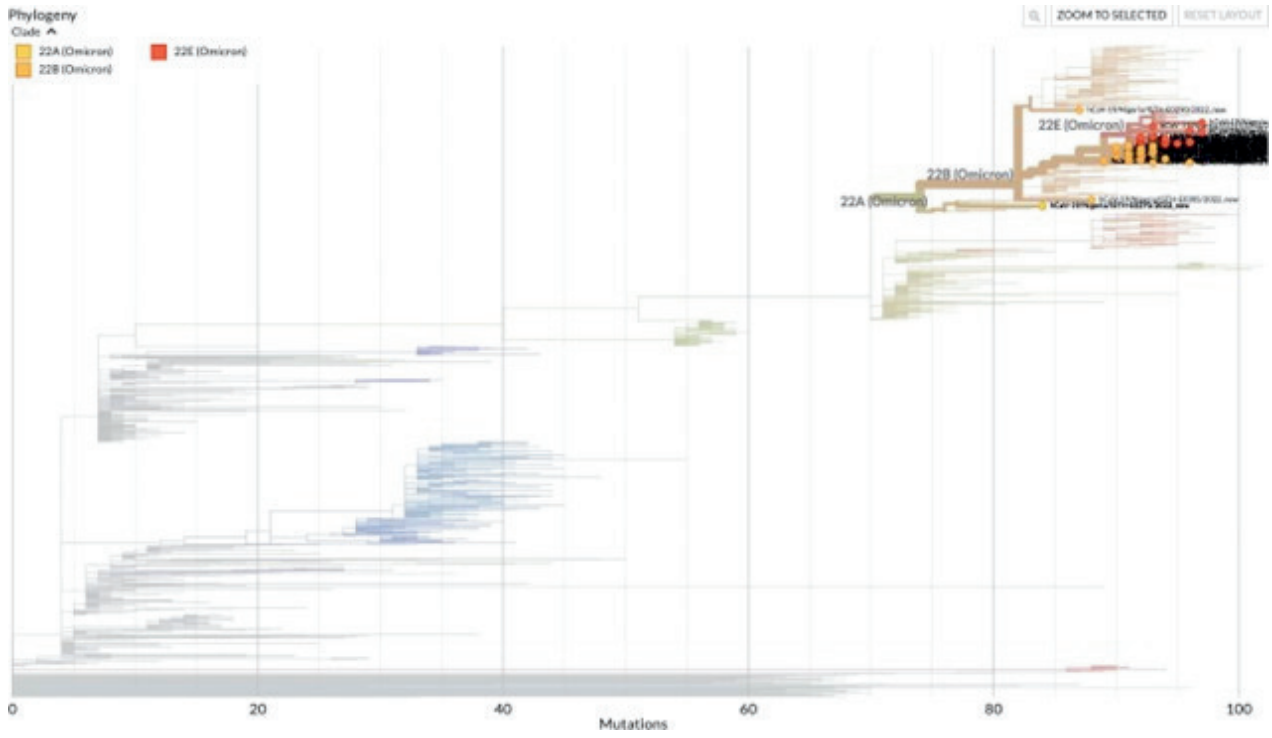


Figure1B.

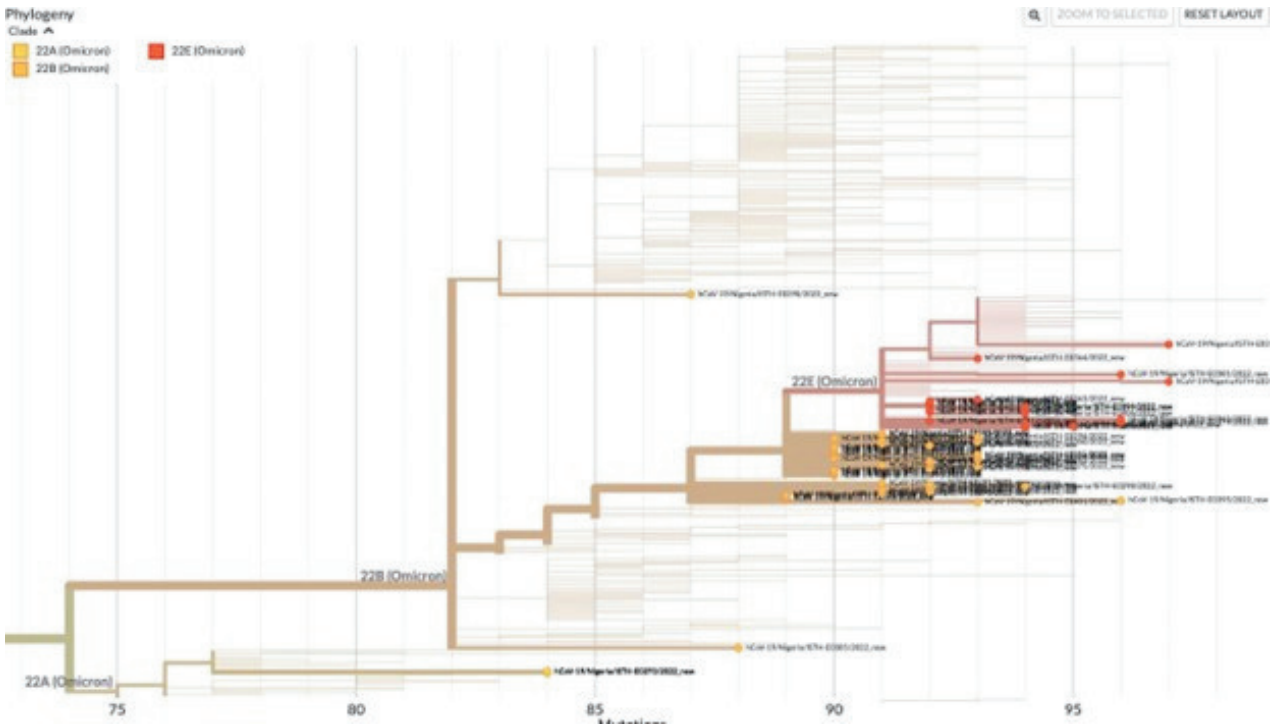


Figure 1C. The diversity of the 22E or BQ.1 lineage is shown. Red dots represent the multiple sub- lineages. At the bottom of the phylogenetic tree is seen the sub-lineage BQ.1.12 with the newly deposited sequence disclosed in this report.

