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Background

Lassa fever (LF) is an acute viral hemorrhagic illness caused by Lassa virus. Lassa virus is enveloped and belongs to the family *Arenaviridae* and genus *Arenavirus* (Bowen et al., 2000). Epidemiologically, an estimated two to three million people in West Africa are infected with LASV annually, causing 10,000 deaths each year (Naeem et al., 2023). In Nigeria, the prevalence of Lassa fever has been fast rising over the years, with over 33 years of national outbreaks and more than 18 years of Lassa fever outbreaks in Plateau State since the detection of the index case in 1969 (Agbonlahor et al., 2021). Plateau state is one of the states with significant increased risk of Lassa virus infection. This study aimed at characterization of the molecular phenotypes of Lassa virus in febrile patients who meet pre-determined criteria for Lassa virus infection, hypothesizing that some mild cases might have been misdiagnosed as other illnesses.

Objectives

The objectives of the study were to:

1. determine the prevalence of Lassa virus in febrile patients within Plateau state, Nigeria.
2. determine the phylogenetic relatedness of the Lassa virus in febrile patients within Plateau state, Nigeria.
3. identify the risk factors associated with Lassa virus infection among febrile patients in Plateau state.

Methods

Ethics statement

Ethical approval for this study was received from the University of Jos Teaching Hospital (JUTH) in Jos, Nigeria with an approval number NHREC/JUTH/05/1022.

