REAL-TIME TRACKING OF LASSA VIRUS GENOME EVOLUTION IN NIGERIA USING NEXTSTRAIN

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Background

- Lassa virus is the etiological agent of Lassa fever

- It is named after Lassa town in Borno state, Nigeria where it was first discovered in 1969 (Frame et al., 1970)

- CEPI and WHO priority pathogen

- Fatality rates vary from 16-60%

- Cases peak in dry season

- No vaccine, only nonspecific treatment with Ribavirin

- Spreads to humans from other animals, specifically the natal multimammate rat or Mastomys natalensis
Lassa Virus Genome

• The virus belongs to the **Arenaviridae** family

• It has a single-stranded and bisegmented, ambisenese RNA genome, composed of an L segment of about 7.3kb and an S segment of 3.5kb.

(Warner et al., 2018)
Why study/track genome evolution?

Pathogen genomes may reveal:

- Evolution of new adaptive variants
- Epidemic origins
- Patterns of geographic spread
- Animal-to-human spillover
- Transmission chains

West African Ebola Phylogeny

Dudas et al., 2017
Using Nextstrain to Track Lassa Virus Genome Evolution in Nigeria

**Nextstrain** is two things:

- a bioinformatics toolkit and visualization app, which can be used for a broad range of datasets
- a collection of real-time pathogen analyses kept up-to-date on the website nextstrain.org

We modified the Nextstrain pipeline and deployed it to track the spread of the virus across different states of the country in real-time and also to track in real-time diversity across the genome of the virus.

Development led by:

Trevor Bedford and Richard Neher

- Align with MAFFT
- Build ML tree with IQ-TREE
- Temporally resolve tree and geographic ancestry with TreeTime

Build accessible at www.nextstrain.org/community/pauloluniyi/lassa/s
Map Data Points

Anambra (2) Bauchi (6) Delta (7) Ebonyi (13) Edo (127) Imo (1) Kaduna (1) Kogi (8) Nasarawa (4) Ondo (78)
Conclusion

- Nextstrain facilitates the real-time monitoring of pathogen spread across different geographical areas of Nigeria.

- Nextstrain facilitates the real-time monitoring of mutations occurring across pathogen genomes.

- Inferences made from phylodynamics analysis with Nextstrain helps inform real-time public health response and surveillance.
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