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Seroprevalence of Lassa Virus Infection and Associated Risk Factors in North-Central Nigeria: A Community-Based Multi-State Study

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ABSTRACT

Background: Lassa fever remains a major public health threat in West Africa, with Nigeria accounting for the highest burden of disease. However, the true extent of population-level exposure is poorly defined, particularly in North-Central Nigeria.

Methods: A community-based cross-sectional seroprevalence of LASV was conducted across five states in North-Central Nigeria (Benue, Kogi, Nasarawa, Plateau, and the Federal Capital Territory-FCT) between January and July 2024. A total of 958 participants were enrolled using a multistage sampling method. Serum samples were tested for LASV-specific IgG and IgM antibodies using a validated recombinant nucleoprotein enzyme-linked immunosorbent assay. All IgM-positive samples and a random subset of IgM-negative samples underwent RT-PCR testing for the detection of active infection. Standardised questionnaires captured sociodemographic, environmental, and behavioural exposures. Multivariable logistic regression was used to identify factors independently associated with seropositivity.

Results: IgM seroprevalence was low (1.15%), and all 91 samples tested by RT-PCR were negative. In multivariable analysis, participants from FCT (adjusted odds ratio [aOR] 0.07, 95% CI 0.03–0.15), Kogi (aOR 0.05, 95% CI 0.02–0.14), Nasarawa (aOR 0.18, 95% CI 0.09–0.40), and Plateau (aOR 0.22, 95% CI 0.10–0.49) had significantly lower odds of IgG seropositivity compared to Benue State. Living in non-concrete houses was associated with increased odds of seropositivity (aOR 2.66, 95% CI 1.79–3.95). In contrast, rodent consumption was associated with reduced odds of seropositivity (aOR 0.23, 95% CI 0.12–0.44).

Conclusion: LASV exposure is widespread but heterogeneously distributed across North-Central Nigeria, with strong influence from geographical and housing-related factors.

Keywords: Lassa virus; Lassa fever; seroprevalence; Nigeria; burial practices; community-based, Multistate

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INTRODUCTION

Lassa fever (LF), caused by Lassa virus (LASV), an Old World arenavirus of the Arenaviridae family, represents a significant public health threat across West Africa, with case-fatality rates among hospitalised patients reaching 15%.[1,2] The virus is estimated to cause 100,000–300,000 infections annually, with Nigeria accounting for over 80% of confirmed cases in recent years, underscoring its position as the primary endemic hotspot in the region.[1,3] The multimammate rat (Mastomys natalensis) serves as the principal reservoir host, perpetuating zoonotic spillover through peridomestic contamination of food and household environments with infected rodent excreta [4,5]. Human-to-human transmission occurs via direct contact with infected bodily fluids, particularly in healthcare settings where infection prevention and control measures are inadequate, with at least 249 health workers infected between 2019 and 2025. Recent modelling studies suggest that such secondary transmission may account for a substantial minority of infections, highlighting the need to consider both zoonotic and human transmission pathways in epidemiological analyses.[6-8]

Since 2018, LASV has demonstrated concerning geographic expansion, spreading to more than 30 of Nigeria's 36 states and the Federal Capital Territory (FCT), with annual outbreaks typically peaking during the dry season (November–March).[9,10] Between 2022 and 2024, over 4,300 confirmed cases were reported nationally, with a case fatality rate among confirmed cases ranging from 13.5% to 18.5%. This proportion substantially exceeds the estimated 1–2% CFR for all infections and reflects persistent challenges in early detection and clinical management.[9,11] The North Central region of Nigeria has emerged as increasingly prominent in the epidemic landscape, with Benue, Kogi, Nasarawa, Plateau states, and the FCT reporting 57 confirmed cases and 20 deaths during the 2025 outbreak alone.[12] Several ecological and socioeconomic factors have been proposed to influence exposure risk and increase regional vulnerability, including a confluence of high population density, intensive agricultural practices that support robust rodent populations, and socioeconomic factors facilitating recurrent rodent-to-human spillover.[11,13]

Reliance on clinical surveillance alone substantially underestimates the true burden of LASV infection, as approximately 80% of infections are asymptomatic or manifest with mild, nonspecific symptoms indistinguishable from other febrile illnesses prevalent in Nigeria, particularly malaria.[14,15] Consequently, only severe cases, typically those presenting with bleeding diathesis, are likely to be diagnosed, while the vast majority of infections remain undetected by routine surveillance systems.[16] This diagnostic blind spot has profound implications for understanding transmission dynamics, assessing population-level immunity, and evaluating the potential impact of future vaccination strategies.

Serological studies detecting LASV-specific antibodies provide a more accurate measure of cumulative population exposure and infection.[16] Immunoglobulin G (IgG) antibodies indicate historical exposure and persist for years, while Immunoglobulin M (IgM) antibodies suggest recent or active infection, enabling differentiation between past and ongoing transmission.[17] Previous seroprevalence surveys across West Africa have reported highly variable IgG positivity rates ranging from 3% to over 50%, reflecting the heterogeneous and microfocal nature of LASV transmission.[16,18] In Nigeria, documented seroprevalence ranges from 18% in Ikorodu Local Government Area of Lagos State to 33% in the Abuja Municipal Area Council and 49.6% among pregnant women attending antenatal clinics in Edo State.[13,19] These variations underscore the importance of localised epidemiological assessments. Despite the classification of North-Central Nigeria as a hyperendemic zone for Lassa fever and its growing contribution to national case counts in Nigeria, important spatial knowledge gaps remain regarding the true population-level exposure to Lassa virus (LASV) and the contextual factors that may influence infection risk in this region. Much of the existing evidence has been derived from facility-based surveillance or studies conducted in single states, with many investigations concentrated in southern Nigeria. These approaches provide valuable information on clinical cases but offer limited insight into the broader patterns of community exposure, particularly in North-Central Nigeria, where ecological and sociocultural conditions differ from other endemic zones.

