

## **Implementation of a nanopore genomic surveillance unit for emerging viral pathogens at the Irrua Specialist Teaching Hospital, Nigeria: experience from a synergistic collaboration**

Ehizojie Ehiremen Emua<sup>1,\*</sup>, Julius Okoeguale<sup>1</sup>, Guiditta Annibaldis<sup>2</sup>, Racheal Omiunu<sup>1</sup>, Sarah Ryter<sup>2</sup>, Precious Omiunu Njigha<sup>1</sup>, Ganiyu Igenegbale<sup>1</sup>, Obchiaghe Benedicta Okogbenin<sup>1</sup>, Paulson Ehichioya Ebhodaghe<sup>1</sup>, Philippe Lemey<sup>3</sup>, Nils Petersen<sup>2</sup>, Mia Le<sup>2</sup>, Liana Kafetzopoulou<sup>3</sup>, Stephan Günther<sup>2</sup>, Sophie Duraffour<sup>2</sup>, Sylvanus Okogbenin<sup>1</sup>, Reuben Eifediyi<sup>1</sup> Cyril Eramah<sup>1</sup>

<sup>1</sup>Irrua Specialist Teaching Hospital, Edo State, Nigeria, <sup>2</sup>Bernhard Nocht Institute for Tropical Medicine, Hamburg, Germany, <sup>3</sup>Rega Institute, KU Leuven, Leuven, Belgium

**\*Corresponding author:** Ehizojie Ehiremen Emua, Irrua Specialist Teaching Hospital, Edo State, Nigeria, **Email:** [eeemua@gmail.com](mailto:eeemua@gmail.com)

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### **Introduction**

In April 2022, the Irrua Specialist Teaching Hospital (ISTH), in collaboration with the Bernhard-Nocht Institute for Tropical Medicine (BNITM), opened its nanopore sequencing facility to monitor SARS-CoV-2 variants and enhance genomic surveillance in the country. Arising from this successful setup of amplicon-based approach, the capacity gradually progressed towards implementing metagenomic nanopore sequencing in 2023. We present here the outcome and contribution to Nigeria's public health efforts to monitor SARS-CoV-2 and Lassa virus variants.

### **Methods**

SARS-CoV-2-positive samples were sequenced using the MinION technology (Oxford Nanopore Technologies, ONT) with the amplicon-based Midnight protocol as part of ISTH surveillance diagnostics activities. Metagenomic nanopore sequencing (SISPA protocol – A and B) was performed on Lassa virus positive with a reverse transcription PCR cycle (RT-PCR) threshold value < 28 (Altona Diagnostics). Basecalling, consensus building using an in-house pipeline, and phylogenetic analysis were performed in-country.

### **Results**

Sequencing of 218 SARS-CoV-2 positive samples collected between 2020 and 2022 revealed that a majority (66% of the sequences acquired at ISTH) were from various clades of the Omicron variant (BA.1 or B.1.1.529), along with others COVID-19 sub-variants. Metagenomic sequencing of 24 Lassa virus-positive samples collected in 2024 yielded genomic recovery ranging from 73.25% to 99.79% for the S segment, and from 52.81% to 99.82% for the L segment. Phylogenetic analysis classified these sequences within lineage II of Lassa virus, which is the dominant clade circulating in Edo State.

### **Conclusion**

The establishment of the sequencing laboratory at ISTH has significantly strengthened Nigeria's genomic surveillance capabilities. Despite challenges such as power interruptions, limited funding, and equipment and computational biology infrastructure constraints, the laboratory's ability to sequence SARS-CoV-2 and Lassa virus underscores its potential for effective viral monitoring and transmission tracking.