Critical Public Health

ISSN: 0958-1596 (Print) 1469-3682 (Online) Journal homepage: www.tandfonline.com/journals/ccph20

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To cite this article: Jude Oluwapelumi Alao (2026) Public genomic visibility of Lassa virus in West Africa: mapping sequence availability, ecological risk, and surveillance gaps, Critical Public Health, 36:1, 2676344, DOI: 10.1080/09581596.2026.2676344

To link to this article: https://doi.org/10.1080/09581596.2026.2676344

CRITICAL PUBLIC HEALTH
2026, VOL. 36, NO. 1, 2676344
https://doi.org/10.1080/09581596.2026.2676344

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Public genomic visibility of Lassa virus in West Africa: mapping sequence availability, ecological risk, and surveillance gaps

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ABSTRACT

Introduction: Lassa fever is a major zoonotic infection in West Africa, but its true epidemiology is difficult to define because diagnostic access, reporting systems, and surveillance capacity vary across countries. Although substantial work has examined LASV ecology, epidemiology, diagnostics, and outbreak response, less is known about how regional burden/risk evidence aligns with publicly visible genomic data.

Theory: This study distinguishes LASV transmission risk from public genomic visibility, viewing sequence availability as the product of ecology, laboratory systems, bioinformatics capacity, governance, research partnerships, and sustained financing.

Method: Public LASV sequence metadata were retrieved from NCBI Nucleotide and summarised across 16 West African countries. Countries were classified by sequence visibility, burden/risk evidence, ecological context, and public genomic surveillance gap category. CHIRPS rainfall data were included as contextual ecological descriptors. A systematic review of 31 studies identified structural, technical, and policy barriers to LASV genomic surveillance.

Results: Public LASV sequences were identified for 9 of 16 countries, totalling 1818 validated records. Sequence visibility was highly concentrated: Nigeria accounted for 71.3% of all records, while Nigeria, Sierra Leone, Guinea, and Liberia accounted for 94.3%. Seven countries had no publicly identifiable sequences despite documented, probable, or ecologically plausible risk.

Discussion: Public LASV genomic visibility does not reflect the broader regional risk landscape. Strengthening surveillance will require integrated genomic systems linked to diagnostics, One Health surveillance, local bioinformatics capacity, equitable data sharing, and sustained long-term investment.

ARTICLE HISTORY
Received 2 April 2026
Accepted 14 May 2026

KEYWORDS
Lassa fever; genome, viral; disease outbreaks; Africa, Western; public health surveillance

Introduction

Lassa fever is a major zoonotic infection in West Africa, but its true epidemiology is still not well defined. Reported cases capture only part of the picture because clinical presentation is often non-specific, diagnostic access is uneven, and routine surveillance systems differ widely across countries. As a result, the observed distribution of Lassa fever is shaped not only by where Lassa virus (LASV) circulates, but also by where cases are recognised, tested, confirmed, reported, and investigated (Simons, 2023). This uncertainty is important for public health planning because countries with few reported cases may not necessarily have low risk; they may instead have limited diagnostic reach, weak sample referral systems, or sparse public documentation.

The ecology of LASV adds another layer of complexity. Transmission is closely linked to rodent reservoirs, particularly multimammate rats, and to environmental and social conditions that influence human-rodent contact (Balogun et al., 2020; Ogundele et al., 2025). Rainfall, vegetation, land use, agricultural activity, housing conditions, and population movement can all affect the likelihood of spillover (Redding et al., 2021). Risk-mapping studies have therefore suggested that the potential geography of LASV exposure may extend beyond the countries that dominate routine reports or

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Supplemental data for this article can be accessed online at https://doi.org/10.1080/09581596.2026.2676344.

published outbreak investigations (Aloke et al., 2023; Besson et al., 2024). However, ecological plausibility is not the same as epidemiological confirmation, and epidemiological confirmation is not the same as public genomic visibility. These distinctions are often blurred in regional surveillance discussions.

Genomic surveillance is now central to infectious disease preparedness because it allows public health systems to track viral lineages, detect cross-border movement, monitor viral evolution, validate diagnostics, and strengthen outbreak response (World Health Organization, 2022a). For LASV, this is particularly important because the virus is genetically diverse and spatially structured across West Africa (Wang et al., 2024). Publicly available sequences are therefore not just research outputs; they are part of the regional evidence base for understanding transmission and viral diversity. Yet LASV genomic data in public repositories are unevenly distributed.

This gap is unlikely to be explained by ecology alone. A country may have suitable ecological conditions, reservoir evidence, or proximity to affected neighbours, but still contribute little to public genomic databases if the surveillance pathway is weak. Case recognition, diagnostic confirmation, biosafety capacity, sequencing access, bioinformatics expertise, metadata curation, data-sharing governance, research partnerships, and funding continuity all shape whether a suspected infection becomes a publicly visible genome. In this sense, public sequence archives can reflect the geography of research capacity and data-sharing systems as much as the geography of viral circulation.

Although substantial work has been done on Lassa fever ecology, epidemiology, diagnostics, and outbreak response, these strands are often examined separately (Arruda et al., 2021; Doohan et al., 2024; Oyelayo & Alao, 2025; Takah et al., 2019). Less attention has been given to the alignment between country-level burden/risk evidence and public LASV genomic sequence visibility across the wider West African region. This is the specific gap addressed by the present study. Combining public sequence metadata, burden/risk classification, rainfall and geographic descriptors, reservoir evidence, border exposure, and a qualitative synthesis of surveillance-system barriers, this study sought to link the biological, ecological, and health-system dimensions of LASV genomic surveillance.

The aim of this study was therefore to map public LASV genomic sequence visibility across West African countries and identify where documented, probable, or ecologically plausible Lassa fever risk is not matched by publicly available genomic data. The study also examined ecological and geographic context and synthesised documented technical, structural, and policy barriers that may explain uneven public genomic visibility. In doing so, it distinguishes LASV transmission risk from public genomic representation and provides a clearer basis for identifying regional blind spots in Lassa fever genomic surveillance.

Methods

Quantitative component

Study design and scope

This study used a descriptive country-level surveillance-mapping design to assess public LASV genomic sequence visibility across 16 West African countries: Benin, Burkina Faso, Cabo Verde, Côte d'Ivoire, The Gambia, Ghana, Guinea, Guinea-Bissau, Liberia, Mali, Mauritania, Niger, Nigeria, Senegal, Sierra Leone, and Togo. Public LASV sequence records were included up to the NCBI extraction date. Because routine country-level Lassa fever reporting is incomplete and heterogeneous across the region, the analysis did not attempt to estimate annual incidence; instead, available evidence was used to classify countries into broad burden/risk groups.

Public LASV sequence metadata

Public LASV sequence metadata were retrieved from NCBI Nucleotide using the rentrez package in R with search terms for '*Lassa mammarenavirus*' and 'Lassa virus'. GenBank XML records were parsed to extract accession number, definition, organism, sequence length, source, country or geographic location, collection date, host, isolate, and isolation source. Country of origin was derived from geo_loc_name where available and otherwise from the country qualifier; collection year was extracted from

collection_date. Synthetic constructs, plasmids, vectors, recombinant or clone-only records, records without identifiable country/geographic origin, and records outside the study region were excluded.

Derived variables included country of origin, collection year, sequence presence, total sequence count, earliest and latest sequence year, host group, sequence-length category, sequence-content type, and metadata completeness. Host was grouped as human, rodent, other, or unknown. Sequence length was classified as short fragment, partial/segment, large or near-complete, or unknown. Metadata completeness was assessed using the presence of country/geographic location, collection year, host, and isolation-source information.