Community-based serological studies are therefore critical for capturing the cumulative burden of LASV infection, including infections that occur without clinical recognition. Detection of LASV-specific immunoglobulin G (IgG) and immunoglobulin M (IgM) antibodies allows estimation of previous and recent exposure, respectively, and can provide a more comprehensive picture of viral circulation within populations. However, few studies in this region have systematically examined how sociodemographic characteristics, environmental conditions, and behavioural practices may interact to influence the likelihood of exposure. Addressing these gaps is important for identifying populations at higher risk and for establishing baseline exposure estimates that can guide public health interventions and future control efforts, including vaccine evaluation. North-Central Nigeria, which includes states such as Benue, Kogi, Nasarawa, and Plateau, as well as the Federal Capital Territory (FCT), is characterised by diverse ecological settings ranging from rural agrarian communities to

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rapidly expanding urban centres. Several of these states have reported confirmed Lassa fever cases during recent outbreaks, suggesting sustained viral circulation within the region. Nevertheless, community-level data describing the distribution of LASV exposure across these settings remain limited. To address this gap, the present study analysed baseline data from a community-based cross-sectional survey conducted across five states in North-Central Nigeria (Benue, Kogi, Nasarawa, Plateau, and the FCT). The objectives were to: (1) estimate the seroprevalence of LASV-specific IgG and IgM antibodies among community residents; (2) explore sociodemographic, environmental, and behavioural factors associated with seropositivity; and (3) generate evidence to support the development of targeted and contextually appropriate public health strategies for Lassa fever prevention and control in this high-burden setting. By integrating serological testing with detailed risk factor assessment, this study aims to contribute to a clearer understanding of LASV exposure patterns in an understudied endemic region.

MATERIALS AND METHODS

Study Area: This study was conducted across five states in North-Central Nigeria: Benue, Kogi, Nasarawa, Plateau, and the Federal Capital Territory (FCT, Abuja), as shown in Figure 1. The North-Central region is characterised by diverse ecological zones, ranging from guinea savanna to derived savanna, with mixed urban and rural settlements. Agricultural activity is intensive, and peridomestic rodent infestation has been widely reported in the region, factors that may influence opportunities for exposure to Lassa virus.[18] Nigeria is divided into six geopolitical regions with 36 states and a Federal Capital Territory, which are further subdivided into Local Government Areas (LGAs) for administrative purposes.[11] The map in Figure 1 includes geographic gridlines and an inset map showing the location of the region within Nigeria.

Study Design and Setting: This analysis forms part of an ongoing longitudinal cohort study investigating the epidemiology of Lassa virus (LASV) infection in North-Central Nigeria. The present report describes findings from the initial phase of the study, comprising a community-based baseline serosurvey designed to estimate population-level exposure and inform surveillance strategies. A population-based cross-sectional study was conducted across selected communities in North-Central, Nigeria.

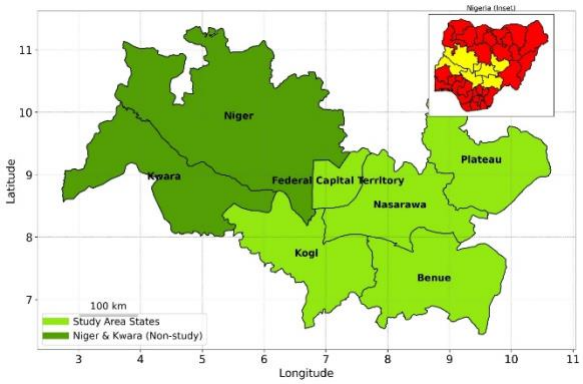

Figure 1: Spatial extent of the North-Central region of Nigeria, indicating the study states.

Ethical Approval: This study obtained ethical approval from the National Health Research Ethics Committee of Nigeria (NHREC/01/01/2007-01/09/2023).
Permission was also secured from the respective State Ministries of Health. Before community entry, we obtained informed consent from traditional leaders (village chiefs, religious leaders) and other community gatekeepers following established community engagement protocols.[11]
All participants provided written informed consent before enrollment. For minors (individuals <18 years) and temporarily incapacitated adults, consent was obtained from a legally authorised representative, with child assent obtained where applicable.[20] For participants with limited literacy, consent was documented via thumbprint after the study information was read and explained in their preferred local language by a trained translator. All study procedures were conducted in accordance with the principles of the Declaration of Helsinki.[21,23] Participant confidentiality was protected through the use of unique study identifiers and restricted data access.

Study Population and Participant Recruitment: The study population comprised apparently healthy individuals and those reporting mild symptoms, recruited from communities across the five states between January 2024 and July 2024. Both healthy and sick participants were included to ensure representation of the full spectrum of community infection. The present analysis focuses on baseline seroprevalence and associated factors among enrolled participants.[19]

Inclusion criteria: Participants were eligible if they were at least six months old, had lived in the study area for at least six months before enrollment, provided informed consent (or assent with parental or guardian consent for minors), and were willing to provide a blood sample and complete the study questionnaire.

Exclusion criteria: Participants were excluded if they refused to provide informed consent or if they had any medical, psychological, or social condition that, in the investigator's

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judgment, could interfere with study participation or follow-up.

Sample Size Determination and Sampling Strategy: Sample size was calculated using Cochran's formula[22] for cross-sectional studies, assuming a 95% confidence level and a 5% margin of error. The minimum required sample size was 384. After adjusting for a 10% nonresponse rate, the target sample size was 426 per state.[23] To enhance statistical power and account for the multistage design, we aimed to enrol approximately 430 participants per state, for a total target of 2,150 participants. It was also decided in advance to collect blood samples from 50% of the households enrolled in the study. The present analysis reports baseline data from the first 958 participants enrolled during the initial phase of the study prior to completion of recruitment across all sites. A multistage sampling technique was employed.[11,24]

In the first stage, two Local Government Areas (LGAs) were selected from each of the five states using purposive sampling. This selection was informed by recent Lassa fever surveillance data obtained from the Nigeria Centre for Disease Control and Viral Hemorrhagic Fever notification records[3], with preference given to LGAs with higher disease burden.

In the second stage, five wards were selected from each chosen LGA using simple random sampling. A comprehensive list of all wards within each LGA served as the sampling frame, and selection was carried out by balloting, ensuring that each ward had an equal probability of inclusion.

In the third stage, one community was selected from each sampled ward using simple random sampling. A list of communities within each ward constituted the sampling frame, and selection was conducted using a random number table.