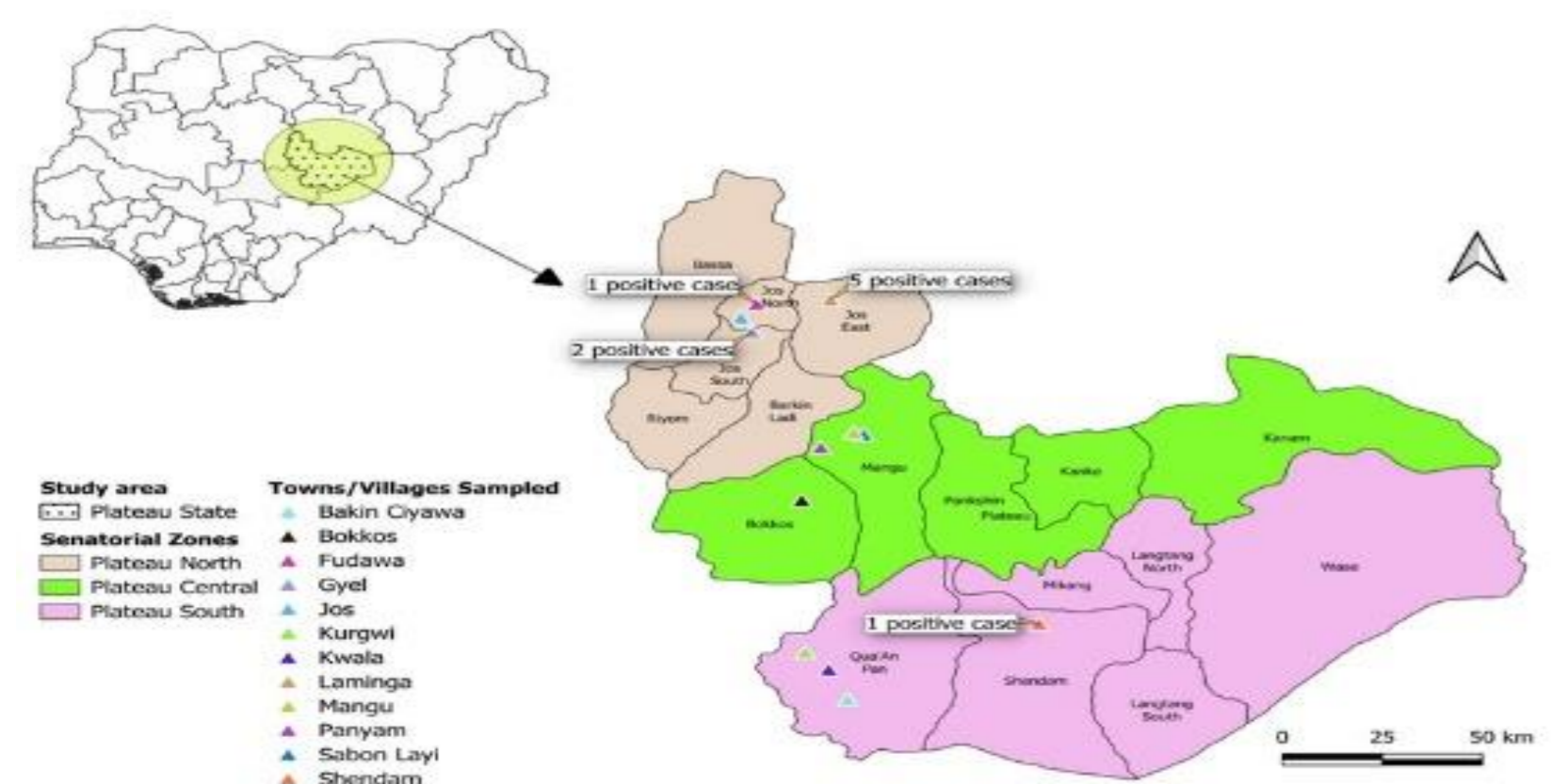
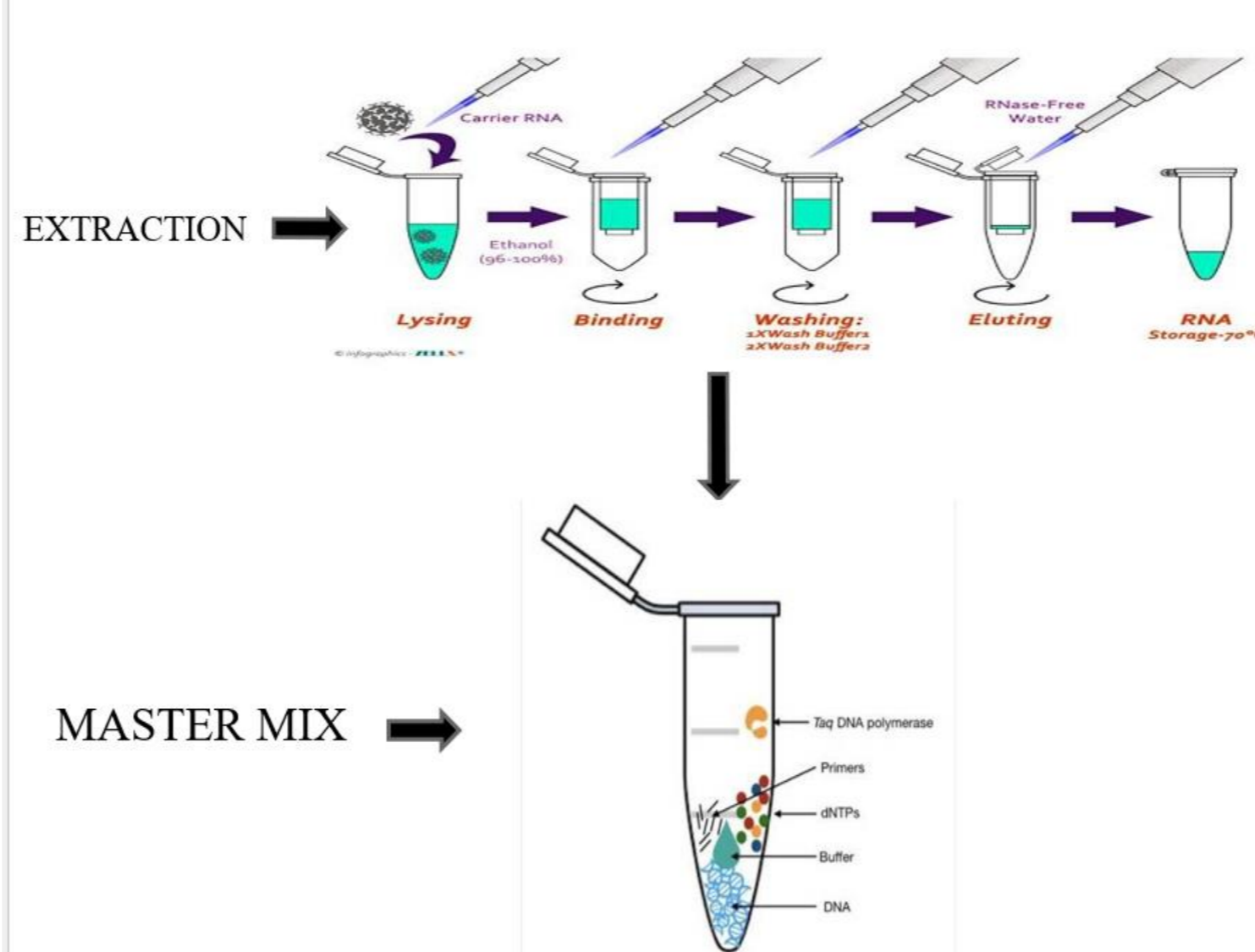