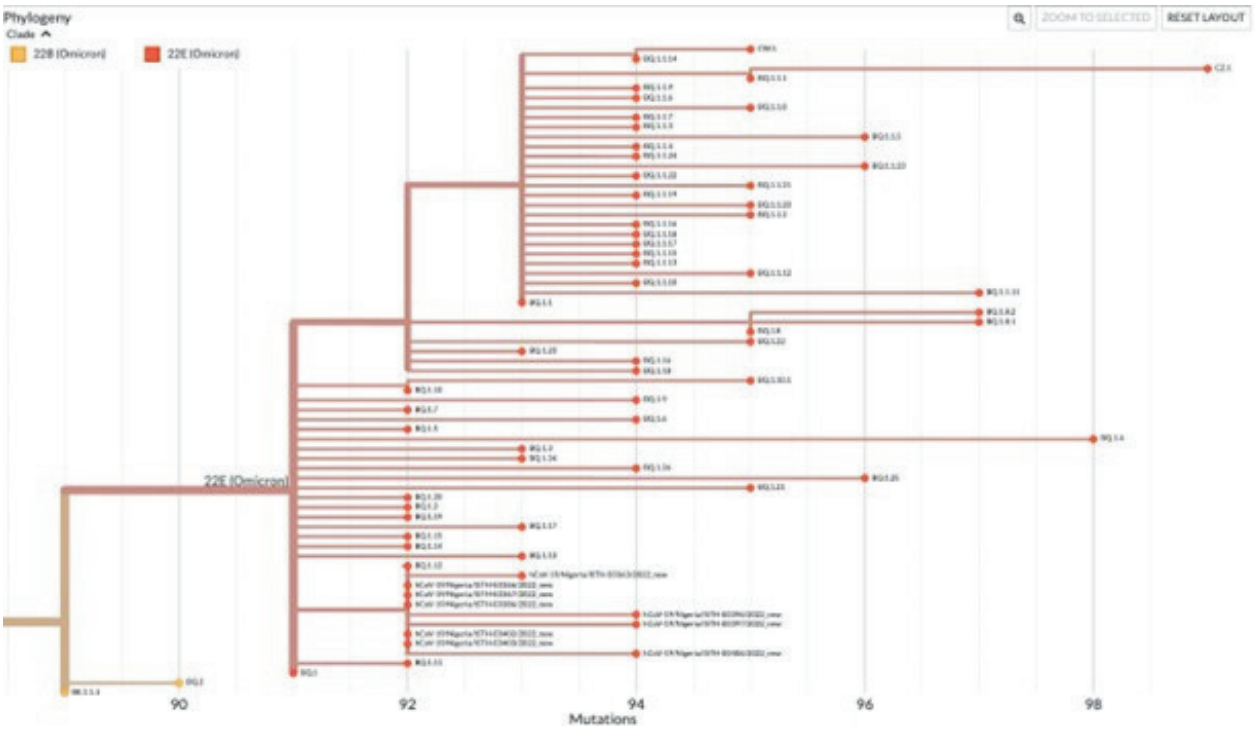
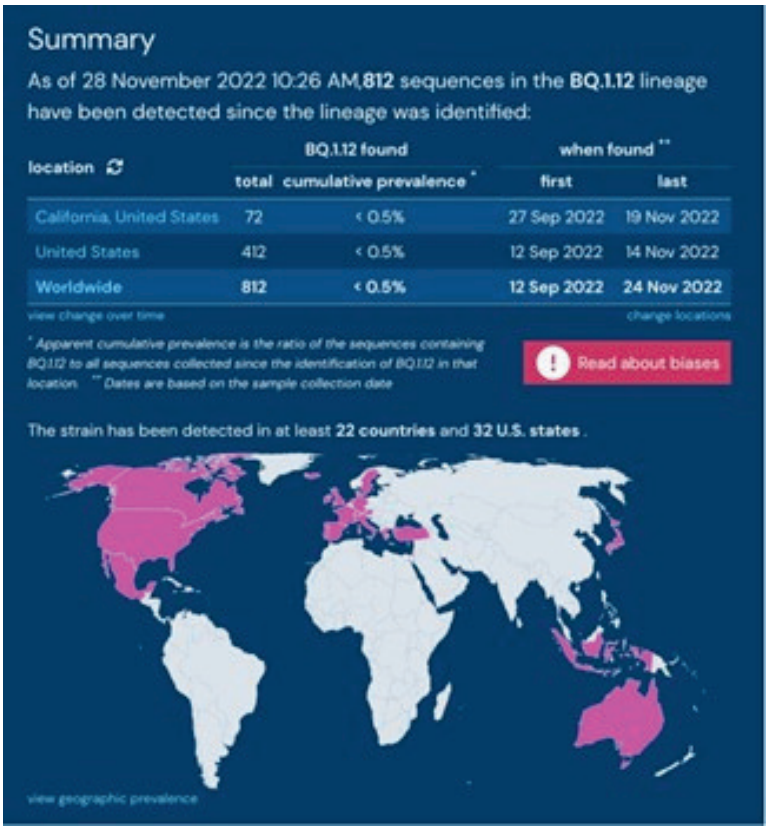


Figure 2: Summary about worldwide BQ1.12 lineage detection as of 3 December 2022 with 812 sequences reported4-6.

See https://outbreak.info/situation-reports?xmin=2022-06-03&xmax=2022-12-03&pango=BQ.1.12, accessed 3 December at 15:00 CET.



TECHNICAL POINT AND PARTNERS

- Sequencing results originate from a jointproject between the following partnerinstitutions and translated into support for COVID-19, namely the Irrua specialist Teaching Hospital (ISTH), Institute for Lassa Fever Research and Control (ILFRC), Irrua, Edo State, Nigeria & the Bernhard-Nocht Institute for Tropical Medicine (BNITM), Hamburg, Germany;
- The German Ministry of Health finances the development and implementation of field sequencing at ISTH in the framework of the Global Health Protection Program (GHPP-CoronaGlobal).
- As part of this program,several trainings of laboratory staffhave been ongoingsince November 2021 to allow for this successful implementation and independent management.
- Sequencing (MinION technology, Oxford Nanopore), bioinformatic analyses, and production of consensus sequences are independently performed by ISTH-laboratory-trained staff.