In the fourth stage, household mapping was conducted within each selected community to establish a sampling frame of all eligible households. Each household was assigned a unique identification number. The sampling fraction was determined by dividing the required number of households by the total number of households in the community, and the sampling interval (k) was calculated as the inverse of the sampling fraction. Households were then selected using systematic random sampling. A random starting point between 1 and k was chosen by balloting, after which every kth household was selected until the desired sample size was achieved. In communities where a household list was not available, a systematic random walk approach was adopted. A central landmark, such as a market, school, or health facility, was identified, a random direction was chosen by spinning a bottle, and households were selected at regular intervals based on the predetermined sampling interval.

Community Engagement and Enrollment

Procedures: A structured community entry plan was implemented before data collection. Research team members, accompanied by community-based organisers and local informants, conducted sensitisation meetings with traditional elders, religious leaders, political representatives, and community-based organisations to explain the study objectives, procedures, and potential benefits.[25] Following community approval, individual households were approached, and the study was explained in detail to household heads. Willing households were geo-referenced using handheld GPS devices (Garmin, USA).[26] At the household level, trained field staff administered a standardised, pre-tested questionnaire to collect information on participants' sociodemographic, environmental, behavioural, and occupational characteristics. Sociodemographic variables included age, sex, occupation, educational attainment, and marital status. Household characteristics captured household size, number of rooms, housing materials (including roof type, wall construction, and presence of structural cracks), and the primary source of water. Participants were also asked about behavioural and cultural practices potentially relevant to exposure risk, including participation in traditional burial practices (such as washing or preparing deceased family members for burial), presence of rodents within the household, consumption of rodent meat, and food storage practices (e.g., drying food in open areas).[27] Information on occupational exposures such as farming, hunting, or healthcare work was also recorded. In addition, participants were asked about their self-reported health history, including prior diagnosis of Lassa fever, recent febrile illness, and contact with individuals known to have had Lassa fever. Questionnaires were administered in English, Pidgin English, or relevant local languages (Tiv, Idoma, Igede, Hausa, or Nupe) according to the participants' preferences, with assistance from trained translators where necessary.

Following completion of the questionnaire, trained phlebotomists collected venous blood samples under sterile conditions. For participants with difficult venous access, capillary blood was obtained via finger prick and transferred into micro collection tubes.[28] Samples were temporarily stored in cold boxes at 4–8°C in the field and transported within 24 hours to the multi-user research laboratory at the Federal University of Health Sciences, Otukpo (FUHSO) for processing. Upon arrival, samples were centrifuged at 1500 rpm for 10 minutes, after which serum and plasma were aliquoted into cryovials and stored at −80°C until shipment to the Irrua Specialist Teaching Hospital, Edo State, Nigeria, for analysis.

Laboratory Analysis

Serological Testing: Serum samples were analysed for Lassa virus (LASV) specific immunoglobulin G (IgG) and

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immunoglobulin M (IgM) antibodies using the Panadea LASV nucleoprotein (NP) IgG/IgM enzyme-linked immunosorbent assay (ELISA) kits (Panadea Diagnostics GmbH, Hamburg, Germany), in accordance with the manufacturer's instructions and established protocols.[29,30]

Briefly, ELISA plates were prepared using three capture formats to optimise antibody detection. For IgG detection, plates were coated with recombinant human FcγRIIA/CD32a (R&D Systems, Minneapolis, MN, USA) at a concentration of 8 µg/mL in phosphate-buffered saline (PBS) containing 0.01% sodium azide and incubated at 4°C for 3–5 days. In parallel, rheumatoid factor (RF)-coated plates (Medac GmbH, Hamburg, Germany) were used as an alternative IgG capture system. For IgM detection, µ-capture ELISA plates coated with anti-human IgM antibodies (Medac GmbH) were employed. All plates were washed three times with PBS containing 0.05% Tween 20 before use. For IgG detection, serum samples diluted 1:20 in PBS containing 1% Triton X-100 were mixed in a 1:1 ratio with biotinylated LASV NP antigen. A total volume of 50 µL was added per well and incubated overnight at 4 °C. For IgM detection, diluted serum (1:20) was first incubated in µ-capture plates for 2 hours at 4°C, followed by washing and incubation with biotinylated.

NP antigen overnight at 4°C.

Following antigen binding, plates were washed three times with PBS–Tween and incubated with streptavidin–horseradish peroxidase conjugate (Sigma-Aldrich, St. Louis, MO, USA) diluted 1:1,000–1:2,000 in PBS for 1 hour at 4°C. After a further wash step, 3,3',5,5'-tetramethylbenzidine (TMB) substrate was added and incubated for 10 minutes at room temperature. The reaction was terminated with 0.5 M sulfuric acid, and optical density (OD) was measured at 450 nm with a reference wavelength of 630 nm using a microplate reader. For quality control and assay standardisation, each plate included positive control sera and three representative negative sera used to establish plate-specific cut-off values. Cut-off values ranged from 0.094 to 0.457, reflecting inter-plate variability in colourimetric response. Results were expressed as the logarithm (base 10) of the sample-to-cut-off ratio ($\log_{10}$ S/CO), and samples with $\log_{10}$ S/CO > 0 were classified as seropositive.

Molecular Testing (RT-PCR): To explore evidence of active infection, all IgM-positive samples (n=11) and a randomly selected subset of 80 serum samples were tested for LASV RNA by RT-PCR.[31] RNA extraction was performed using the QIAamp Viral RNA Mini Kit (Qiagen, Germany) according to manufacturer instructions [20]. Real-time RT-PCR targeting the LASV nucleoprotein gene was conducted using the Altona RealStar® Lassa Fever RT-PCR Kit 2.0 (Altona Diagnostics, Germany) on a CFX96 Real-Time PCR Detection System (Bio-Rad, USA), following established protocols.[32,33] Positive and negative controls were included in each run.