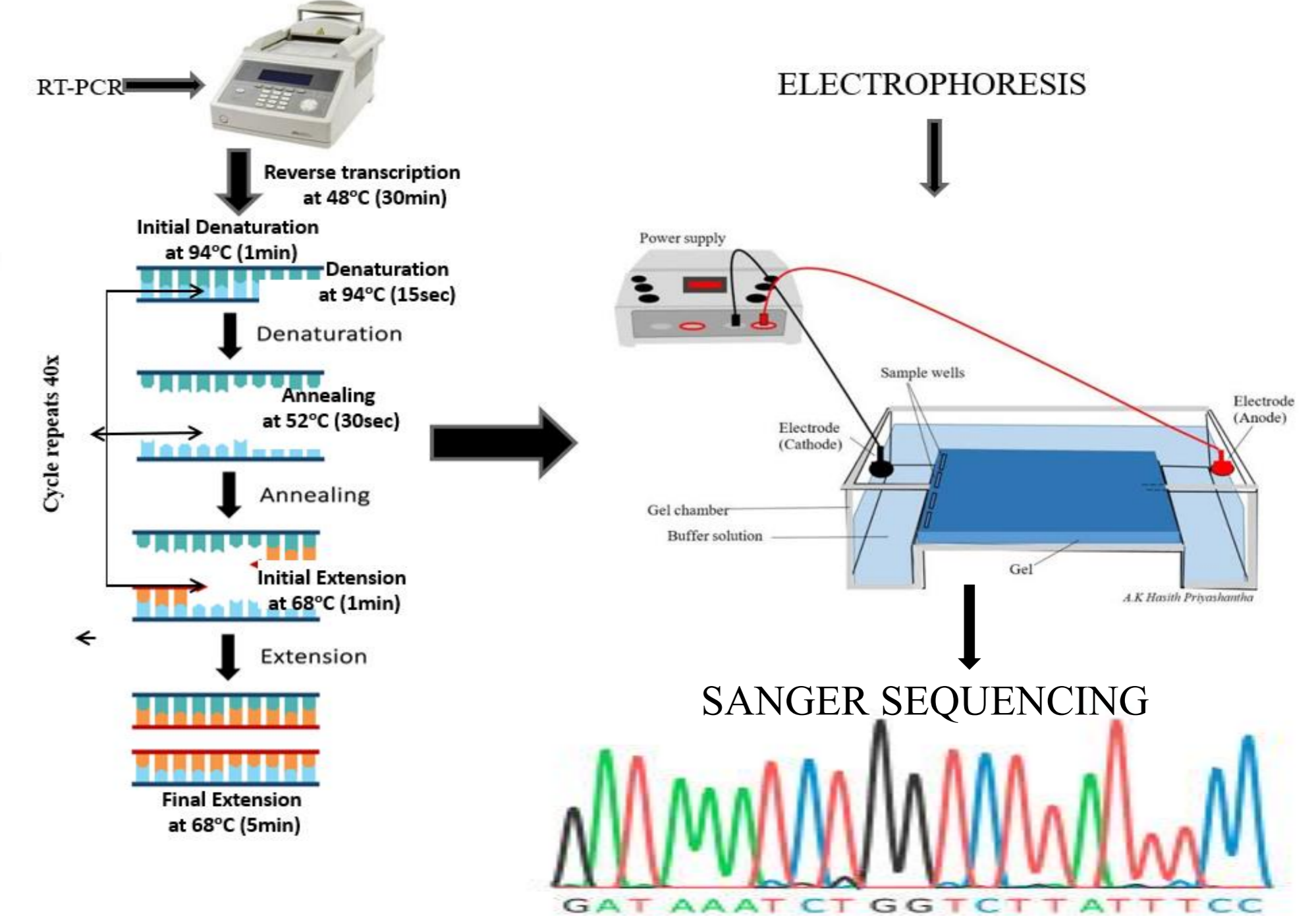
Figure 1: Map of Nigeria showing location of sample collection (Generated using QGIS version 3.38.3)