The MinION technology (Oxford Nanopore) is used for this program.A direct coronavirus amplification approach is performed following the ONT Midnight protocol in combination with the analysis shared by epi2me/wf-artic. The work presented in this report comes from a collaborative project of ISTH and BNITM in the coronavirus response.

REFERENCES

For the reportto be accessed using: https://cov-lineages.org/lineage.html?lineage=BQ.1.12 and for Nextstrain visualization (Figure 1):

1. **A dynamic nomenclature proposal for SARS-CoV-2 lineages to assistgenomic epidemiology.** Rambaut A, Holmes EC, et al (2020) Nature Microbiology DOI:10.1038/s41564-020-0770-5
2. **Tracking the international spread of SARS-CoV-2 lineages B.1.1.7 and B.1.351/501Y-V2**. O'Toole Á, Hill V, Pybus OG et al. (2021) Wellcome Open Res DOI:10.12688/wellcomeopenres.16661.1
3. **Assignment of epidemiological lineages in an emerging pandemic using the pangolin tool.** Áine O'Toole, Emily Scher, et al (2021) Virus Evolution DOI:10.1093/ve/veab064
4. For the report to be accessed using: https://outbreak.info/situation-reports?xmin=2022-06-

For the report to be accessed using: https://outbreak.info/situation-reports?xmin=2022-06-03&xmax=2022-12- 03&pango=BQ.1.12:

4. **BQ.1.12 Lineage Report.** Karthik Gangavarapu, Alaa Abdel Latif, et al (available at https://outbreak.info/situation-reports?xmin=2022-06-02&xmax=2022-12-02&pango=BQ.1.12). Accessed 3 December 2022.
5. **Outbreak.info genomic reports: scalable and dynamic surveillance of SARS-CoV-2 variants and mutations.** Karthik Gangavarapu, Alaa Abdel Latif, et al. medRxiv (2022). doi: 10.1101/2022.01.27.22269965
6. **GISAID's Role in Pandemic Response.** Khare, S., et al. (2021). China CDC Weekly,3(49): 1049-1051. doi: 10.46234/ccdcw2021.255 PMCID: 8668406

Report done at ISTH, Irrua, on 30 June 2022

Dr. Cyril Erameh, Director of ILFRC

Prof. Sylvanus Okogbenin, Chief Medical Directorof ISTH

OFFICIAL REPORT N°05

IMPLEMENTATION of a METAGENOMIC SEQUENCING CAPACITY AT IRRUA SPECIALIST TEACHING HOSPITAL (ISTH) RELEASE of LASSA VIRUS SEQUENCING RESULTS

Date: 26 July 2023

SUMMARY

- Since its implementation in April 2022, the SARS-CoV-2 sequencing laboratory at Irma Specialist Teaching Hospital (ISTH) has sequenced and deposited more than 200 SARS-CoV-2 sequences on GISAID.
- To strengthen the sequencing capacity at ISTH, six ISTH scientific staff were trained on metagenomic sequencing in the past months (theory, benchwork and bioinformatic analysis), including attendance to two workshops at the Laboratoire des Fievres Hemorragiques Virales de Guinee (LFHVG) in Conakry, Guinea (Figure 1).
- During the pre-implementation training phase, 4 Lassa virus (LASV) positive samples collected between February 2022 and September 2022 in Edo and Kogi States, Nigeria, were retrospectively sequenced at ISTH and the results are shared in this report (Table 1).
- Lassa Virus (LASV) genomic recovery ranged from 99.3 % to 99.8% of the full genome (Table 1).
- Phylogenetic analyses revealed that the 4 sequences obtained belong to lineage II of Lassa virus, which is known to circulate in Nigeria (Table 1 and Figure 2). Phylogenetic analysis also shows four independent virus transmission events.
- Planning of sequence submissions to Genebank before publication of results.
- The program to build a genomic surveillance capacity at ISTH is continuing.

BACKGROUND

- The Irrua Specialist Teaching Hospital (ISTH) is a federal government of Nigeria teaching hospital located in Irrua, Edo State, Nigeria, which includes the Institute of Viral Haemorrhagic Fevers and Emergent Pathogens (IVEP). The later diagnoses and monitors viral hemorrhagic fevers, with special reference to Lassa Fever. Since April 2022, a sequencing capacity for SARS-CoV-2 has been set-up at ISTH-IVEP. Since January 2023, the implementation of a broad genomic surveillance capacity at ISTH is currently ongoing.
- The work presented in this report originates from a collaborative project between several partner institutions: ISTH; the Bernhard-Nocht Institute for Tropical Medicine (BNITM), Hamburg, Germany; the Evolutionary and Computational Virology (ECV), Catholic University (KU Leuven), Leuven, Belgium; and the Laboratoire des Fievres Hemorragiques Virales de Guinee (LFHVG), Conakry, Guinea.
- The German Ministry of Health finances the development and implementation of a genomic surveillance capacity at ISTH in the framework of the Global Health Protection Program (GHPP-CELESTA).
- Metagenomic sequencing (MinION technology, Oxford Nanopore), bioinformatic analyses, production of consensus sequences and generation of phylogenetic trees were independently performed by ISTH-laboratory trained staff.

OVERVIEW OF TRAINING ACTIVITIES

As part of this program, two on-site trainings of laboratory staff from ISTH have taken place early 2023 in Conakry, Guinea, to allow for the successful implementation and independent management of metagenomic sequencing at ISTH **(Figure 1).**