Specimen Handling, Packaging, and Transport: All biological specimens were handled following international biosafety guidelines for Category B infectious substances[34]. Samples were packaged using a triple-layer system: (1) primary watertight, leak-proof receptacle containing the specimen, wrapped in absorbent material; (2) secondary durable, watertight, leak-proof receptacle enclosing the primary receptacle(s); and (3) outer shipping package providing physical protection and maintaining cold chain (4–8°C) during transit.[35] Samples were transported to Irrua Specialist Teaching Hospital (ISTH) Institute of Viral and Emerging Pathogens Control and Research, a WHO-accredited reference laboratory for Lassa fever diagnostics,[36] under a material transfer agreement between FUHSO and ISTH. At ISTH, samples were stored at −80°C until analysis.[29]

Data Management and Statistical Analysis: Data were double-entered into a secure REDCap database (Vanderbilt University, USA) with range and consistency checks to minimise entry errors[37]. Statistical analyses were performed using Stata version 17.0 (StataCorp, College Station, TX, USA) at a 5% significance level[38]. *Descriptive statistics:* Participant characteristics were summarised using frequencies and percentages for categorical variables, and means (with standard deviations) or medians (with interquartile ranges) for continuous variables, as appropriate.[39]

Seroprevalence estimation: LASV IgG and IgM seroprevalence estimates were calculated with 95% confidence intervals using the Wilson score method, with clustering at the household level accounted for where appropriate.[40]

Risk factor analysis: Bivariate associations between seropositivity (IgG and IgM) and potential risk factors were examined using chi-square tests (or Fisher's exact test where expected cell counts were <5) for categorical variables and t-tests or Wilcoxon rank-sum tests for continuous variables[41]. Variables with $p<0.20$ in bivariate analysis were considered for inclusion in multivariable logistic regression models[42]. Multivariable logistic regression models were constructed to estimate adjusted odds ratios (aORs) for factors associated with seropositivity. Variables with $p<0.20$ in bivariate analysis or considered biologically relevant based on prior literature were included in the initial model[11]. Model building employed a purposeful selection approach, with variables retained if they significantly improved model fit based on the likelihood ratio test or if their exclusion altered other coefficients by >15% [43]. Multicollinearity was assessed using variance inflation factors (VIF), with values >10 indicating potential collinearity concerns.[44]

Molecular analysis: RT-PCR results were reported qualitatively (detected/not detected). Due to the low

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number of IgM-positive samples, descriptive analysis only was performed for this subset.[31]

Quality Assurance: All field and laboratory staff underwent standardised training on study protocols, including ethical conduct of research, questionnaire administration, phlebotomy techniques, and biosafety procedures[45]. The ELISA assays were performed by trained laboratory scientists blinded to participant clinical and demographic data[20]. Internal quality controls (positive, negative, and calibrator controls) were included in each assay run. A subset of 10% of samples was randomly selected for repeat testing to assess reproducibility, with concordance >95% required for continued analysis[46]. External quality assurance was ensured through participation in the ISTH laboratory's proficiency testing program for Lassa fever diagnostics[36]

RESULTS

Distribution of Lassa fever Diagnosis across Study Locations: Figure 1 shows the Lassa fever diagnosis across the study locations. Among the 958 participants enrolled, only 8 individuals (0.84%) reported a previous diagnosis of Lassa fever. While Kogi State accounted for four of these cases, Benue and Nasarawa States did not report any confirmed case. FCT and Plateau State recorded 2 cases each, indicating a generally low self-reported history of Lassa fever diagnosis across the study area.

Seroprevalence and viral antigen across Study Locations: From the IgG and IgM seroprevalence results across the study locations, as displayed in Table 2, 182 respondents (19.0%) tested positive for IgG, indicating previous exposure to Lassa virus. In contrast, IgM positivity was 1.15%, suggesting that there were limited recent or acute infections at the time of the survey. IgG seroprevalence was highest in Benue State (n = 56), followed by Nasarawa (n = 31), while the lowest IgG prevalence was recorded in Kogi (n = 8) and the FCT (n = 21). For IgM, Kogi State recorded the highest seroprevalence (n = 5), while Nasarawa State recorded no IgM-positive cases. All 91 RT-PCR-tested samples (11 IgM+ and 80 random) were negative, suggesting that no virus antigen was detected.

Table 1: Table of Socio-demographic Characteristics

Demographic Characteristics	n	%
State		
Benue	118	12.3
FCT	302	31.5
Kogi	135	14.1
Otukpo	127	27.6
Plateau	276	28.8
Age	75	7.8
Under 10		
11 – 20	166	17.3
21 – 30	215	22.4
31 – 40	205	21.4
41 – 50	149	15.6
51 – 60	74	7.7
Above 60	74	7.7
Gender	442	46.1
Male		
Female	516	53.9
Occupation	117	12.2
Pupil		
Student/higher education	117	12.2
Health facility staff – direct contact with patients	19	2.0
Health facility staff – no direct contact with patients	11	1.1
Farmer	124	12.9
Trader/petty	36	3.8
Business	226	23.6
Self-employed	73	7.6
Private sector	22	2.3
Civil Servant	87	9.1
Unemployed	17	1.8
Housewife	84	8.8
Other	25	2.6