A total of 240 blood samples were collected from febrile Patients $\geq 38^{\circ}\text{C}$ across selected Hospitals within the three zones in Plateau state, Nigeria and analysed at the National Veterinary Research Institute (NVRI), Vom, in a BSL3 laboratory as follows:

THE EXTRACTION AND MASTER MIX PROCESS



THE PCR AND ELECTROPHORESIS PROCESS



Results

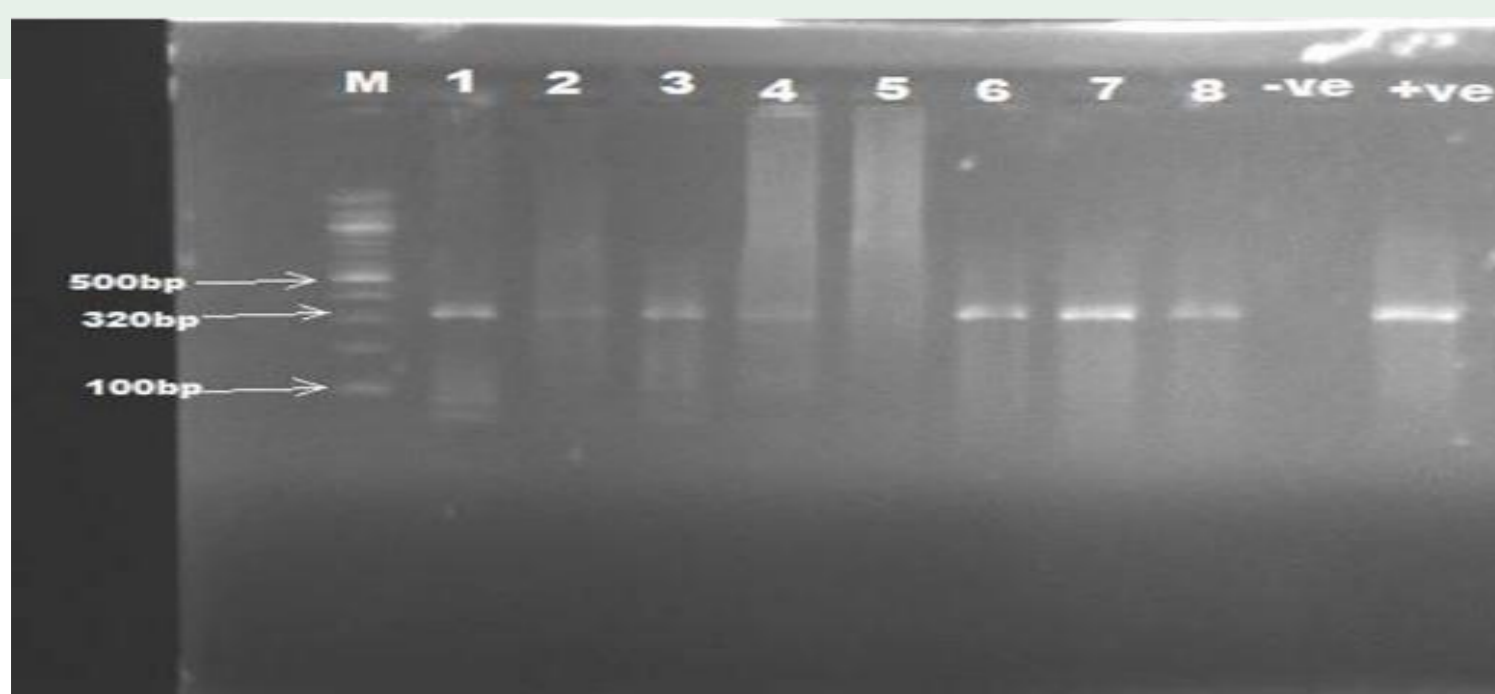