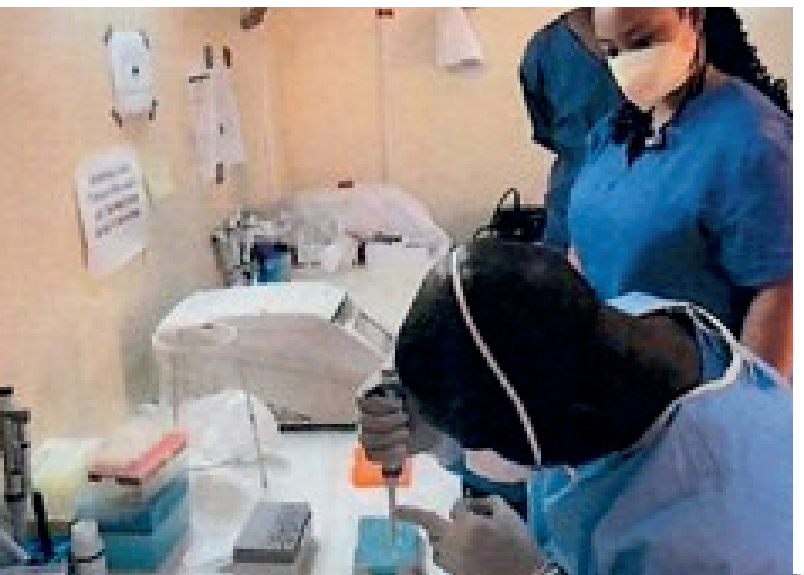


Figure 1. Top, Four ISTH sequencing lab staff with a BNITM trainer during the introductive training on phylogenetics analysis at LFHVG in Conakry, Guinea. Copyright: ISTH&BNITM. **Bottom left and right**, ISTH staff during practical hands-on sessions of metagenomic sequencing at LFHVG in Conakry, Guinea.

RESULT

- ISTH scientific staff independently sequenced and analyzed 4 Lassa virus positive samples which were collected between February and September 2022 in Edo and Kogi States, Nigeria.
- Close to full length Lassa virus genomes were recovered from each sample with a genomic recovery ranging from 99.3 to 99.8% for both segments (Table 1).
- Phylogenetic analyses (Figure 2) revealed that the 4 sequences belong to Lassa virus lineage II (Figure 2) which is a lineage known to circulate in these regions of Nigeria. The analysis further shows four independent virus transmission events.

Table 1. Results of the 4 LASV positive samples analyzed and collected between February and September 2022. All samples have been de-identified to protect patient confidentiality.

N°	*Sequencing Identifier*	*Sampling date*	*Ct Value* (Cycle Threshold)*		*%Consensus recovery*		*Location*	*Lineage***
			S	***L***	**S**	***L***		
1	E0466	25th April, 2022	26.36	28.75	99.76	99.75	**IDAH,** KOGI	II
2	E0457	22nd April, 2022	28.04	28.88	99.85	99.82	IRUEKPEN, EDO	II
3	E0460	14th February, 2022	22.63	22.78	99.29	99.73	**BENIN,** EDO	II
4	E0463	17th February, 2022	23.69	22.68	99.79	99.76	AUCH!, EDO	II

*RealStar® LASV RT-PCR kit 2.0, altona Diagnostics (Hamburg,Germany)
**Lineage assignment was made using the phylogenetic analyses presented in Fig. 2.

RESULTS

For another visualization of the results, the samples are shown in **Figure 1 A-B.** Figure 1A shows the relationship between the four L samples worked on so far and the reference sequences, while figure 1B shows the S samples. It can be seen that these samples fall into the same clades with previous samples from the same region in Edo State, Nigeria.