Country-level sequence visibility and burden/risk classification

The primary outcome was public LASV genomic sequence visibility, measured using sequence presence/absence, total public sequence count, earliest and latest collection year, and sequence records per country-year. Countries were grouped descriptively as having no sequences (0), low visibility (1–9 sequences), moderate visibility (10–99), or high visibility (≥100). These categories were used to describe public data visibility and were not intended as thresholds of surveillance adequacy.

Country-level burden/risk evidence was manually compiled from peer-reviewed literature, public health reports, and grey literature. Extracted indicators included documented human Lassa fever evidence, endemicity/risk status, recent outbreak or case evidence, reservoir/ecological evidence, and evidence strength. Countries were classified as documented or high risk, probable or possible risk, or limited public evidence. A public genomic surveillance gap category was then derived by comparing burden/risk group with sequence-visibility group: documented/high-risk countries with no or low visibility were classified as priority gaps; probable/possible-risk countries with no or low visibility as possible gaps; and countries with limited public evidence and no sequences as limited burden and sequence evidence. Moderate sequence visibility was interpreted as partial representation rather than adequate routine surveillance.

Ecological and geographic context

Rainfall, climate zone, reservoir evidence, and geographic exposure were retained as contextual descriptors. Mean monthly rainfall, rainfall seasonality, and rainfall coefficient of variation were derived from CHIRPS monthly rainfall data for 2000–2024 and summarised at country level (Funk et al., 2015). Additional descriptors included climate zone, documented reservoir evidence, border with Nigeria, border with a validated LASV sequence-reporting country, number of bordering LASV sequence-reporting countries, mainland contiguous exposure, and mainland/island status.

Data analysis

Analyses were conducted in R version 4.5.2 using R GUI 1.82 High Sierra build (8556). The analysis was descriptive and exploratory; multivariable models were not fitted because the unit of analysis was the country and the dataset contained only 16 countries. NCBI search yield, metadata completeness, sequence visibility, sequence characteristics, temporal distribution, burden/risk classification, and ecological/geographic descriptors were summarised using counts, percentages, and country-level tables. Temporal distribution was assessed by aggregating sequence records by country and collection year.

Exploratory supplementary analyses included Fisher's exact tests for binary country-level comparisons and Spearman rank correlations between sequence counts and selected contextual variables. Statistical significance was set at 0.05. The main R packages used were rentrez, xml2, readr, dplyr, tibble, stringr, purrr, ggplot2, forcats, terra, sf, geodata, and R.utils.

Qualitative component

Study design and search strategy

A systematic qualitative literature review was conducted to identify structural, technical, policy, and health-system barriers relevant to LASV genomic surveillance and public genomic visibility across the study countries. Searches were conducted in PubMed, Scopus, Web of Science, ScienceDirect, and Google Scholar

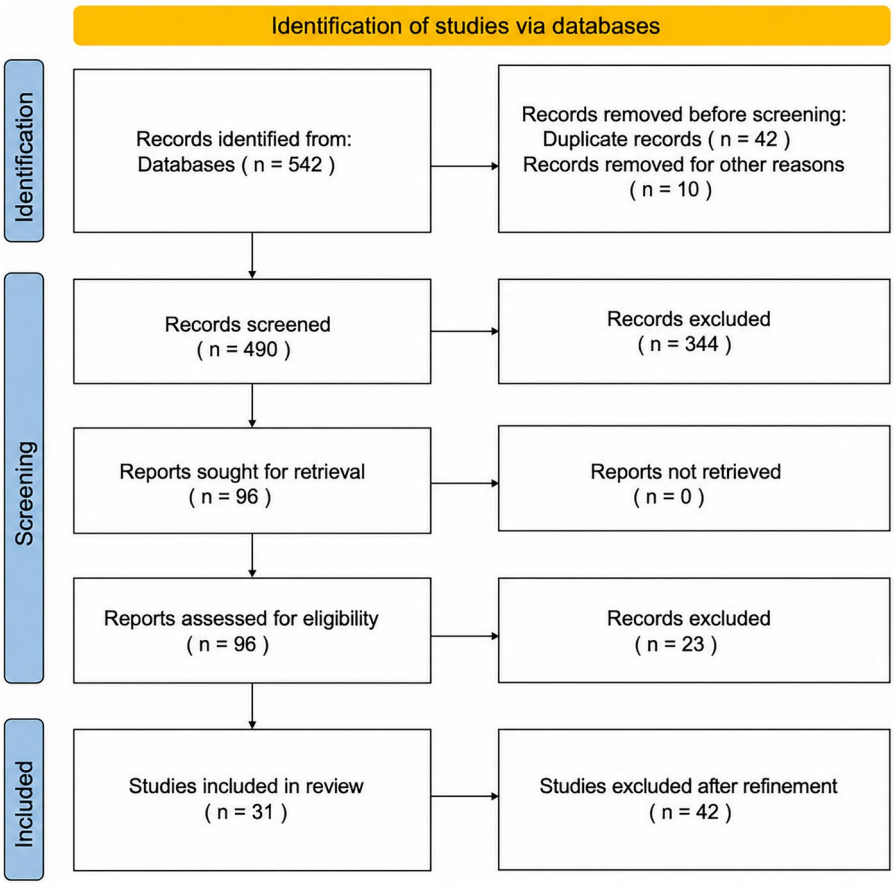

Figure 1. PRISMA flowchart for study selection in the qualitative evidence synthesis.

for English-language literature published between January 2000 and March 2026. Search terms combined LASV terms with genomics/surveillance, geographic, and barrier/capacity terms (Supplementary File 1).

Eligibility, study selection, and synthesis

Eligible sources were original empirical studies or other policy-relevant sources addressing LASV surveillance in one or more study countries and contributing evidence relevant to a predefined surveillance-related domain. Studies were excluded if they were outside the geographic scope, lacked relevance to surveillance barriers or genomic visibility, lacked sufficient methodological detail, editorials, commentaries, opinion pieces, or conference abstracts without full text. Studies focused only on therapeutics, vaccine design, clinical management, or basic virology without a direct link to surveillance capacity or genomic visibility were excluded from the present synthesis.

The selection process followed PRISMA guidance. Of 542 records identified, 31 studies were included in the final qualitative evidence base (Figure 1). Data were extracted into a structured matrix capturing study setting, methodological approach, surveillance relevance, barrier type, and implications for LASV genomic visibility, and findings were synthesised narratively across the surveillance pathway from case detection and sample referral through sequencing, bioinformatics, data governance, and public data deposition.

Results

Quantitative component

Public LASV sequence visibility across West Africa

Public LASV sequences were identified for 9 of the 16 West African countries included in the analysis, from a total of 1818 validated sequence records (Figure 2). Sequence availability was highly uneven

