

VARIATION IN LINEAGE 2 STRAIN OF LASSA FEVER VIRUS IN NIGERIA

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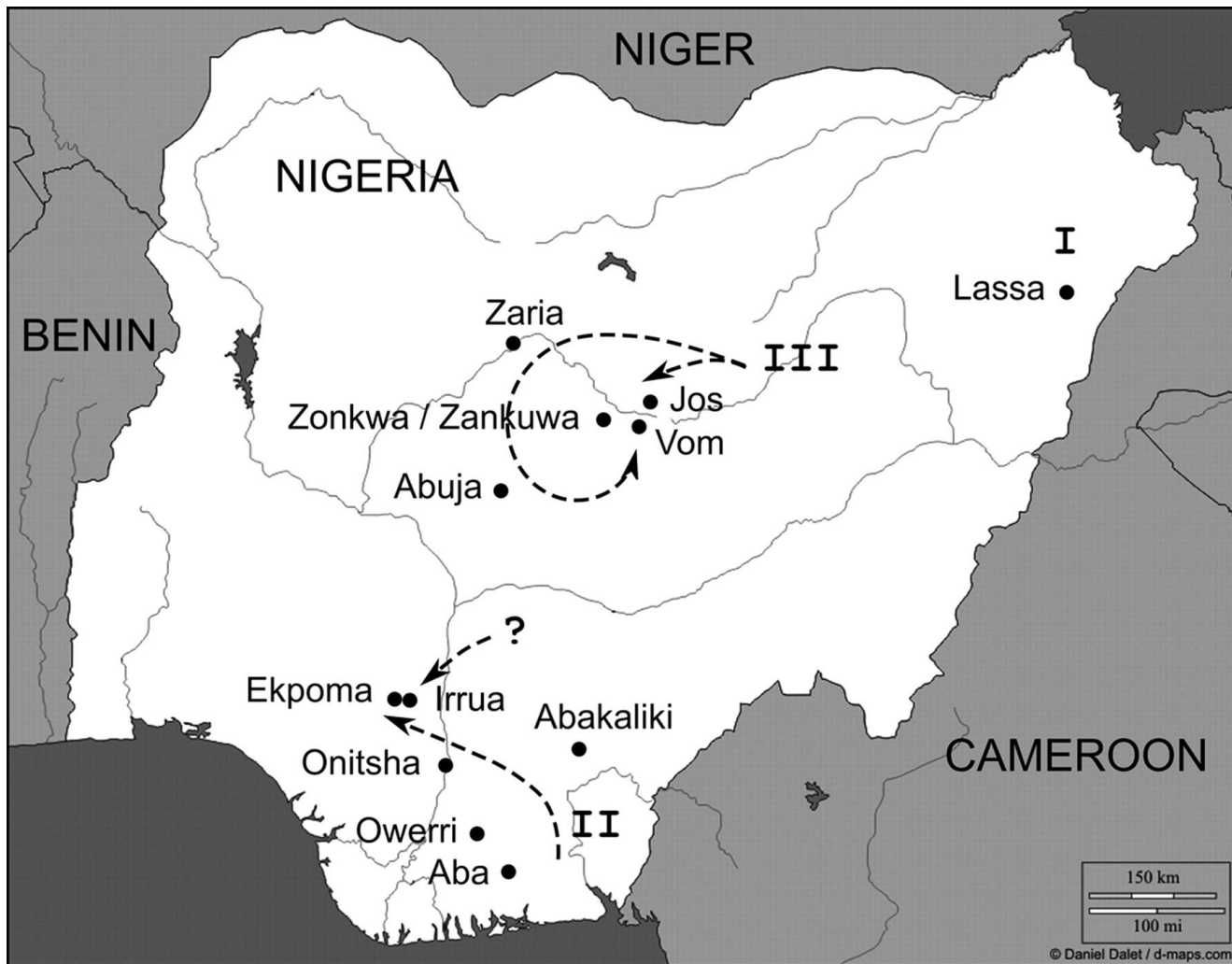
BACKGROUND

- Nigeria harbours three of the four established strains of Lassa Fever (LF) in West Africa.
- Lineages 2 and 3 occur dominantly in the southern and Northern regions of the country respectively.
- In the south, the South West(S.W) and South East (S.E) axes are most endemic for LF.
- Casual observation/anecdotes suggesting increased complications among SE cases raised the question : are there variations in the LF strains in the SW and SE axes that may suggest a difference in virulence ?

Methodology

- Following the 2014 epidemic with fifteen positive cases among (HCWs) in the SE axes, genomic studies elucidating their nucleic acid sequences were conducted in Nagasaki University.
- Ten years study of nucleic acid sequences of lineage 2 strains of LF from Nigeria covering the period 2004-2014 gleaned from the GENBANK pool was conducted.
- . Included were the fifteen positive samples of 2014 epidemic, totalling 79 LF glycoprotein precursor (GPC) gene sequences.

Map of Nigeria showing sites of Lassa virus circulation.



Ehichioya D U et al. J. Clin. Microbiol. 2011;49:1157-1161

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Methodology

- Using MEGA 6 software, Phylogenetic and BLAST analysis of the homologous identity of all the 79 strains were conducted.
- Fifty of the 79 LF lineage two strains were of SW origin while 29 were of SE.
- Alignments of various gene sequences (GPC, NP and L) from readily available sequences was conducted

Findings

- Three probable distinct clades/sublineages of the SE strain were observed and clustered around Nig 05-SE40, Nig 08-04 and Nig 11-186 strains.
- . Diversity among the clades of the SE strains ranged between 18 – 21 %. The SW strains were essentially of one clade and exhibited good homologous identity of 97-100%.
- Sequences of LF viruses at the boundary of the SE/SW may be “outliers” that gave the SE strains the diversity

FINDINGS

- Alignments of various gene sequences (GPC, NP and L) from readily available sequences reveal marked diversity of South-east strains.
- South west strains of same lineage show less diversity.
- Phylogeny of the sequences suggests at least 3 different clades of the South east strain- the 2013 -99% homologue of Nig 08-04 belonging to a separate clade.
- Some of the strains identified in the south west region aligned with South east clades in the phylogeny tree.

Conclusion

- This suggests less diversity among the SW strains than SE strains. Between the SW and SE strains diversity was up to 20%.
- Though fewer NP gene sequences are available for alignment than GP gene sequences, NP appeared to show greater diversity for the Lassa virus strains than GP sequences.
- Most of sequences available were “PARTIAL SEQUENCES” and will have its influence on the findings unlike if full sequences of all LF analyzed were available
- There is need for evaluation for mutation among clades of SE origin.

- Map of Nigeria showing sites of Lassa virus circulation. The possible spread of virus is indicated by dashed arrows. The Lassa virus lineages are indicated with the corresponding areas in which the virus is endemic. The potential lineage/sublineage represented by strain Nig05-A08 is indicated with a question mark. (Modified from a map by Daniel Dalet that is freely available at <http://d-maps.com>.)