Figure 1A

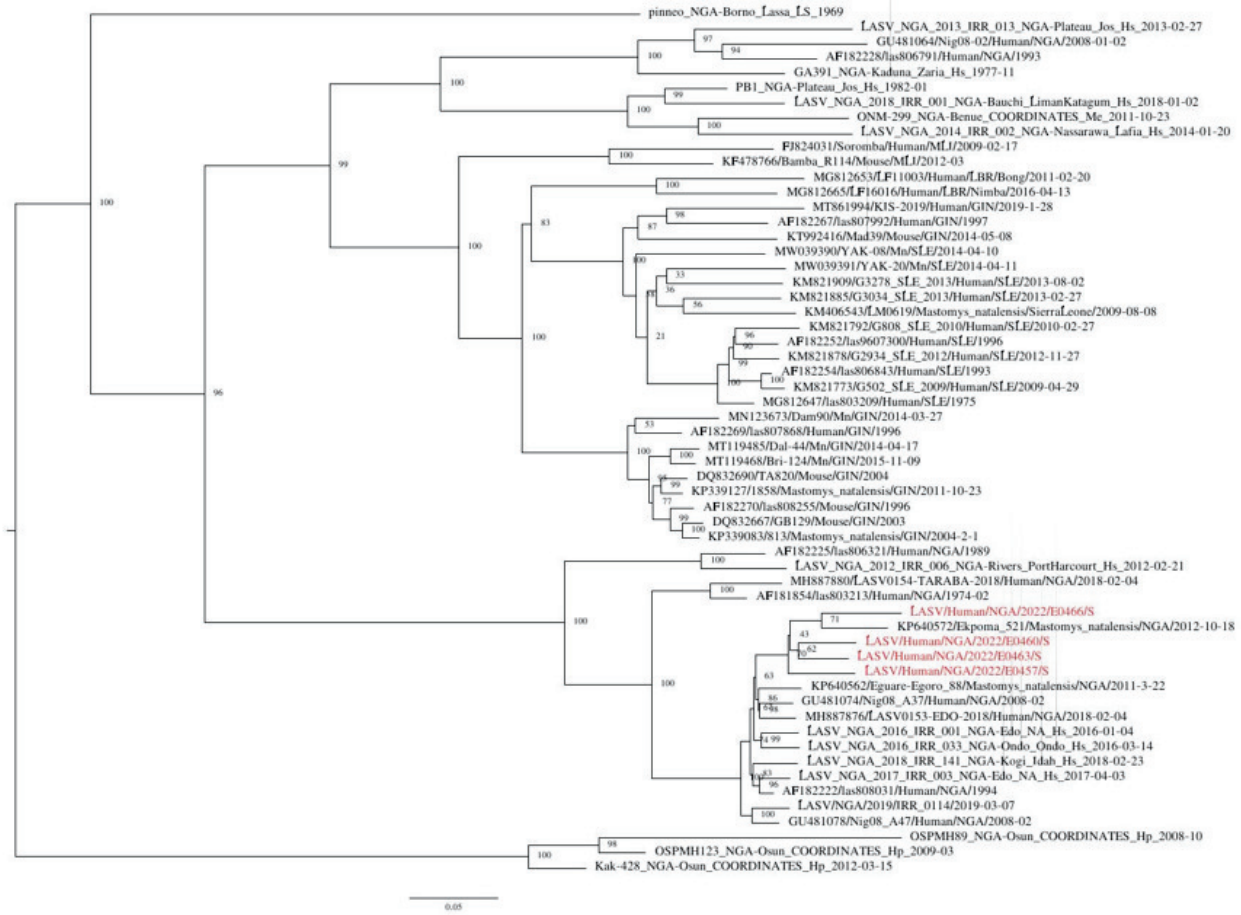


Figure 1B

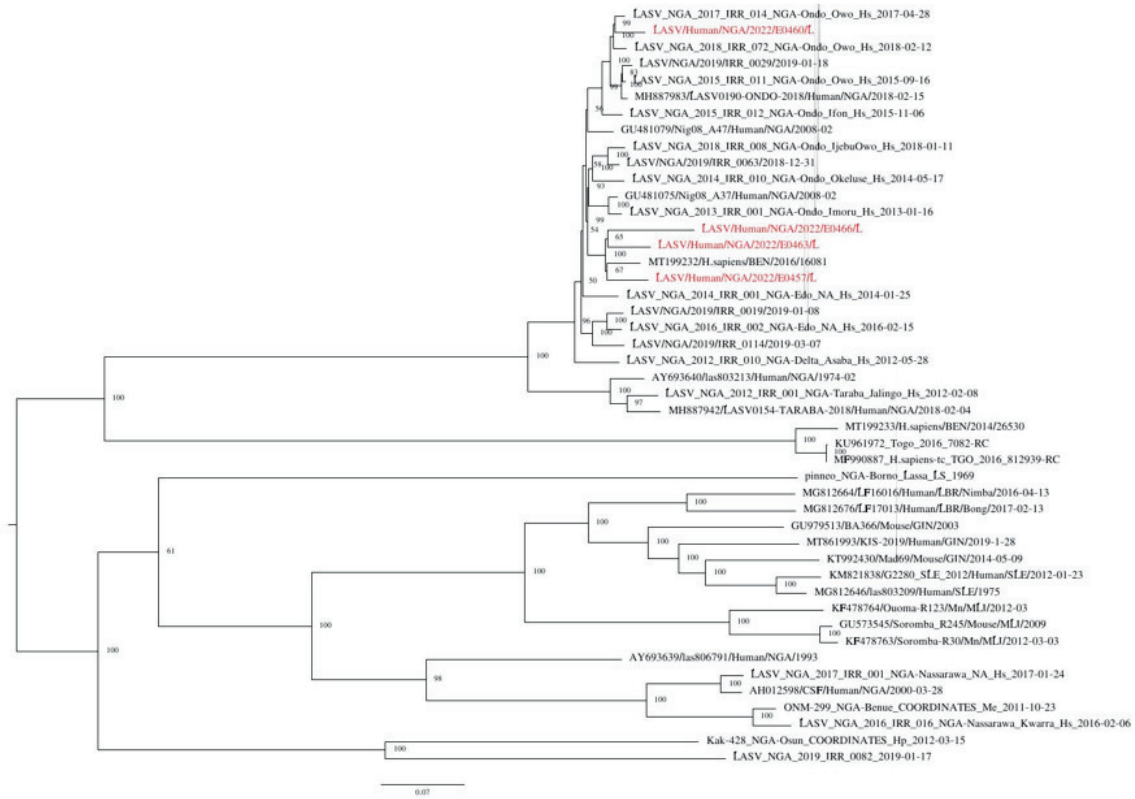


Figure 1: Phylogenetic tree of the LASV samples sequenced here. (A) Overall phylogenetic tree with L sequences. (B) Overall phylogenetic tree with S sequences.

TECHNICAL POINT AND PARTNERS

The MinION technology (Oxford Nanopore) is used for this program. The metagenomic protocol is followed with the aim of Targeting the Lassa Virus. The work presented in this report comes from a collaborative project of ISTH and BNITM.etic tree with S sequences.

DISSEMINATION OF RESULTS

This report and associated unpublished sequences are shared under the following conditions: the Irrua specialist Teaching Hospital (ISTH), Irrua, Nigeria and the Bernhard Nocht Institute of Tropical Medicine (BNITM), Hamburg, Germany, agree to share data to support the public health response. Data may be used and analyzed for these purposes. It is not permitted to use these sequences and data for publication purposes. If you intend to do so, please contact us directly. Prof. Reuben. A. Eifediyi, agbonsgloria@gmail.com, Irrua specialist Teaching Hospital (ISTH), Irma, Nigeria & Prof. Stephan Gunther, guenther@bni.uni-hamburg.de, Director of the WHO Collaborating Centre for Reference and Research on Arboviruses and Haemorrhagic Fevers, BNITM.

Report done at ISTH, Irrua, on 26 July 2023

Dr. Cyril Erameh, Director of ILFRC

Prof. Reuben. A. Eifediyi, Chief Medical Director of ISTH

OFFICIAL REPORT N°06

Breaking Ground: ISTH Establishes Locally Operated Next-Generation Metagenomic Sequencing Facility for RNA Virus Surveillance

Date: 12 April, 2024

SUMMARY

- Inauguration of the new metagenomic sequencing facility at ISTH, expanding local SARS-CoV-2 sequencing capacity and empowering local scientists to conduct comprehensive RNA-virus genomic surveillance (Figure 1)
- Real-time support during the current 2024 Lassa fever outbreak with sequencing and associated molecular epidemiology of 6 Lassa virus (LASV) positive samples collected in January 2024 (Table 1) from different patients.
- Retrospective analysis of one additional LASV positive sample collected in February 2022 which was part of the training process.
- Lassa virus genomic recovery ranged from 66% to 99 .6% for the S-segment and from 54.7% to 99.5% for the L-segment (Table 1).
- The 7 LASV sequences belong to lineage II which is known to circulate in Nigeria (Figure 2) and analysis further shows independent virus transmission events which reflects the main mode of LASV transmission.
- Planning of sequence submissions to Genebank before publication of results.
- ISTH scientific staff independently sequenced and analyzed the results presented here.

Figure 1A. Group picture following the inauguration of the metagenomic sequencing laboratory at ISTH, attended by the laboratory staff, the Director of the IVEPCR, alongside trainers from BNITM.