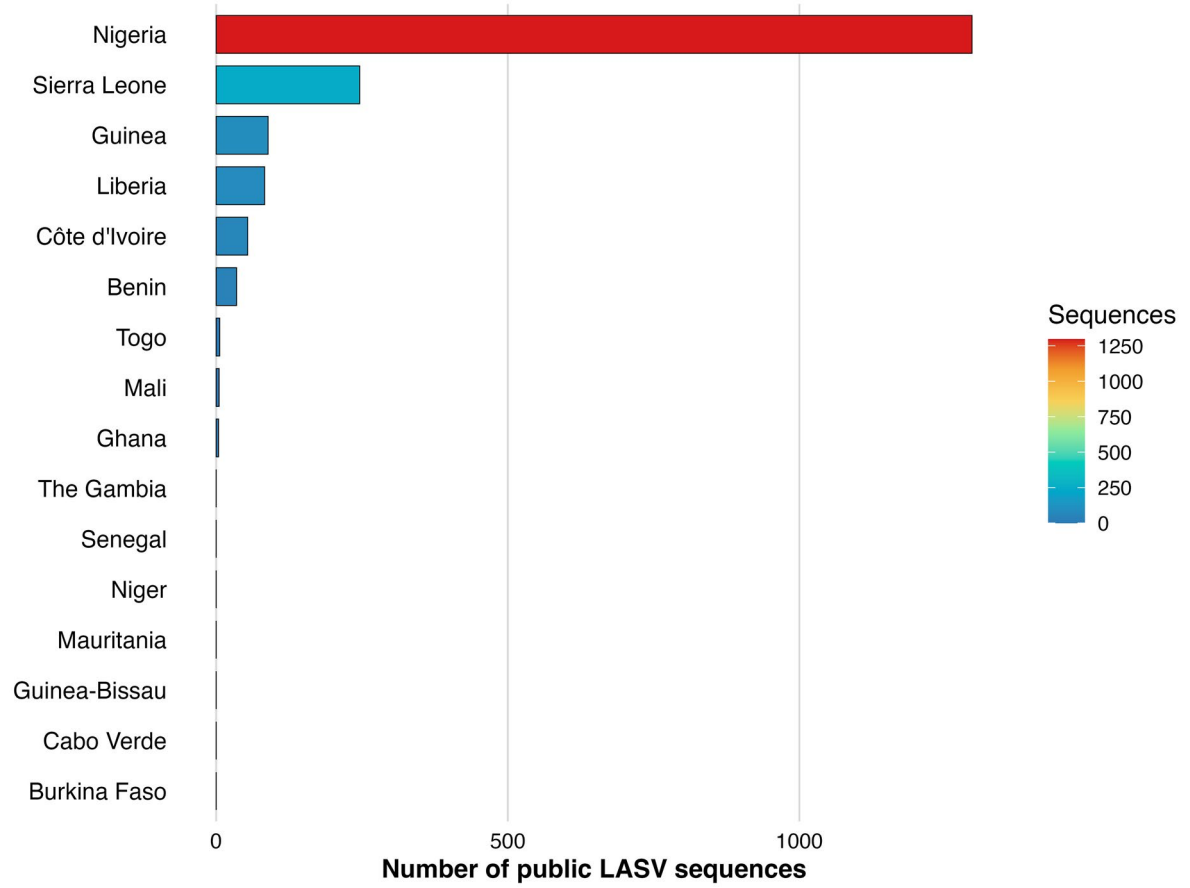

Figure 2. Public LASV sequence counts by country.

across countries, with seven countries; Burkina Faso, Cabo Verde, The Gambia, Guinea-Bissau, Mauritania, Niger, and Senegal, contributing no publicly identifiable records.

Public LASV sequence data were concentrated in a small number of countries. Nigeria alone accounted for 71.3% of all identified records, and the four most represented countries; Nigeria, Sierra Leone, Guinea, and Liberia accounted for 94.3%. The remaining five countries with any sequences collectively contributed less than 6% of the regional total. The temporal depth of available sequences also varied markedly. Nigeria had the longest apparent record (1969–2022), followed by Sierra Leone (1975–2023), Liberia (1972–2018), and Guinea (1981–2024). Countries with fewer sequences had correspondingly more restricted temporal coverage (Figure 3).

Ecological and geographic context

Country-level rainfall varied substantially across West Africa, reflecting the expected gradient from Guinea Coast to Sahelian settings. Mean monthly rainfall ranged from 8.5 mm/month in Mauritania to 211.7 mm/month in Sierra Leone (Figure 4). Most countries experienced peak rainfall between July and September, with the magnitude of the rainy season varying considerably. Rainfall coefficient of variation was highest in the more arid Sahelian countries and lowest in wetter coastal settings, consistent with the ecological classifications applied across the region.

Several countries without public LASV sequences bordered at least one sequence-reporting country, including Burkina Faso, Guinea-Bissau, Niger, and Senegal (Figure 5). Exploratory Fisher's exact tests did not identify clear associations between public sequence presence and bordering Nigeria (OR = 0.76, $p = 1.00$) or bordering any validated LASV sequence-reporting country (OR = 2.46, $p = 0.596$).

Spearman correlation analyses indicated a positive association between sequence count and mean monthly rainfall ($\rho = 0.69$, $p = 0.004$) and a negative association between sequence count and rainfall coefficient of variation ($\rho = -0.67$, $p = 0.006$); the association with rainfall seasonality was weaker and

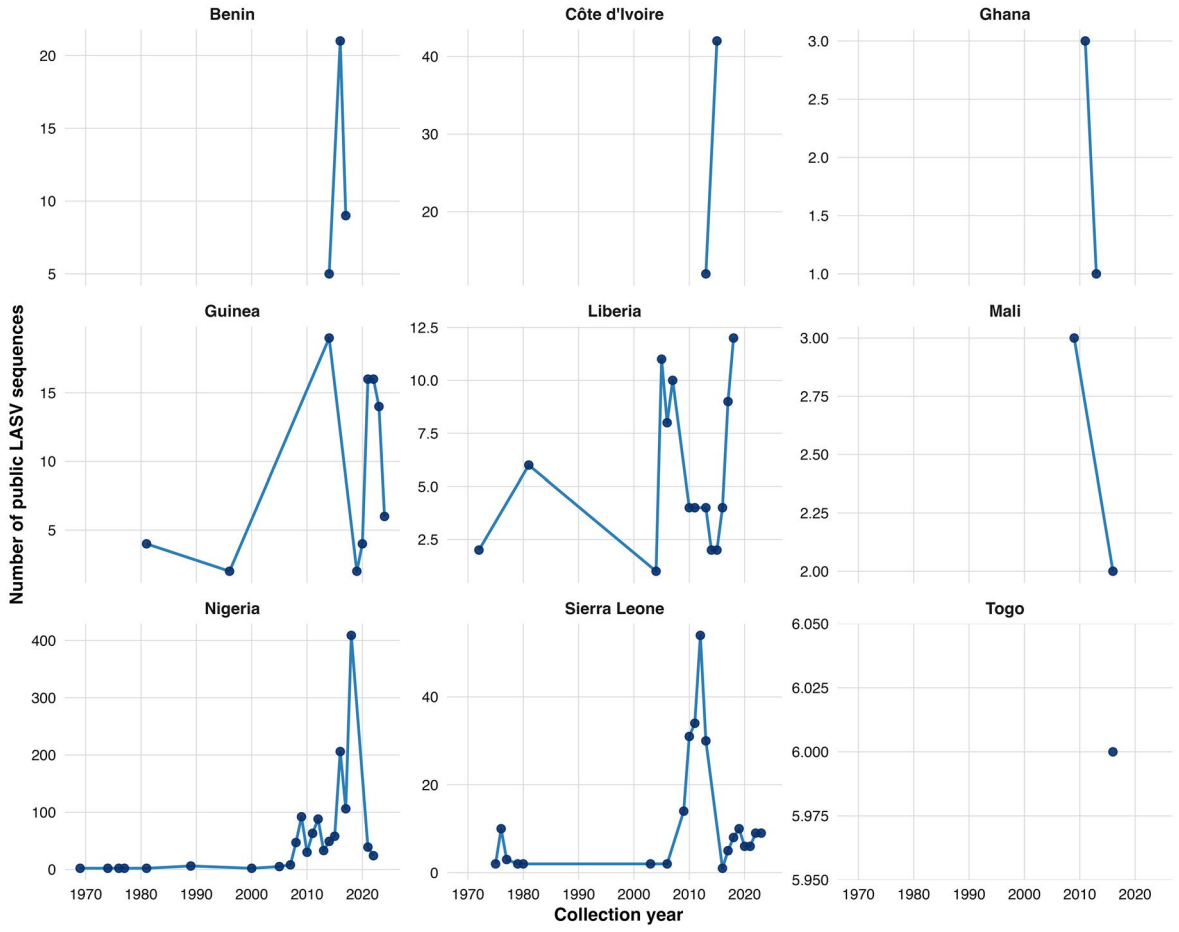

Figure 3. Public LASV sequence availability by country and collection year.

