Irrua Specialist Teaching Hospital, ISTH
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METAGENOMICS SEQUENCING RESULTS AT IRRUA SPECIALIST TEACHING HOSPITAL (ISTH): 2024 LASSA OUTBREAK SEQUENCING RESULTS AND PHYLOGENETIC ANALYSIS

Summary

- Real – time genomics support was provided during the 2024 Lassa fever outbreak, including sequencing and molecular epidemiology analysis.
- A total of **26 Lassa virus (LASV) positive** samples with cycle threshold (CT) values <25, collected between **January 2024 and April 2024,** were selected for sequencing and analysis.
- Of these, **18 yielded sufficient LASV genomic material** for phylogenetic analysis **(Table 1).** Two samples, with segment recoveries of 35.9% (S segment) and 21.3% (L segment) were excluded from the segment–specific phylogenetic analysis due to insufficient genome coverage **(Figure 1 and Table 1).**
- Genomic recovery among the 18 LASV-positive samples ranged from **73.3%** to **99.8%** for the **S-segment,** and from **52.8%** to **99.8%** for the **L-segment (Table 1).**
- All the **18 LASV** genomes belong to **lineage II,** consistent with the known circulating strain in Nigeria **(Figure 1),** and analysis further shows independent virus transmission events.
- Sequencing and data analysis were independently conducted by scientific staff at ISTH.

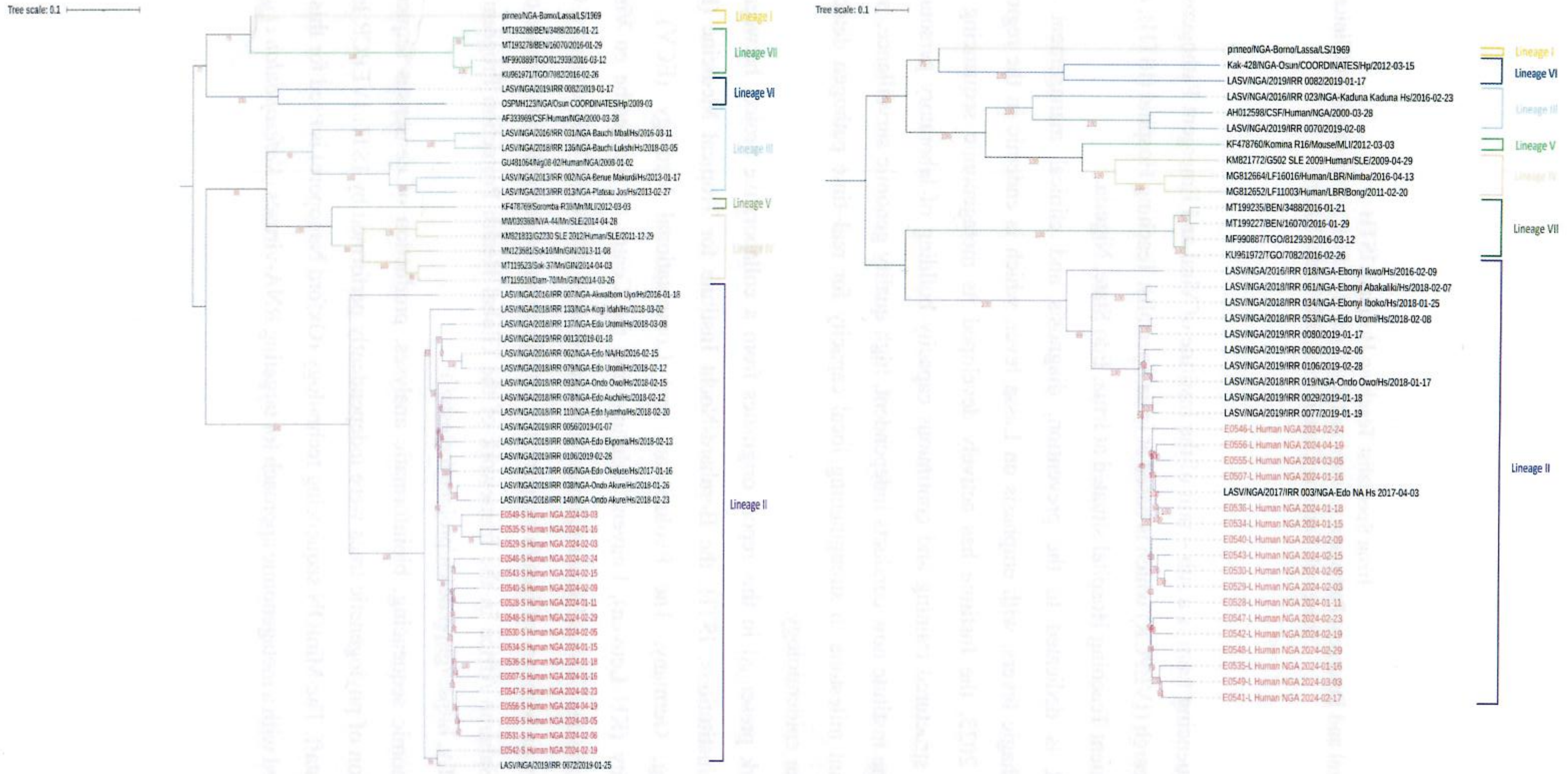

Figure 1: Phylogenetic trees of the new Lassa virus sequences; S segment (left) and L segment (right). The lineages I to VII, representing the diversity of Lassa virus, are indicated on the right-hand side of the trees in different colors. Sequences from samples collected and sequenced in 2024 in red (text). All the sequences obtained at ISTH from 2024 outbreak cluster within lineage II which is known to circulate in Nigeria.

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This report and associated unpublished sequences are shared under the following conditions: the Irrua Specialist Teaching Hospital (ISTH), Irrua, Nigeria and the Bernhard Nocht Institute of Tropical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 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 & Prof. Stephan Günther; guenther@bni.uni-hamburg.de, Director of the WHO Collaborating Centre for Reference and Research on Arboviruses and Haemorrhagic Fevers, BNITM.

Reports done at ISTH, Irrua on 23rd June, 2025

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