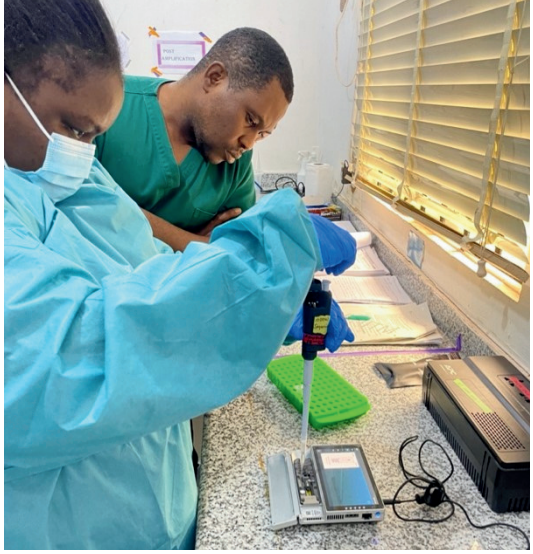


Figure IB. Personnel at the ISTH bioinformatic laboratory are seen loading the MinION device from Oxford Nanopore Technologies, initiating metagenomic sequencing .

Figure 1C. Laboratory staff engage in analysis to align LASV sequences and establish phylogenetic relationships.

Table 1. Sequencing outcome of 7 LASV positive samples collected in February 2022 (retrospective testing)and in January 2024 (prospective testing). All samples have been de identified to protect patient confidentiality.

No	*Sequencing Identifier*	*Sampling date*	*Ct Value (Cycle threshold)**		*% Consensus recovery*		*State*	*Lineage***
			GPC	*L*	*S*	*L*		
I	E0467	20/02/2022	13.5	20.7	98.3	57.6	EDO	II
2	E0498	11/01/2024	20.9	21.1	99.6	95.6	EDO	II
3	E0499	13/01/2024	21.5	19.7	91.6	**87.8**	EDO	II
4	E0504	02/01/2024	19.0	20.7	97.0	54.7	EDO	II
5	E0505	5/01/2024	16.3	18.7	66.0	-	EDO	II
6	E0506	14/01/2024	15.2	14.6	99.5	**84.1**	EOO	II
7	E0507	16/01/2024	33.3	18.9	99.4	99.5	EOO	II

*Rea/Star® LASV RT-PCRkit 2.0, a/tonaDiagnostics (Hamburg, Germany), Ct values from the diagnostic test performed at ISTH

**Lineage assignment was made using the phylogeneticanalyses presented in Fig. 2.

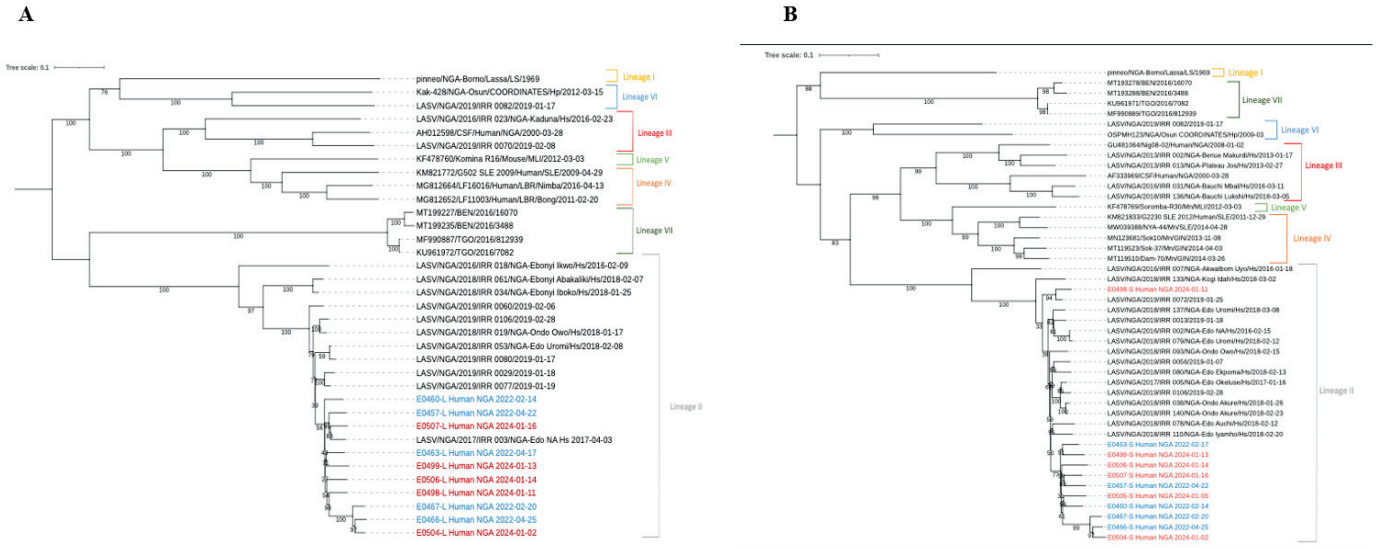


Figure 2: Phylogenetic trees of the new Lassa virus sequences; L segment (A) and S segment (B). The lineages I to VI, representing the diversity of Lassa virus, are indicated on the right-hand side of the trees in different colors. Sequences from samples collected in 2022 are shown in blue (text), while sequences from samples collected in 2024 in red (text). All the sequences obtained at ISTH from 2022 and from 2024 cluster within lineage II which is known to circulate in Nigeria.

BACKGROUND

- The Irua Specialist Teaching Hospital (ISTH) is a Federal Government Teaching Hospital located in Irrua, Edo State,Nigeria, which includes the Institute of Viral and Emergent Pathogens Control and Research (IVEPCR). The later diagnoses and monitors viral hemorrhagic fevers, with special reference to Lassa Fever. Since 2018, the feasibility toimplement LASVsequencing capacity was assessed. In April 2022,a sequencing capacity for SARS-CoV-2 has been set-up at ISTH-IVEPCR. The implementation of a broad genomic surveillance capacity at ISTH has been pursued since January 2023 through several trainings of laboratory staff.
- The work presented in this report originates from a collaborative project between several partner institutions: ISTH; the Bernhard-Nocht Institute for Tropical Medicine (BNITM), Hamburg, Germany; theEvolutionary and Computational Virology (ECV), Catholic University (KU Leuven), Leuven, Belgium; and theLaboratoire des Fievres Hemorragiques Virales de Guinee (LFHVG),Conakry, Guinea.
- The German Ministry of Health supports the establishment of genomic surveillance capcities in Sub-Saharan Africa in the framework of the Global Health Protection Program (GHPP-CELESTA, https://ghpp.de/en/projects/celesta/).
- Metagenomic sequencing (MinION technology, Oxford Nanopore), bioinformatic analyses, production of consensus sequences and generation of phylogenetic trees were independently performed by ISTH-laboratory-trained staff. The MinION sequencing technology (Oxford Nanopore) is used for this program. A metagenomic approach is followed with the aim of targeting RNA-viruses (Kafetzopoulou et al., 2019).