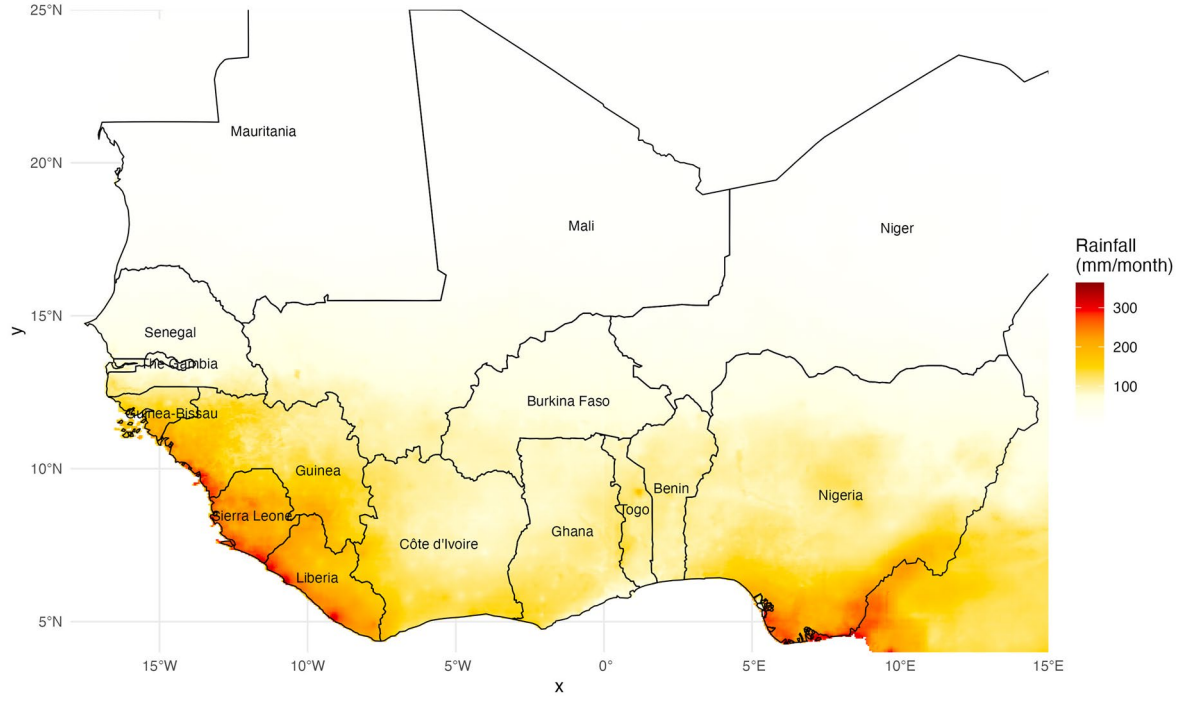

Figure 4. Long-term mean monthly rainfall across West Africa, derived from CHIRPS data for 2000–2024.

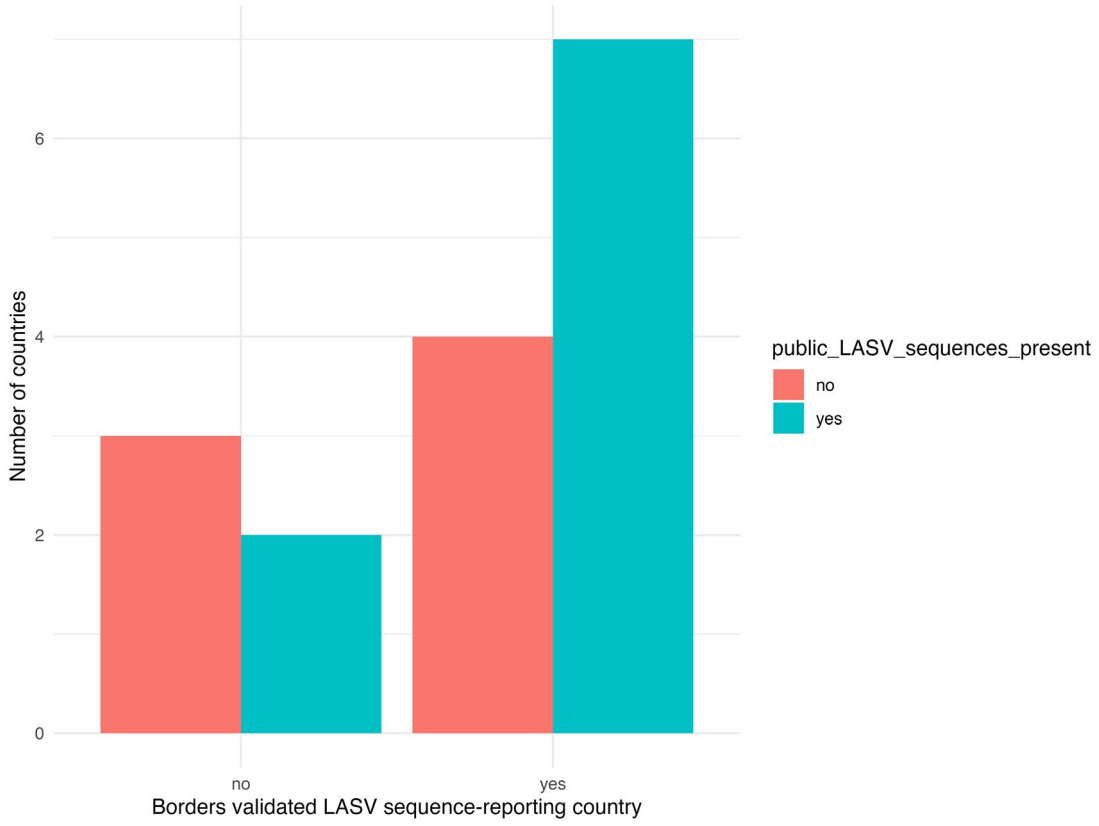

Figure 5. Public LASV sequence presence by border exposure.

inconclusive (ρ = 0.44, $p = 0.098$). The mean rainfall association persisted after excluding Nigeria (ρ = 0.75, $p = 0.002$) and after additionally excluding Sierra Leone and Guinea (ρ = 0.59, $p = 0.042$) (Figure 6).

Country-level Lassa fever burden and risk classification

Nine countries were classified as documented or high risk for Lassa fever: Nigeria, Sierra Leone, Liberia, Guinea, Benin, Côte d'Ivoire, Ghana, Mali, and Togo. Evidence was strongest for Nigeria, Sierra Leone, Liberia, and Guinea, which had documented endemicity, repeated human case reports, and reservoir or seroepidemiological support; the remaining five had confirmed or probable human or ecological evidence of moderate strength. Burkina Faso, Guinea-Bissau, Niger, and Senegal were classified as probable or possible risk based on historical, ecological, or modelling evidence alone, without repeated confirmed human outbreaks. Cabo Verde, Mauritania, and The Gambia were classified as limited evidence (Supplementary file 2; Macher & Wolfe, 2006; Fichet-Calvet & Rogers, 2009; Safronetz et al., 2013; Kouadio et al., 2015; Bonwitt et al., 2017; Patassi et al., 2017; Safronetz et al., 2017; Mateo et al., 2019; Zhao et al., 2020; Yadouleton et al., 2020; Basinski et al., 2021; Quandelacy et al., 2021; Shaffer et al., 2021; Ocansey et al., 2023; Dwalu et al., 2024; Tiamiyu et al., 2024; Akowuah et al., 2025; Mariën et al., 2025; Agboka et al., 2026; Moore et al., 2025; Seye et al., 2026). Comparing these classifications against public sequence availability identified potential genomic surveillance gaps across the region (Figure 7).