Plate 1. Shows agarose gel electrophoresis picture for amplified GPC gene of Lassa virus (320bp). Line M: DNA molecular weight marker (100 bp); Line 1-8 showed the sample IDs. Line -Ve: Negative control; Line +Ve: Positive control.

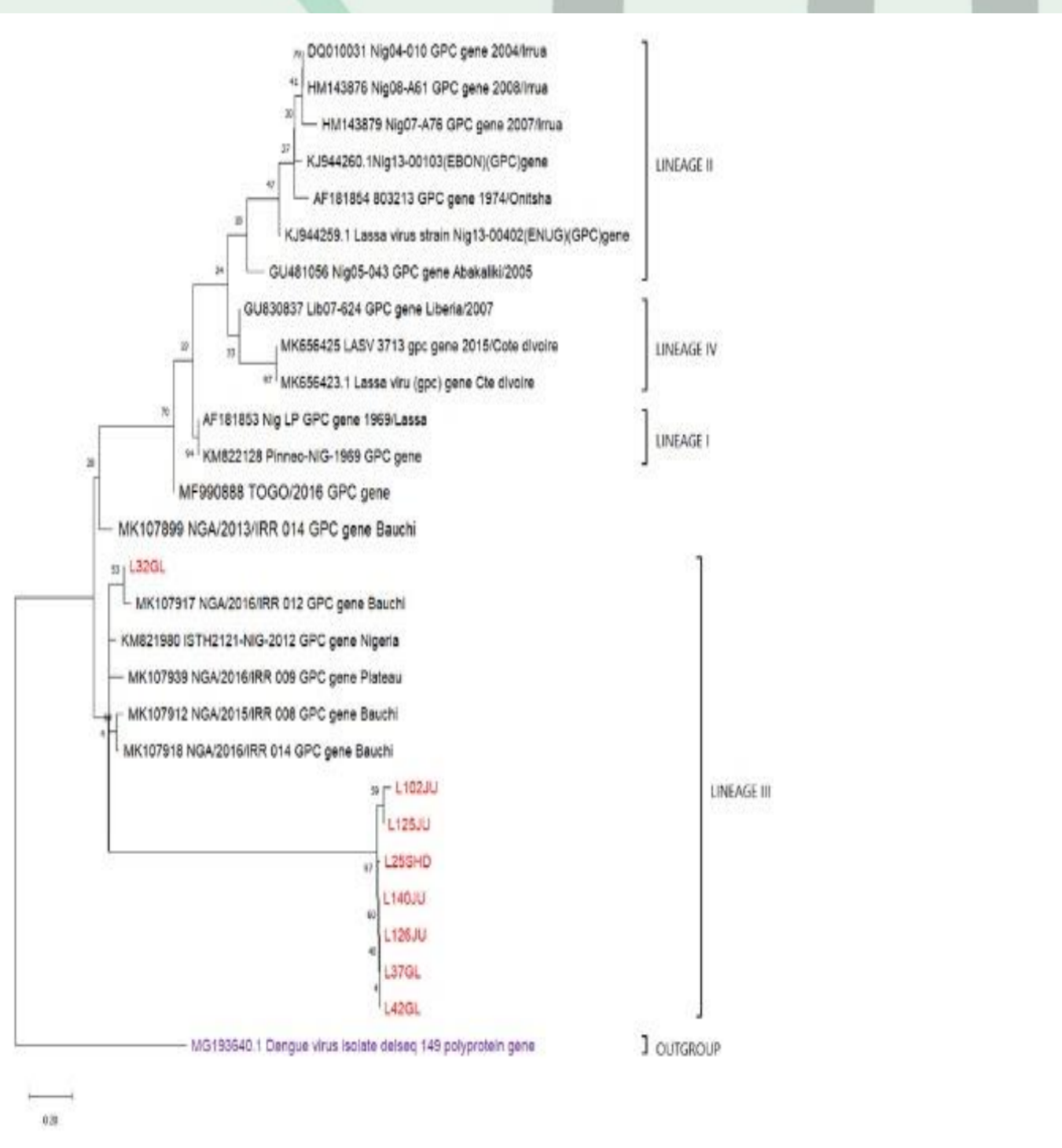


Figure 3. A maximum likelihood phylogenetic tree inferred from GPC gene in Jos, Nigeria