DISSEMINATION OF RESULTS

- This reportand associated unpublished sequences are shared under the following conditions: the Irrua specialist Teaching Hospital(ISTH), Irrua, Nigeria and the Bernhard Nocht Institute of TropicalMedicine (BNITM), Hamburg, Germany, agree to share data to supportthe public health response. Data may be used and analyzed for these purposes. It is not permitted to use these sequences and data for publication purposes. If you intend to do so, please contact us directly. Prof. Reuben. A. Eifediyi, agbonsgloria@gmail.com, Irrua specialist Teaching Hospital (ISTH), Irrua, Nigeria & Prof. Stephan Gunther, guenther@bni.uni-hamburg.de, Director of the WHO Collaborating Centre for Reference and Research on Arboviruses and Haemorrhagic Fevers, BNITM.

Report done at ISTH, Irrua, on 12 April, 2024

Dr. Joseph Okoeguale, Director IVEPCR

Prof. Reuben. A. Eifediyi, Chief Medical Director of ISTH

STAKEHOLDERS' ENGAGEMENT MEETING NATIONAL GENOMICS SURVEILLANCE STRATEGY

OVERVIEW OF GENOMICS SEQUENCING ACTIVITIES

INTRODUCTION

The Institute of Viral and Emergent Pathogens Control and Research (IVEPCR), Irrua Specialist Teaching Hospital commenced sequencing activities in April, 2022 through the support of our collaborators including The Bernhard Nocht Institute for Tropical Medicine (BNITM) Hamburg Germany, the Evolutionary and Computational Virology (ECV) Catholic University (KU Leuven) Leuven, Belgium, and the Laboratoire des Fievres Hemorrhagiques Virales de Guinee (LFHVG) Guinea, to implement the SARS-CoV-2 sequencing Laboratory.

To strengthen the sequencing capacity at ISTH, six ISTH scientific staff were trained on metagenomic sequencing in 2023 (theory, benchwork and bioinformatic analysis), including attendance to two workshops at the (LFHVG) in Conakry Guinea.

During the pre-implementation training phase, 4 Lassa virus (LASV) positive samples collected between February 2022 and September 2022 in Edo and Kogi States, Nigeria, were retrospectively sequenced at ISTH.

Lassa Virus (LASV) genomic recovery ranged from 99.3 % to 99.8% of the full genome Phylogenetic analyses revealed that the 4 sequences obtained belong to lineage II of Lassa virus, which is known to circulate in Nigeria.analysis also shows four independent virus transmission events. The program to build a genomic surveillance capacity at ISTH is continuing.

PATHOGENS OF INTEREST (FOR SEQUENCING)

- Lassa virus
- COVID-19
- Monkeypox
- etc

DATA SHARING

- These sequences have been submitted to GISAID (https://www.gisaid.org/)
- Future plans to submit LASV sequences from Metagenomics to Genbank

CHALLENGES

- Power
- Funding
- Equipment
- Computational Biology Laboratory

The Sequencing team with Partners from BNITM

The Chief Medical Director, Professor Reuben Eifediyi in Search of collaborative partnership in Metagenomic study

The Director of the Institute Dr Joseph Okoeguale in a visit to the Team in Preparedness for a step-down training with our collaborators

Team Member loading Nanopore flowcell

Molecular Laboratory Ambulance

The Sequencing Team Lead, Dr Ehizojie Emua (Bioinformatician) at BNITM Hamburg, Germany for analysis pipeline training.