Qualitative component

Study selection and research profile

The included literature covered epidemiological, genomic, ecological, health-system, and modelling dimensions relevant to LASV surveillance. Earlier studies were concentrated in epidemiology and rodent-reservoir ecology, while diagnostics, genomics, health-system analysis, and predictive modelling became more prominent in later years. The evidence base was geographically uneven, with most studies focused on Nigeria and Sierra Leone and little or no primary-study evidence from several other countries in the study region.

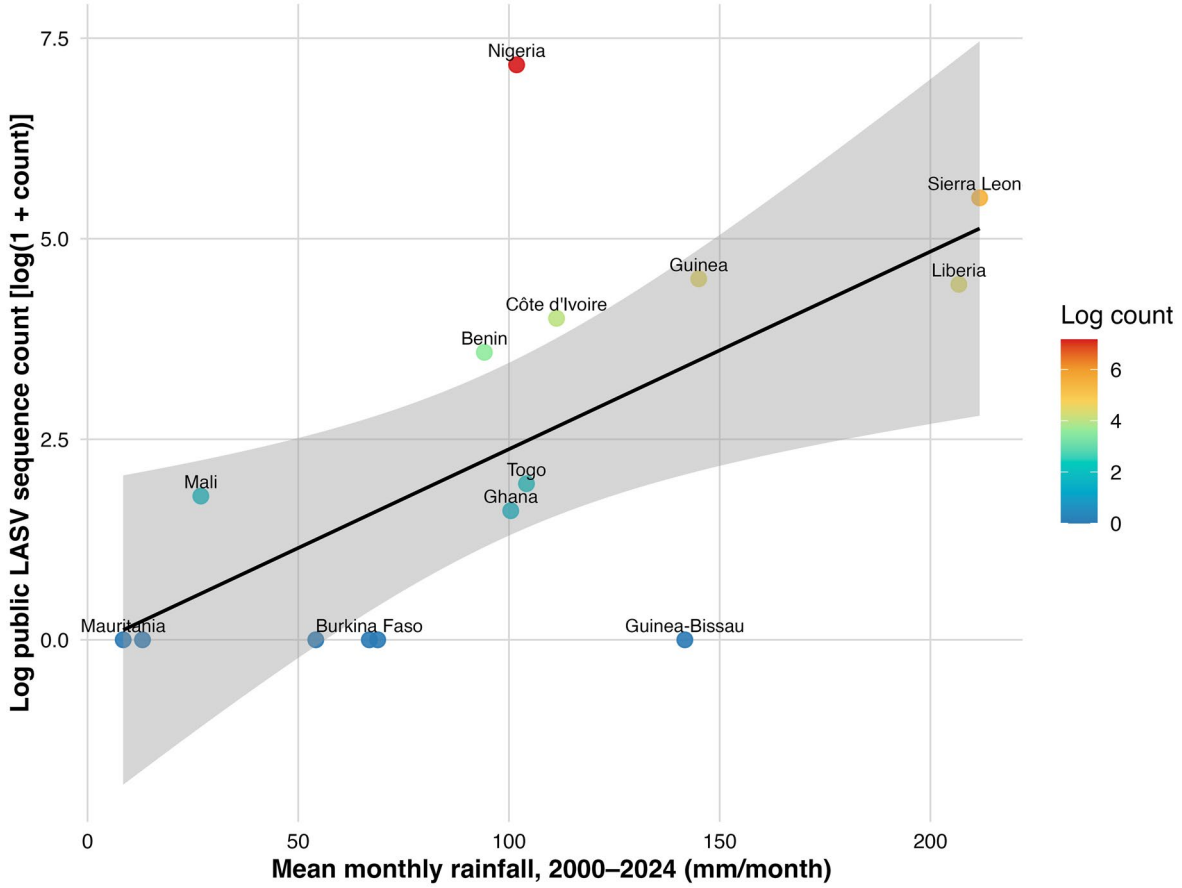

Figure 6. Exploratory association between rainfall and public LASV sequence visibility.

Epidemiology, spatial distribution, and risk mapping

The epidemiological and risk-mapping literature showed that LASV risk is geographically heterogeneous and extends beyond the most intensively studied countries. Studies in this theme used ecological niche modelling, spatial analysis, outbreak data, and phylogeography to identify broad areas of transmission risk and viral diversity (Table 1). However, several studies also showed that these outputs are affected by uneven sampling and data availability. Risk maps identified potential LASV transmission zones beyond traditional foci, while phylogeographic studies demonstrated that important viral diversity could remain undetected in countries with limited genomic surveillance.

Diagnostics, genomics, and laboratory surveillance

The diagnostic and laboratory literature showed that tools for LASV detection and genomic characterisation are available, but their implementation remains uneven across the region. The studies identified recurrent barriers including assay variability arising from LASV genetic diversity, dependence on centralised laboratories, limited cold-chain and sample-handling capacity, high reagent and equipment costs, inadequate sequencing investment, and weak bioinformatics and data-governance systems (Table 2). The literature also indicated that sequencing is commonly outbreak-driven or project-based rather than embedded in routine surveillance.

Ecological drivers, rodent reservoirs, and One Health surveillance

The ecological and One Health literature established that effective LASV surveillance requires integration of human, animal, and environmental data. Studies described rodent-reservoir ecology, household-level human–rodent contact, anthropogenic drivers of spillover, and One Health surveillance models (Table 3).