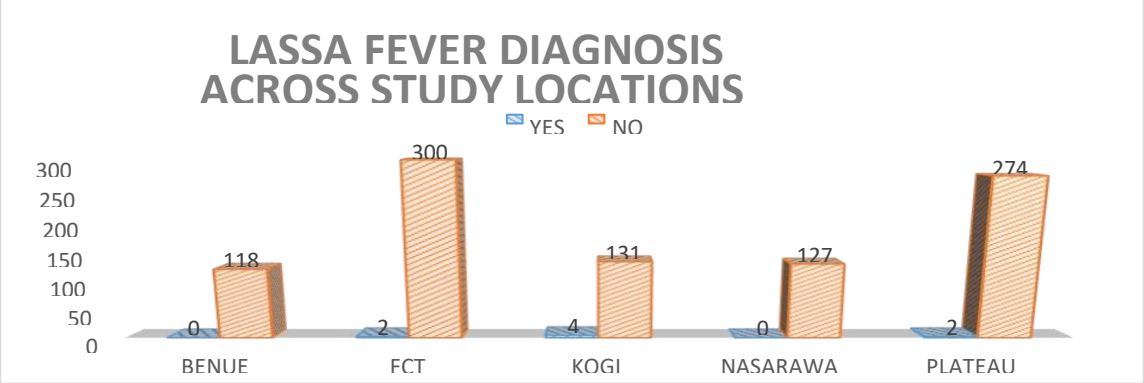

Figure 1: Lassa fever diagnosis across the study locations

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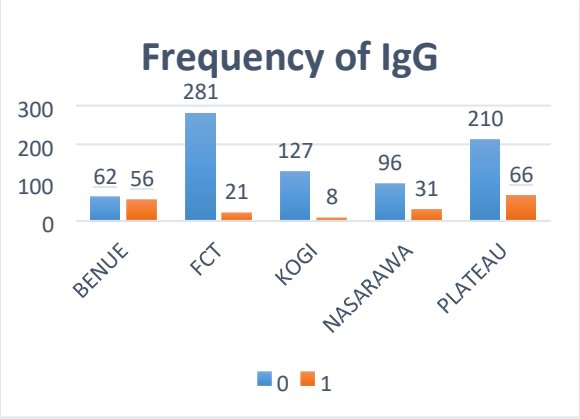

Figure 2: Frequency of IgG across locations

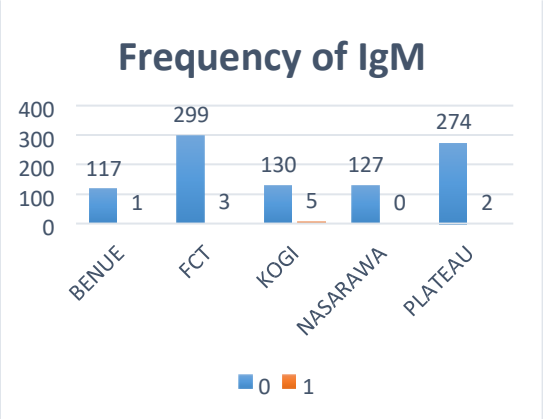

Figure 3: Frequency of IgM across locations

Multiple Logistic Regression Analysis for IgG

Table 2: Adjusted Odds Ratio (AOR) for factors associated with IgG Seropositivity

Variable	Category	AOR	95%CI	P-value
Intercept	-	0.65	0.12 – 3.51	0.619
State	Benue (Ref)	1.00	-	-
	FCT	0.07	0.03 – 0.15	<0.001
	Kogi	0.05	0.02 – 0.14	<0.001
	Nasarawa	0.18	0.09 – 0.40	<0.001
	Plateau	0.22	0.10 – 0.49	<0.001
House type (grouped)	Concrete (Ref)	1.00	–	–
	Non-concrete	2.66	1.79 – 3.95	<0.001
Sex	Female (Ref)	1.00	–	–
	Male	1.27	0.85 – 1.88	0.240
Occupation (grouped)	Healthcare (Ref)	1.00	–	–
	Other	1.31	0.40 – 4.32	0.657
	Student	0.59	0.17 – 2.06	0.406
	Working	0.80	0.26 – 2.46	0.698
Rodent burrows around house	No (Ref)	1.00	–	–
	Yes	1.54	0.77 – 3.08	0.218
Rodent consumption	No (Ref)	1.00	–	–
	Yes	0.23	0.12 – 0.44	<0.001
Burial practices (contact with corpse)	No (Ref)	1.00	–	–
	Yes	1.34	0.72 – 2.47	0.354
Ceiling present in house	No (Ref)	1.00	–	–
	Yes	1.29	0.68 – 2.45	0.428
Number of persons in household	Continuous	0.93	0.88 – 0.98	0.007
Participant age (years)	Continuous	1.01	1.00 – 1.03	0.118

overall LASV IgG

DISCUSSION

This community-based serosurvey, the most comprehensive multi-state assessment of Lassa virus (LASV) exposure in North-Central Nigeria to date, reveals several critical findings with implications for public health policy and our understanding of transmission ecology in this hyperendemic region. The seroprevalence of 19% confirms substantial historical exposure across the five studied states, while the low IgM prevalence (Figure 3) and absence of detectable viremia among tested individuals indicate sporadic, seasonal transmission rather than widespread ongoing outbreaks. Participation in traditional burial practices was explored as a potential behavioural risk factor; however, burial practices involving contact with corpses

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were not significantly associated with LASV IgG seropositivity in the adjusted analysis. While this finding may suggest a potential behavioural correlate of exposure, the cross-sectional design of this study precludes determining whether such practices represent a direct transmission pathway. Table 2 indicates key environmental and structural determinants of Lassa fever virus (LFV) exposure, as measured by IgG seropositivity, with notable geographical variation across the study area. Participants residing outside Benue State had significantly lower odds of exposure, with particularly strong reductions observed in FCT, Nasarawa, and Plateau. These findings reinforce the characterisation of Benue as a high-burden setting[47,48,49] and suggest that localised ecological and environmental conditions may play a critical role in sustaining transmission.

Housing quality emerged as a major predictor of exposure, with individuals living in non-concrete houses having nearly threefold higher odds of IgG seropositivity, as shown in Table 2. This finding is consistent with the established role of poor housing structures in facilitating rodent entry and colonisation [50,51,52]. Materials such as mud, thatch, and wood are more permeable and often contain structural gaps that increase human–rodent contact. This underscores the importance of structural interventions, including improved housing design and materials, as part of long-term LFV control strategies.[53,54]

Interestingly, rodent consumption was associated with significantly lower odds of seropositivity. While this finding appears counterintuitive given the zoonotic nature of LFV, it may reflect residual confounding, behavioural differences, or context-specific practices such as cooking methods that reduce infection risk rather than a true protective effect. Alternatively, individuals who consume rodents may differ systematically in ways not fully captured in the model, including exposure to other environmental risk factors. This finding should therefore be interpreted with caution and warrants further investigation.

Contrary to expectations, the presence of rodent burrows around households was not significantly associated with seropositivity after adjustment, suggesting that observable indicators of rodent activity may not independently capture exposure risk and that their effect may be mediated through broader structural factors such as housing quality. Similarly, burial practices involving contact with corpses were not significantly associated with IgG seropositivity, suggesting that burial-related exposures were not independently associated with cumulative LASV exposure in this analysis; however, given the absence of viral sequencing and the cross-sectional design, the relative contributions of zoonotic and human-to-human transmission cannot be determined. The lack of association with ceiling presence and occupation further supports the dominant influence of structural and environmental factors over individual socioeconomic characteristics.