LASSA FEVER **VISIONEERS**

OUR COLLABORATORS

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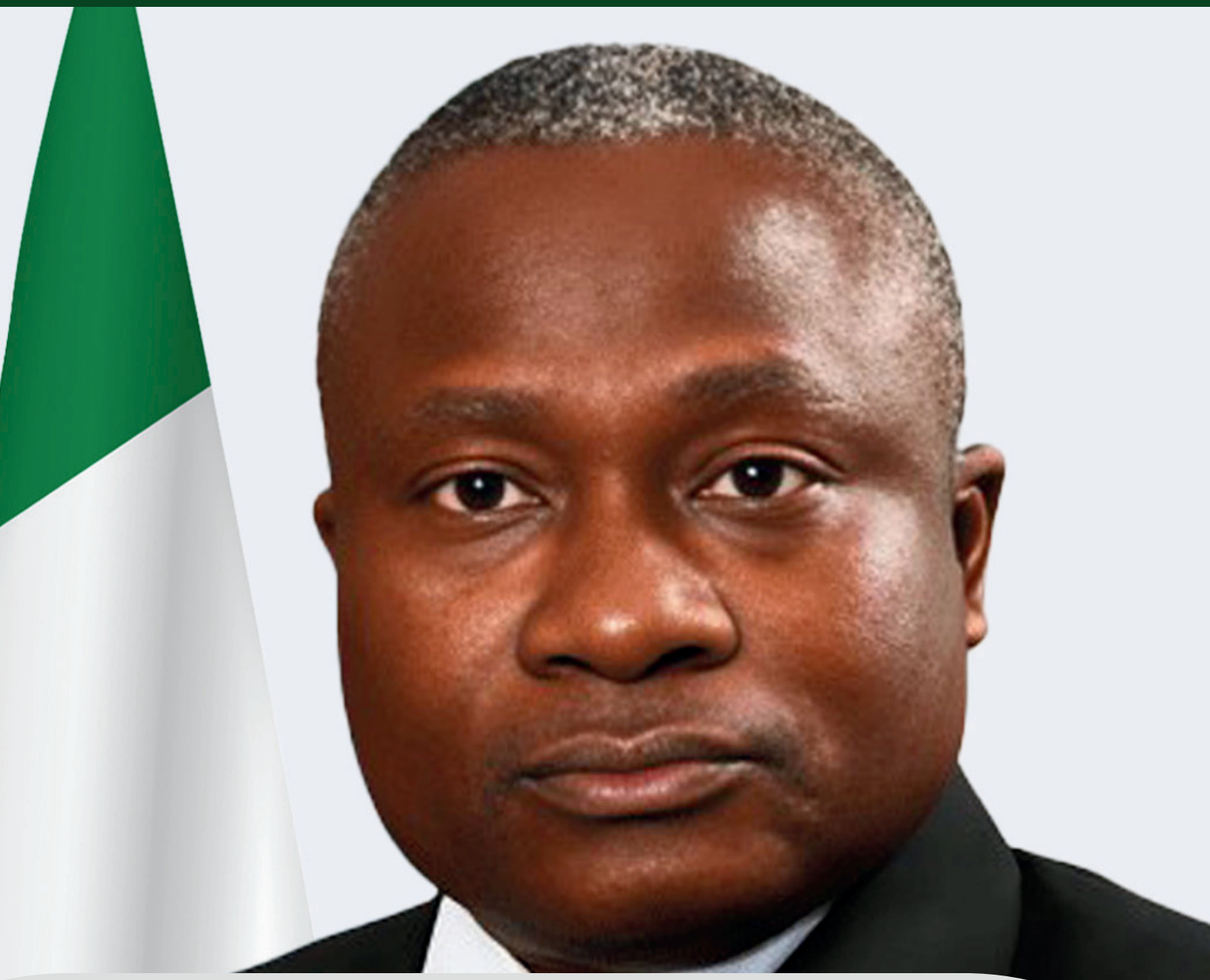
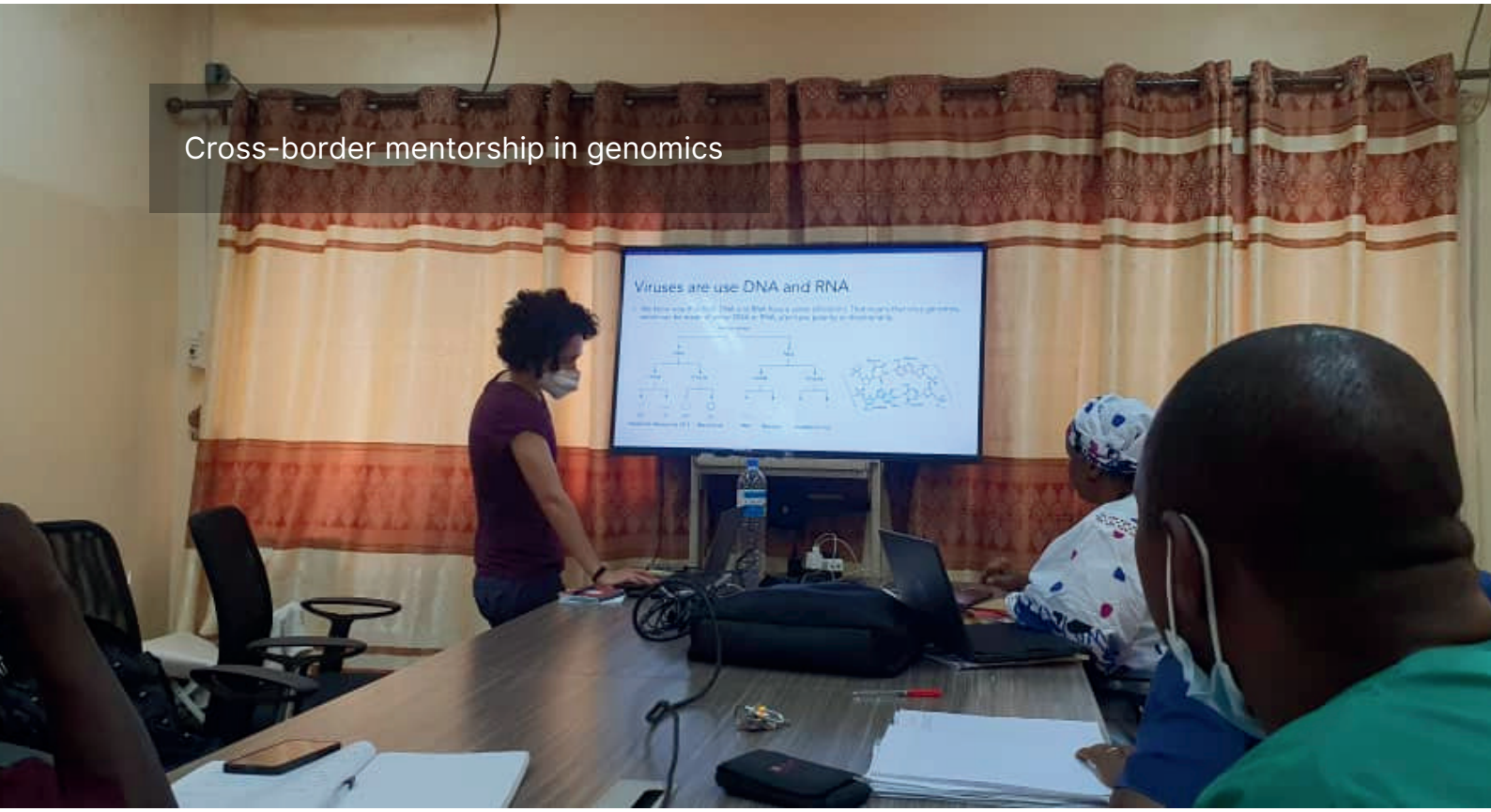


Dr Jide Idris, DG, NCDC, Key stakeholder, and support framework of our Institute

SEQUENCING **TEAM MEMBERS**

From left to right: Njigha Precious Igenegbale Ganiyu, Ebhodaghe Paulson, Omiunu Racheal (Assistant Team Lead), Emua Ehizojie (Team Lead), Okogbenin Benedicta

PHOTO **GALLERY**



Cross-border mentorship in genomics


BNITM
Bernhard-Nocht-Institut für Tropenmedizin

Hands-on mentorship and intenship continuing in Conakery Guinea

CENTRE OF EXCELLENCE FOR DIAGNOSIS, CASE MANAGEMENT, CONTROL AND RESEARCH OF VIRAL AND EMERGENT PATHOGENS

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