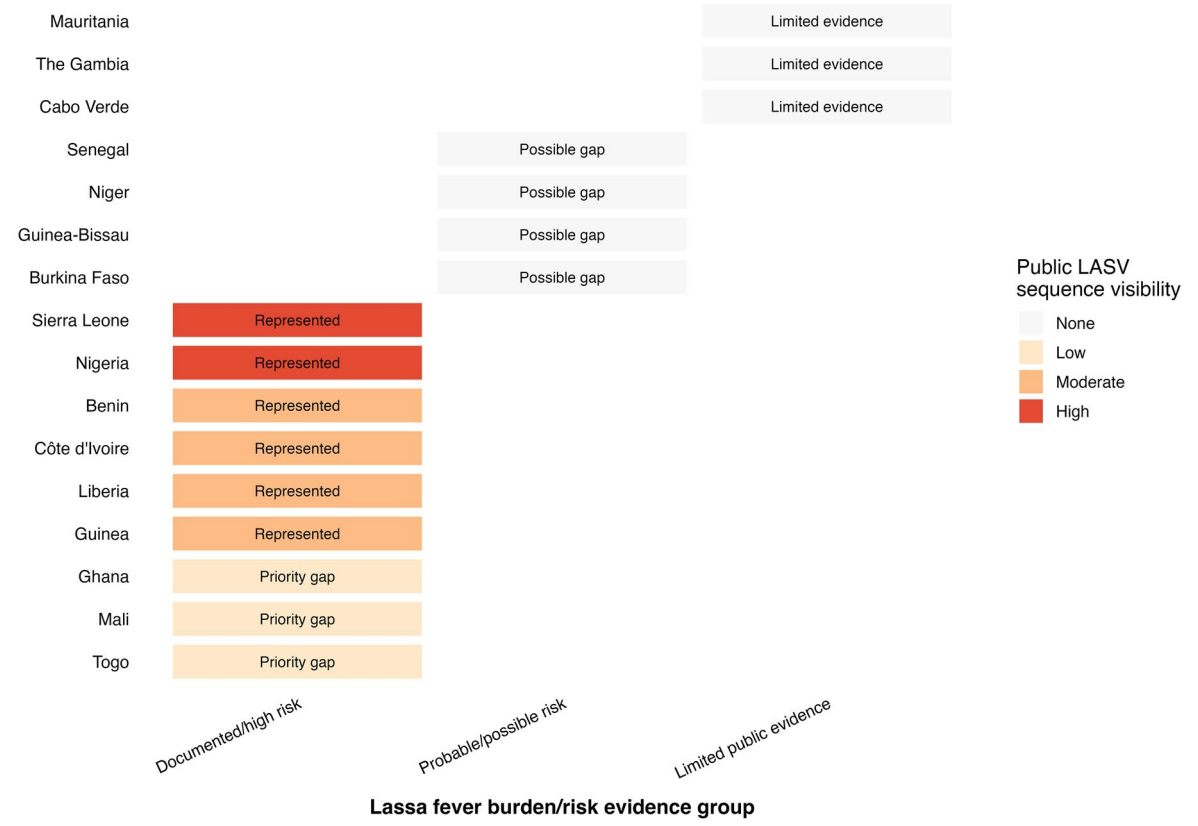

Figure 7. Public LASV genomic surveillance gaps by country.

However, integrated human–rodent–environment sampling remained uncommon and was largely confined to discrete research programmes rather than routine national systems. The evidence also showed that systematic genomic sampling of rodent reservoirs is limited, leaving public LASV sequence datasets dominated by human-derived sequences from a small number of countries.

Health systems, policy, and structural barriers

Health-system and policy barriers were the most consistently reported constraints on sustained LASV genomic surveillance. Across the included literature, recurrent barriers included limited diagnostic coverage, inadequate sample transport, weak laboratory biosafety, shortages of trained personnel, unreliable and project-dependent funding, and fragmented governance. Data-sharing constraints, unclear ownership of pathogen genomic data, and limited cross-border coordination were also repeatedly identified.

These barriers affected the entire surveillance pathway, from case recognition and sample collection through diagnostic confirmation, sequencing, bioinformatic analysis, and public data deposition. The literature further showed that LASV genomic surveillance is often reactive, externally supported, and insufficiently integrated into routine national systems, limiting continuity between outbreaks.

Predictive modelling, data analytics, and outbreak forecasting

The modelling literature showed increasing use of machine learning, mechanistic modelling, precision epidemiology, wastewater surveillance, and other data-driven approaches for LASV prediction and outbreak intelligence. These approaches can support early detection and resource prioritisation, but their performance depends on complete, timely, and geographically representative data (Table 4). Sparse surveillance, inconsistent reporting, incomplete metadata, and under-representative genomic datasets were repeatedly identified as constraints on model utility. The evidence therefore linked limited public genomic visibility not only to sequence generation, but also to downstream analytical capacity and outbreak forecasting.

Table 1. Included studies on LASV epidemiology, spatial distribution, and risk mapping.

ID	Focus area	Methodological approach	Key findings	Implications for LASV genomic surveillance	Reference
IS0	Continental risk mapping	Environmental niche modelling with *M. natalensis* occurrence and environmental data	Broad LASV risk belt confirmed from Guinea through Nigeria; risk correlated with rainfall and vegetation indices	Provides baseline spatial priorities but reflects sampling-effort bias rather than true risk distribution	(Fichet-Calvet & Rogers, 2009)
IS1	Risk map quality control	Quality control and sampling-bias weighting of occurrence records	Sampling bias distorts risk maps; areas proximate to research institutions appear disproportionately high-risk	Genomic databases may be similarly biased toward well-resourced sites, overstating sequence coverage	(Peterson et al., 2014)
IS2	Refined continental risk mapping	Boosted regression tree modelling with environmental covariates	Extended endemic potential to Mali, Ivory Coast, and Ghana beyond traditional foci	Viral lineages from these understudied areas are likely absent from or underrepresented in public databases	(Mylne et al., 2015)
IS3	Real-time outbreak genomics	Near-real-time whole-genome sequencing during 2018 Nigeria outbreak	Multiple co-circulating lineages identified; genomic data enabled real-time lineage tracking	Demonstrates feasibility and value of integrating sequencing into outbreak response; not yet routine	(Siddle et al., 2018)
IS4	Novel lineage discovery	Phylogenetic analysis of LASV isolates from Mali and Ivory Coast	A novel fifth lineage discovered; greater genetic diversity than previously recognised	Confirms that significant uncharacterised diversity exists in areas with limited surveillance infrastructure	(Manning et al., 2015)
IS5	Long-term outbreak epidemiology	Temporal and spatial analysis of 52 years of Nigerian Lassa fever outbreak data	Geographic expansion of reported cases from traditional epicentres to new states documented	Implies a growing number of distinct viral populations requiring genomic characterisation	(Agbonlahor et al., 2021)
IS6	Climate-driven risk modelling	Generalised linear modelling of climate and human factors on case distribution in Ondo State	Temperature, rainfall, and population density were significant predictors of case occurrence	Surveillance strategies should be dynamically adjusted to environmental conditions to remain representative	(Arotolu et al., 2025)

Integrated qualitative synthesis of barriers to public LASV genomic visibility

Across the five directly relevant themes, the qualitative synthesis identified five recurrent barrier domains:

1. **Laboratory and diagnostic infrastructure:** limited access to standardised diagnostics, sequencing platforms, biosafety capacity, and referral systems.
2. **Sample collection and referral systems:** incomplete clinical detection, weak transport networks, and uneven geographic sampling.
3. **Workforce and analytical capacity:** shortages of trained laboratory scientists, genomic epidemiologists, and bioinformaticians.
4. **Data governance and regional coordination:** inconsistent data-sharing policies, unclear ownership arrangements, and limited cross-border harmonisation.
5. **Sustainability of surveillance investment:** reliance on project-based or outbreak-driven funding rather than routine, nationally embedded systems.

Discussion

The central contribution of the analysis is conceptual rather than only descriptive. It suggests that Lassa fever burden and ecological plausibility are not the same thing as public genomic visibility, and the qualitative synthesis suggests that the gap between the two is structural, not accidental. In that sense, the study is not only mapping where public LASV genomes are found; it is mapping where the region is able to convert suspected transmission into shared genomic intelligence. That distinction matters because deposition in public repositories depends on much more than laboratory capability. During COVID-19, genomic surveillance in Africa often relied on hub-and-spoke referral arrangements rather

Table 2. Included studies on LASV diagnostics, genomics, and laboratory surveillance.