Household size was inversely associated with IgG seropositivity, suggesting that individuals in larger households had slightly lower odds of exposure. While this finding is not immediately intuitive, it may reflect shared protective behaviours, differences in housing types, or dilution of exposure risk within households. Increasing age was not significantly associated with seropositivity after adjustment, although the direction of effect suggests a potential cumulative exposure pattern that did not reach statistical significance in this model.

These findings emphasise that LFV exposure is driven primarily by modifiable environmental and structural determinants, particularly housing quality and geographical context.[55] Public health interventions should therefore prioritise improvements in housing infrastructure, enhanced environmental sanitation, and targeted control efforts in high-risk areas such as Benue State. A comprehensive One Health approach that integrates human, animal, and environmental perspectives will be essential for sustainable control of Lassa fever in endemic regions. A key strength of this study is its large, community-based sample across multiple states, combined with robust laboratory confirmation and multivariable analysis, enabling reliable identification of factors associated with Lassa fever virus exposure. Such integrated perspectives will be essential for sustainable control of Lassa fever in endemic regions.

This study has limitations. A pilot study was not conducted before data collection, which may have limited the opportunity to identify and address potential issues with the questionnaire and study procedures. Its cross-sectional design precludes causal inference, and self-reported data are subject to recall and social desirability biases. The small number of IgM-positive cases limited analysis of recent infection. The absence of concurrent rodent sampling restricts our ability to directly link human seroprevalence with local reservoir dynamics, and the lack of viral sequencing restricts inference on transmission pathways; thus, the relative contributions of zoonotic and human-to-human transmission could not be determined. Although we employed a standardised assay with high sensitivity and specificity, cross-reactivity with other arenaviruses cannot be entirely excluded. Finally, while the sample was large and multi-state, it may not be fully representative of all communities in the region.

Implications for Policy and Future Research

These findings carry several implications for Lassa fever control in North-Central Nigeria and similar endemic

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settings. First, the lack of a significant association between burial practices involving corpse contact and LASV IgG seropositivity highlights the need for further investigation into the role of social and cultural practices in exposure risk, particularly given evidence that adherence to modern burial practices is associated with significantly improved infection control behaviours compared to traditional rituals involving close contact with the deceased[56]. If confirmed in longitudinal or outbreak studies, these findings could inform community-based prevention messaging.[29,57,58] Such interventions must be co-developed with community leaders, traditional rulers, and religious authorities to ensure cultural sensitivity and acceptance.

Second, the geographic heterogeneity in seroprevalence underscores the need for spatially targeted interventions. High-burden areas such as Benue State may warrant enhanced surveillance, prioritised rodent control, and consideration as priority sites for future vaccine trials.[59] Understanding the relative contributions of different transmission pathways is also critical for vaccine strategy design, as populations experiencing higher levels of secondary transmission may derive disproportionate benefit from immunisation compared to those where exposure is predominantly driven by sporadic zoonotic spillover. Conversely, lower-burden areas might benefit from strengthened surveillance to detect emerging hotspots.

Third, the weak association with self-reported rodent presence reinforces calls for more objective measures of human-rodent interaction in epidemiological studies. Future research should integrate household-level rodent trapping, environmental sampling, and geospatial analysis to better characterise exposure pathways.[60,61]

Fourth, the observed association between rodent consumption and lower odds of seropositivity, while requiring confirmation, suggests that public health messaging should emphasise reducing peridomestic rodent contact through improved housing and food storage rather than simply discouraging rodent meat consumption, which may be culturally important and, if properly cooked, may not represent the primary pathway of exposure.[60]

Fifth, the absence of detectable viremia despite substantial IgG seroprevalence highlights the importance of serological surveillance for understanding true population exposure. Reliance on clinical case counts alone dramatically underestimates infection burden and may misdirect resources toward outbreak response at the expense of prevention.[60]

From a public health perspective, although burial-related exposures were not significantly associated with seropositivity in this study, behavioural and social factors may still interact with environmental determinants in shaping exposure risk and warrant further investigation.

CONCLUSIONS

This study demonstrates that Lassa fever virus exposure is primarily driven by environmental and structural factors, particularly geographical location and housing conditions. Living in non-concrete houses and residing in high-burden areas such as Benue State were significant predictors of IgG seropositivity, while larger household size and rodent consumption showed inverse associations. These findings highlight the importance of targeted, context-specific interventions, including improvements in housing quality and intensified control efforts in endemic regions. Strengthening environmental sanitation and adopting a One Health approach will be critical to reducing the burden of Lassa fever in affected communities. Further multidisciplinary studies integrating ecological, behavioural, and genomic data will be essential for clarifying the relative contributions of different transmission pathways. Future research should combine serosurveys with ecological sampling, geospatial analysis, and qualitative methods to elucidate the complex, multifactorial drivers of LASV transmission and to design effective, contextually appropriate interventions. As Lassa fever continues to expand geographically and vaccine candidates advance toward clinical trials, understanding true population exposure and its determinants becomes ever more critical for outbreak prediction, intervention targeting, and eventual vaccination strategies.