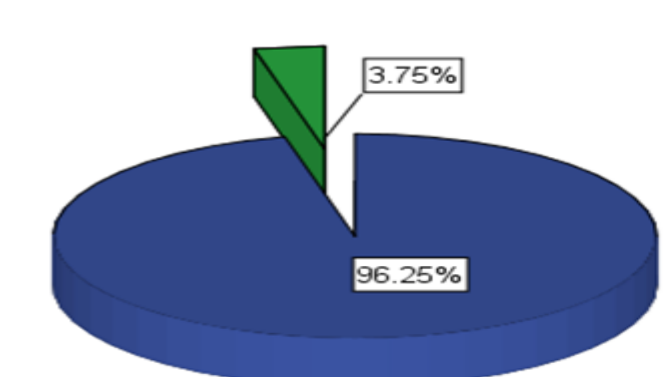


Figure 2: Prevalence of Lassa fever in Plateau state

Table 1 Prevalence of Lassa virus infection in relation to sociodemographic factors in Jos, Nigeria

Variable	Category (years)	No. examined	Positive	Prevalence (%)	χ^2	p-value
Age group	0-10	41	2	4.9	6.151	0.525
	11-20	47	1	2.1		
	21-30	29	2	6.9		
	31-40	43	0	0.0		
	41-50	30	2	6.7		
	51-60	20	0	0.0		
	61 and above	30	2	6.7		
Total		240	9			
Sex	Female	120	4	3.3	0.115	0.734
	Male	120	5	4.2		
Total		240	9			
Occupation	Farming	4	0	0.0	4.643	0.461
	Managerial	1	0	0.0		
	Professional	15	2	13.3		
	Skilled	48	2	4.2		
	Student/Pupil	61	3	3.7		
Zones within Plateau state	Plateau Central	80	0	0.0	13.160	0.001*
	Plateau North	80	6	10.0		
Plateau South	80	1	1.3			
Total		240	9			
Residence	Rural	187	5	2.7	2.717	0.099
	Urban	53	4	7.5		
	Total	240	9			

*value is statistically significant at

Table 2 Exposure related factors associated with the prevalence of Lassa Virus infection in Jos, Nigeria

Variable	Category	No. examined	Positive	Prevalence (%)	χ^2	p-value
Involved in animal farming	No	155	6	3.9	0.018	0.894
	Yes	85	3	3.5		
	Total	240	9			
Contact with rodents?	No	108	5	4.6	0.526	0.839
	Yes	128	4	3.1		
	Unknown	4	0	0.0		
Total		240	9			
Travelled to an area with febrile illness?	No	219	9	4.1	0.897	0.672
	Yes	18	0	0.0		
	Unknown	3	0	0.0		
Total		240	9			
Contact with febrile patients within the last three weeks?	No	216	9	4.2	1.039	0.595
	Yes	23	0	0.0		
	Unknown	1	0	0.0		
Total		240	9			

Conclusions and Recommendations

- The 3.75% prevalence from febrile Patients recorded in our study indicate that just using case definition to screen Lassa fever will lead to a lot of missed cases.
- The sequences obtained in our study phylogenetically clustered with Lassa virus strains obtained from Bauchi state in Northern Nigeria
- Lassa infection differed significantly ($p < 0.05$) across zones with higher infection observed in Jos North Zone of Plateau State.
- There was no significant association observed between Lassa infection and exposure risks in the study.

This study highlights the presence of Lassa fever among febrile patients who might not typically be screened for the disease, as they do not meet the standard case definition for suspected Lassa fever. This call for an active screening of all patients with fever at presentation and not just focusing on those that meet the standard case definition.

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