ID	Focus area	Methodological approach	Key findings	Implications for LASV genomic surveillance	Reference
IS7	Diagnostic platforms	Review of diagnostic challenges arising from LASV genetic diversity	Genetic diversity and lack of standardised assays create diagnostic variability across settings	Undermines comparability of surveillance data; limits case confirmation and sample forwarding for sequencing	(Mazzola & Kelly-Cirino, 2019)
IS8	Diagnostic constraints	Review of platform-specific limitations in resource-limited settings	High reagent costs, cold chain requirements, and equipment needs limit access outside national reference laboratories	Systematic underrepresentation of cases from peripheral and remote settings in sequence databases	(Hassan et al., 2020)
IS9	Pathogen genomics in Africa	Analysis of data barriers across multiple African outbreak contexts	Absent data-sharing agreements, insufficient sequencing investment, and weak governance frameworks identified	Majority of LASV genomic data generated by external groups rather than national public health institutes	(Mboowa et al., 2024)
IS10	Serological detection	Antibody detection in HIV patients in North-West Cameroon	IgG/IgM antibodies detected in a non-traditional endemic area, suggesting broader viral circulation	Indicates wider LASV exposure than case counts imply; absence of concurrent molecular confirmation limits genomic inference	(Abongwa et al., 2025)
IS11	Improved molecular detection	RT-PCR targeting conserved 5′ region of S RNA across diverse LASV lineages	Enhanced detection across lineages compared to existing assays; reduces lineage-driven false negatives	Continuous validation against circulating strains required; depends on representative sequence data from surveillance	(Ölschläger et al., 2010)
IS12	Genomic surveillance capacity in Africa	Analysis of infrastructure, funding, and human resource gaps in pathogen genomics	Persistent gaps across platforms, bioinformatics, and funding; genomic data generated reactively during outbreaks	Argues for national sequencing platforms integrated into existing disease surveillance systems	(Mwapagha, 2023)
IS13	Neuroinvasive LASV	Detection of LASV RNA in cerebrospinal fluid of paediatric patients in Edo State, Nigeria	Evidence of neuroinvasive Lassa fever in children; LASV RNA confirmed in CSF	Highlights need for expanded specimen types beyond blood to capture full pathogenesis for sequencing	(Müller et al., 2026)
IS14	Metagenomic surveillance	mNGS applied to undiagnosed febrile illness in Nigeria	Most patients had no identifiable etiological agent despite broad-spectrum sequencing	mNGS alone insufficient for LASV detection; requires optimised protocols and expanded reference databases	(Vaziri et al., 2026)
IS15	Biomarker detection	Characterisation of soluble glycoprotein 1 shedding during acute LASV infection	sGP1 detectable in blood and may serve as an early biomarker of acute infection	Could enhance case detection efficiency and sequencing prioritisation; requires cross-lineage validation	(Branco et al., 2010)
IS16	Comprehensive diagnostic review	Review of LASV laboratory diagnostic methods, advantages, and limitations	No single method sufficient for all surveillance purposes; tiered approach recommended	Tiered implementation requires coordinated laboratory networks with clear referral pathways and QA mechanisms	(Kazachinskaia et al., 2022)
IS17	Sample inactivation	Methanol fixation and Giemsa staining efficacy for LASV inactivation in blood smears	Methanol fixation inactivates LASV; Giemsa staining alone does not	Enables safer transport of samples from field sites to centralised sequencing laboratories in low-BSL settings	(Relich et al., 2020)

than evenly distributed national platforms, with some countries sequencing on behalf of others (Adepoju, 2021). The experience of variant disclosure in southern Africa suggested that rapid data sharing could carry perceived political and economic costs, reinforcing concerns about sovereignty, attribution, and downstream consequences (Christoffels et al., 2023; Moodley et al., 2022). WHO's genomic surveillance strategy was shaped by exactly this problem, it explicitly frames sequencing as one part of an end-to-end system that includes sample collection, diagnostics, data sharing, and analysis, and it treats timely access to publicly accessible sequence data as a core public-health objective (World Health Organization, 2022a). In that light, the absence of public LASV sequences should not be interpreted as proof of no surveillance activity, but it is highly policy-relevant because it marks where regional situational awareness is weakest.

A further layer is the role of externally funded research collaborations. For pathogens such as LASV, foreign-supported projects can be an important mechanism through which samples are collected,

Table 3. Included studies on LASV ecological drivers, rodent reservoirs, and One Health surveillance.

ID	Focus area	Methodological approach	Key findings	Implications for LASV genomic surveillance	Reference
IS18	Anthropogenic ecosystem surveillance	Mixed-methods observational cohort integrating human, rodent, and landscape sampling across West Africa	Landscape structure, rodent density, and human activity patterns modulate spillover risk	Provides a model for integrated human–rodent–environment genomic sampling; rare in the LASV literature	(Friant et al., 2026)
IS19	Zoonotic spillover drivers	Comparative analysis of eight viral epidemic events in Africa	Deforestation, agricultural expansion, and urbanisation are common and recurrent spillover drivers	Surveillance should monitor ecological and anthropogenic change alongside viral sequence data	(Isibor et al., 2023)
IS20	One Health framework	Review and proposal for integrated human–animal–environment LASV surveillance	Fragmented sectoral surveillance is inadequate for a pathogen as ecologically embedded as LASV	Sequencing should extend to rodent populations and environmental samples to capture full viral diversity	(Abdullahi et al., 2020)
IS21	Domestic human–rodent contact	Observational study of household-level human–rodent interactions in Sierra Leone	Construction materials, food storage practices, and daily routines significantly influence exposure probability	Genomic sampling should be stratified by household-level risk factors to improve representativeness	(Bonwitt et al., 2017)
IS22	One Health prevention strategy	Review of proactive versus reactive approaches to zoonotic disease prevention	Proactive approaches addressing ecological root causes of spillover are more cost-effective	Surveillance integration across human, animal, and environmental health sectors is structurally lacking for LASV	(Heymann & Dixon, 2013)

sequenced, and analysed, especially where domestic genomic infrastructure is still developing. However, externally enabled sequence generation does not automatically become publicly visible sequence generation. Cross-institutional collaborations may be governed by project-specific arrangements on sample export, data ownership, publication rights, intellectual property, and benefit sharing; where these arrangements are restrictive, unclear, or slow to resolve, they can delay or limit open deposition even when genomes have been generated (Amoakoh-Coleman et al., 2023; Christoffels et al., 2023; Selormey et al., 2025). This concern sits within a wider African genomics debate about equitable benefit sharing, local control over samples and data, and the need for governance models that support both collaboration and timely public-health use of pathogen sequence data (Dos S. Ribeiro et al., 2018; World Health Organization, 2022b).

The concentration of publicly visible LASV genomes in a few national systems is consequential because LASV diversity is strongly structured in space (Bangura et al., 2024; Ehichioya et al., 2019; Manning et al., 2015; Whitmer et al., 2018). In-country sequencing from Guinea further shows how quickly the apparent map of LASV diversity can change once local capacity is established (Camara et al., 2026). The implication is that public archives are liable to become maps of where sequencing systems are mature rather than maps of where viral diversity is greatest. Under these conditions, under-sequenced countries are not only 'missing data', but are also potential sources of mis-specified phylogeographic inference, understated cross-border connectivity, and under-appreciated lineage diversity.

That bias is not only an evolutionary problem. LASV is genetically diverse enough that assay performance can deteriorate when primers and probes are not repeatedly validated against the strains circulating across settings (Ölschläger & Günther, 2012). Studies have shown that sequence mismatches can contribute to false negatives and that diagnostic performance is challenged by the breadth of LASV diversity (Nikisins et al., 2015; Ölschläger & Günther, 2012). Public genomic underrepresentation can therefore feed back into case ascertainment itself. The more incomplete the regional archive, the greater the risk that divergent lineages remain both epidemiologically and diagnostically under-recognised, making public sequence concentration not only a visibility problem, but also a constraint on the accuracy of the surveillance system that generates future cases and sequences.

The rainfall signal in the study is biologically plausible, but it should be interpreted as ecological context rather than confirmation of transmission. Foundational risk-mapping work linked Lassa occurrence to rainfall gradients and other environmental variables, and subsequent analyses have shown that climate, poverty, agriculture, and urbanisation all shape where spillover and recognised disease are likely

Table 4. Included studies on LASV predictive modelling, data analytics, and outbreak forecasting.