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REFERENCES

1. World Health Organization. Lassa fever fact sheet. Geneva: WHO; 2025.
2. McCormick JB, Fisher-Hoch SP. Lassa fever. In: Oldstone MBA, editor. Arenaviruses I. Berlin: Springer; 2002. p. 75–109.
3. Nigeria Centre for Disease Control. Lassa fever situation report 2024. Abuja: NCDC; 2024.
4. Monath TP, Newhouse VF, Kemp GE, Setzer HW, Cacciapuoti A. Lassa virus isolation from Mastomys natalensis rodents during an epidemic in Sierra Leone. Science. 1974;185(4147):263–5.
5. Happi AN, Olumade TJ, Ogunsanya OA, Sijuwola AE, Oguzie JU, Oluniyi PE, et al. Increased prevalence of Lassa fever virus-positive rodents and diversity of infected species during human Lassa fever epidemics in Nigeria. Microbiol Spectr. 2022;10(4):e0036622.
6. Omotehinwa TO, Edegbene AO, Audu O, Abah SO, Shittu OS, Agbo EB, Ujah IAO, Idoko JA, Anejo-Okopi J. Modelling household, behavioural, and environmental determinants of Lassa virus exposure using formative risk indices. Zoonotic Dis. 2026; 6:8. doi:10.3390/zoonoticdis6010008.
7. Edegbene AO, Omotehinwa TO, Anejo-Okopi J, Yaagoubi SE, Shittu OS, Audu O, et al. Serological evidence of Lassa virus exposure in non-Mastomys small mammals within a hyperendemic region of North-Central Nigeria: a pilot study. Viruses. 2025;17(10):1368.
8. Bamidele OO. Epidemiology of Lassa fever in Nigeria, 2015–2025: a descriptive study. J Infect Dis. 2025;1(9):1–9.
9. Eneh SC, Obi CG, Ephraim IU, Okon IJ, Udom GU, Bassey IA, et al. The resurgence of Lassa fever in Nigeria: economic impact, challenges, and strategic public health interventions. Front Public Health. 2025; 13:1574459.
10. Asogun D, Arogundade B, Unuabonah F, Oladipo EK, Ogunlade S, Fowotade A, et al. Review of the epidemiology of Lassa fever in Nigeria. Microorganisms. 2025;13(6):1419.
11. Tiamiyu AB, Adegbite OA, Freides O, Ogunleye OO, Afolabi MO, Okoeguale J, et al. Seroprevalence and risk factors for Lassa virus infection in South-West and North-Central Nigeria: a community-based cross-sectional study. BMC Infect Dis. 2024;24(1):1118.
12. Nigeria Centre for Disease Control. Lassa fever situation report 2025 (week 46). Abuja: NCDC; 2025.
13. Ogundele GO, Jolayemi KO, Bello S. Lassa fever in West Africa: a systematic review and metaanalysis of attack rates, case fatality rates and risk factors. BMC Public Health. 2025;25(1):2948.
14. Moore SM, Rapheal E, Mendoza GS, Lo Iacono G, Grant DS, Schieffelin JS, et al. Estimation of Lassa fever incidence rates in West Africa: development of a modelling framework to inform vaccine trial design. PLoS Negl Trop Dis. 2025;19(7):e0012751.
15. Richmond JK, Baglole DJ. Lassa fever: epidemiology, clinical features, and social consequences. BMJ. 2003;327(7426):1271–5.
16. Ogbu O, Ajuluchukwu E, Uneke CJ. Lassa fever in West African sub-region: an overview. J Vector Borne Dis. 2007;44(1):1–11.
17. Gabriel M, Adomeh DI, Ehimuan J, Oyakhilome J, Ogbaini-Emovon E, Olomu SC, et al. Development and evaluation of antibody-capture immunoassays for detection of Lassa virus nucleoprotein-specific immunoglobulin M and G. PLoS Negl Trop Dis. 2018;12(3):e0006361.
18. Fichet-Calvet E, Rogers DJ. Risk maps of Lassa fever in West Africa. PLoS Negl Trop Dis. 2009;3(3):e388.
19. Kayem ND, Okogbenin S, Okoeguale J, Asogun D, Akhideno P, Okonofua M, et al. Seroepidemiology of Lassa virus in pregnant women in Southern Nigeria: a prospective hospital-based cohort study. PLoS Negl Trop Dis. 2023;17(5):e0011350.
20. Abongwa LE, Njefi K, Tamanjong CD, Nfor EG, Ashu NE, Nchang WA, et al. Detection of Immunoglobulin G and/or IgM antibodies specific for Lassa virus among HIV patients in the Northwestern region of Cameroon. Virol J. 2025;22(1):125.
21. World Medical Association. World Medical Association Declaration of Helsinki: ethical principles for medical research involving human subjects. JAMA. 2013;310(20):2191–4.
22. Cochran WG. Sampling techniques. 3rd ed. New York: John Wiley & Sons; 1977.
23. Lwanga SK, Lemeshow S. Sample size determination in health studies: a practical manual. Geneva: World Health Organization; 1991.
24. Dimas HJ, Sambo NM, Ibrahim MS, Ajayi IO, Ajumobi OO, Nguku PM, et al. Coverage of indoor residual spraying for malaria control and factors associated with its acceptability in Nasarawa State, North-Central Nigeria. Pan Afr Med J. 2019;33:84.
25. Tindana PO, Singh JA, Tracy CS, Upshur RE, Daar AS, Singer PA, et al. Grand challenges in global health: community engagement in research in developing countries. PLoS Med. 2007;4(9):e273.
26. Eisen L, Eisen RJ. Using geographic information systems and decision support systems for the prediction, prevention, and control of vectorborne diseases. Annu Rev Entomol. 2011;56:41– 61.

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27. Bonner PC, Schmidt WP, Belmain SR, Oshin B, Baglole D, Borchert M. Poor housing quality increases risk of rodent infestation and Lassa fever in rural communities of Sierra Leone. Am J Trop Med Hyg. 2007;77(5):954–8.
28. World Health Organization. WHO guidelines on drawing blood: best practices in phlebotomy. Geneva: WHO; 2010.
29. Gabriel M, Adomeh DI, Ehimuan J, Oyakhilome J, Ogbaini-Emovon E, Olomu SC, et al. Development and evaluation of antibody-capture immunoassays for detection of Lassa virus nucleoprotein-specific immunoglobulin M and G. PLoS Negl Trop Dis. 2018;12(3):e0006361.
30. Bundo K, Kato H, Yamada K, Nwafor CD, Umeokonkwo CD, Anjorin OO, et al. Seroprevalence of Lassa virus in healthcare workers and community members in Nigeria. J Infect Dis. 2023;228(5):612–20.
31. Asogun DA, Adomeh DI, Ehimuan J, Odia I, Hass M, Gabriel M, et al. Molecular diagnostics for Lassa fever at Irrua Specialist Teaching Hospital, Nigeria: lessons learnt from two years of laboratory operation. PLoS Negl Trop Dis. 2012;6(9):e1839.
32. Nikisins S, Rieger T, Patel P, Müller R, Günther S, Niedrig M. International external quality assessment study for molecular detection of Lassa virus. PLoS Negl Trop Dis. 2015;9(5):e0003793.
33. Olschlager S, Lelke M, Emmerich P, Panning M, Drosten C, Hass M, et al. Improved detection of Lassa virus by reverse transcription-PCR targeting the 5' region of S RNA. J Clin Microbiol. 2010;48(6):2009–13.
34. World Health Organization. Guidance on regulations for the transport of infectious substances 2021-2022. Geneva: WHO; 2021.
35. International Air Transport Association. Dangerous goods regulations. 63rd ed. Montreal: IATA; 2022.
36. Irrua Specialist Teaching Hospital. Institute of Viral and Emerging Pathogens Control and Research annual report. Irrua: ISTH; 2023.
37. Harris PA, Taylor R, Thielke R, Payne J, Gonzalez N, Conde JG. Research electronic data capture (REDCap) a metadata-driven methodology and workflow process for providing translational research informatics support. J Biomed Inform. 2009;42(2):377–81.
38. StataCorp. Stata statistical software: release 17. College Station, TX: StataCorp LLC; 2021.
39. Altman DG. Practical statistics for medical research. London: Chapman and Hall; 1991.
40. Newcombe RG. Two-sided confidence intervals for the single proportion: comparison of seven methods. Stat Med. 1998;17(8):857–72.
41. Agresti A. Categorical data analysis. 3rd ed. Hoboken, NJ: John Wiley & Sons; 2013.
42. Hosmer DW, Lemeshow S, Sturdivant RX. Applied logistic regression. 3rd ed. Hoboken, NJ: John Wiley & Sons; 2013.
43. Greenland S. Modeling and variable selection in epidemiologic analysis. Am J Public Health. 1989;79(3):340–9.
44. Kutner MH, Nachtsheim CJ, Neter J, Li W. Applied linear statistical models. 5th ed. New York: McGraw-Hill; 2005.
45. World Health Organization. Laboratory quality management system: handbook. Geneva: WHO; 2011.
46. Westgard JO. Basic quality control practices. 4th ed. Madison, WI: Westgard QC; 2018.
47. World Health Organization. Benue State: WHO expands Lassa fever response with community-level outreach campaigns [Internet]. 2025 [cited 2026 Apr 4]. Available from: https://www.afro.who.int/countries/nigeria/news/benue-state-who-expands-lassa-fever-response-community-level-outreach-campaigns
48. Nigeria Centre for Disease Control and Prevention. Lassa fever situation report: Epi Week 11, 2026 [Internet]. Abuja: NCDC; 2026 [cited 2026 Apr 4]. Available from: https://ncdc.gov.ng/themes/common/files/sitreps/83306284bfecdf4a04cdebfbe7d462a8.pdf
49. Mbaave TP, Onyilo O, Echekwube PO, Swende TZ, Igbah TI. Lassa fever: patients' profile and treatment outcomes at Benue State University Teaching Hospital Makurdi, North-Central Nigeria. Adv Infect Dis. 2023;13(4):58. doi:10.4236/aid.2023.134058
50. Bonwitt J, Sáez AM, Lamin J, Ansumana R, Dawson M, Buanie J, et al. At home with Mastomys and Rattus: human–rodent interactions and potential for primary transmission of Lassa virus in domestic spaces. Am J Trop Med Hyg. 2017;96(4):935–43. doi:10.4269/ajtmh.16-0675
51. Taboe HB, Pilyugin SS, Ngonghala CN. Revealing hidden drivers of Lassa fever through a model-informed approach for reproducing and predicting disease dynamics and guiding control strategies. Sci Rep. 2025; 15:33786. doi:10.1038/s41598-025-01176-y
52. Uppala PK, Karanam SK, Kandra NV, Edhi S. Lassa fever: a comprehensive review of virology, clinical management, and global health implications. World J Virol. 2025;14(3):108405. doi:10.5501/wjv.v14.i3.108405
53. McCormick JB, Webb PA, Krebs JW, Johnson KM, Smith ES. A prospective study of the epidemiology and ecology of Lassa fever. J Infect Dis. 1987;155(3):437–44.
54. Kamara ABS, Moseray A, Fatoma P, et al. Socioeconomic and environmental predictors of Lassa fever transmission in Lower Bambara Chiefdom, Kenema District, Eastern Sierra Leone. BMC Public

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Health. 2025; 25:3710. doi:10.1186/s12889-025-24973-6

55. Madaki PD, Husaini DC, Frazzoli C, Nwokocha CR, Orisakwe OE. Understanding Lassa fever through a One Health lens: how climate, land use, and poverty shape transmission in Nigeria. The Microbe. 2026; 10:100649. doi:10.1016/j.microb.2026.100649
56. Kobie AG, Okeibunor JC, Gonah L. Risk factors and determinants of Lassa fever transmission in Eastern Sierra Leone. J Glob Health Econ Policy. 2025;5:e2025021. doi:10.52872/001c.142074
57. World Health Organization. Ebola virus disease: manual for safe and dignified burial. Geneva: WHO; 2014.
58. Tiffany A, Dalziel BD, Kagume Njenge H, Johnson G, Nugba Ballah R, James D, et al. Estimating the number of secondary Ebola cases resulting from an unsafe burial and risk factors for transmission during the West Africa Ebola epidemic. PLoS Negl Trop Dis. 2017;11(6):e0005491.
59. Asogun DA, Adomeh DI, Ehimuan J, Odia I, Hass M, Gabriel M, et al. Molecular diagnostics for Lassa fever at Irrua Specialist Teaching Hospital, Nigeria: lessons learnt from two years of laboratory operation. PLoS Negl Trop Dis. 2012;6(9):e1839.
60. World Health Organization. Lassa fever fact sheet. Geneva: WHO; 2017.
61. Salami K, Gouglas D, Schmaljohn C, Saville M, Tornieporth N. A review of Lassa fever vaccine candidates. Curr Opin Virol. 2019; 37:105–11.

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