ID	Focus area	Methodological approach	Key findings	Implications for LASV genomic surveillance	Reference
IS23	ML-based outbreak prediction	Framework integrating clinical, laboratory, and environmental data for early Lassa detection in Nigeria	Multi-stream ML integration improves predictive accuracy; implementation tested in Nigerian context	Faces challenges of data standardisation, system interoperability, and analytical capacity in endemic settings	(Ogah et al., 2026)
IS24	Mechanistic disease modelling	Compartmental model incorporating human–rodent and human–human LASV transmission pathways	Seasonal and ecological drivers identified; control strategies simulated quantitatively	Predictions sensitive to poorly constrained viral genetic diversity parameters; comprehensive genomic data needed	(Taboe et al., 2025)
IS25	Wastewater-based surveillance	Review of wastewater epidemiology for pathogens with pandemic potential	Wastewater surveillance could detect LASV before clinical cases emerge; sequencing enables lineage monitoring	Technical and infrastructure barriers substantial in West Africa; requires coordinated regional approach	(Grassly et al., 2025)
IS26	Precision epidemiology	Framework for integrating genomic, epidemiological, and environmental data for targeted control	Genomic integration enables more targeted interventions and resource allocation	Implementation requires high-quality, representative genomic data unavailable for LASV in most endemic areas	(Ladner et al., 2019)
IS27	Big data analytics	Review of big data applications for infectious disease surveillance in sub-Saharan Africa	Mobile, satellite, and social-media data can complement traditional surveillance; substantial infrastructure gaps identified	Barriers include absent digital infrastructure, shortage of data scientists, and weak data governance frameworks	(Achieng & Ogundaini, 2024)
IS28	Recursive outbreak forecasting	Recursive prediction model applied to historical Lassa fever outbreak data from Nigeria	Reasonable two-week case forecasts achieved; accuracy degrades substantially at longer horizons	Performance limited by reporting delays, underreporting, and inconsistencies in underlying surveillance data	(Okwonu et al., 2023)
IS29	Point-of-care diagnostics	Review of obstacles to POC diagnostic deployment in sub-Saharan Africa	High cost, regulatory gaps, and supply chain constraints are primary barriers to deployment	POC integration with sequencing referral networks could increase sample volume and geographic representativeness	(Ofori et al., 2024)
IS30	Class imbalance in surveillance data	SMOTE and Random Forest applied to imbalanced Lassa fever epidemic surveillance datasets	SMOTE significantly improved sensitivity for detecting true cases from imbalanced data	Model performance remains contingent on training data representativeness; existing surveillance biases are perpetuated	(Njama-Abang et al., 2025)

to occur (Fichet-Calvet & Rogers, 2009; Redding et al., 2021). WHO recognises endemic Lassa fever in a broader set of West African countries than those that dominate the public sequence archive, reinforcing that the epidemiological footprint is wider than the visible genomic one (World Health Organization, 2024). Yet, the border-exposure observations in this study are revealing. Geography alone does not self-correct surveillance inequality. Proximity to a country that generates or shares LASV genomes does not automatically translate into public visibility next door.

A sensible hypothesis would be that ecology sets the stage for spillover, while public visibility is produced by surveillance systems, research pathways, and governance. National rainfall averages can signal macroecological suitability, but they collapse the local heterogeneity that shapes rodent abundance, household exposure, diagnostic access, and outbreak detection. A study suggested that oversampling in well-studied locations can materially distort Lassa risk maps; the same logic applies to genomic databases (Peterson et al., 2014). Countries classified in this study as documented, probable, or ecologically plausible LASV settings but still sparse in public archives should therefore be treated as regional blind spots in genomic situational awareness, not as peripheral areas of low relevance.

The qualitative synthesis adds its greatest explanatory value by showing that the dominant constraints are distributed across the surveillance cascade: case recognition, specimen referral, diagnostic confirmation, biosafety, laboratory throughput, bioinformatics, metadata curation, data governance, and sustained financing. That picture is closely aligned with literature which have argued that the main challenge is not a simple 'sequencer gap' but the fragility of the systems surrounding sequencing (Christoffels et al., 2023;

Garry, 2023; Inzaule et al., 2021; Mboowa et al., 2024). The most encouraging lesson is that this fragility is not fixed. Work from Guinea shows how capacity seeded during the COVID-19 period can be integrated into a national viral haemorrhagic fever laboratory network and then redirected towards LASV (Camara et al., 2026). At continental level, Africa CDC's Pathogen Genomics Initiative, associated workforce programmes, and networked efforts such as AFROSCREEN are all explicitly attempting to turn emergency pandemic investments into more durable, multi-pathogen surveillance ecosystems (Holden, 2024; Ochola, 2025; Poublan et al., 2026).

For policy, the results of this study argue against stand-alone investment in hardware or one-off outbreak sequencing. What is needed is an end-to-end surveillance architecture linking febrile illness surveillance, viral haemorrhagic fever diagnostics, reservoir and One Health intelligence, specimen referral, in-country analysis, and routine deposition of genomes with usable metadata. A hub-and-spoke model is pragmatic for rare, high-consequence pathogens, but it must be coupled to attribution, standardised metadata, and credible benefit-sharing arrangements; otherwise, data may be generated operationally without becoming regionally visible. Several limitations should nevertheless temper interpretation. Public database absence are an underestimate of total surveillance activity, especially where referral sequencing, delayed release, incomplete metadata, or unpublished datasets are common. The ecological analyses were exploratory and country-level, so they cannot resolve subnational hotspots or separate epidemiology from research intensity. The small number of country units also limits statistical interpretation, and the qualitative evidence base, although systematically assembled was constrained by English-language publication and what is publicly documented. Even with those caveats, the central implication is robust, the regional LASV problem is not simply under-sequencing, but under-visibility in the very places where shared genomic data would most improve cross-border preparedness.

Conclusion

This study shows that public LASV genomic visibility across West Africa remains highly uneven and only partly aligned with known or plausible Lassa fever burden. The findings indicate that the regional problem is not simply the absence of sequencing, but the limited capacity to convert suspected transmission, diagnostic confirmation, and genomic analysis into publicly accessible sequence data with usable metadata. Public repositories therefore reflect not only viral ecology, but also the strength of surveillance systems, sample referral networks, bioinformatics capacity, data governance, collaboration agreements, and sustained financing. This distinction is critical because countries with sparse or absent public LASV sequences may still have ecological risk, human exposure, or undocumented surveillance activity, but remain largely invisible to regional genomic intelligence systems.

LASV genomic surveillance should be embedded as a routine component of West African viral haemorrhagic fever surveillance, not treated as an episodic research output or outbreak-only activity. Regional and national investments should prioritise end-to-end systems that link case detection, diagnostic confirmation, specimen referral, in-country or regionally coordinated sequencing, bioinformatics, metadata curation, and timely public data sharing. Hardware alone will not close the visibility gap. Sustainable progress will require clear data-sharing policies, equitable collaboration agreements, local analytical ownership, One Health sampling, and long-term financing. Without these changes, the region will continue to face a fragmented public genomic record that limits lineage tracking, diagnostic validation, cross-border preparedness, and shared situational awareness for Lassa fever.

Author contributions

CRediT: **Jude Oluwapelumi Alao**: Conceptualization, Data curation, Formal analysis, Investigation, Methodology, Validation, Visualization, Writing – original draft, Writing – review & editing.

Disclosure statement

No potential conflict of interest was reported by the author(s).

Funding

The author did not receive support from any organisation for the submitted work.

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Data availability statement

All data used in this study are derived from publicly available sources. LASV sequence data were obtained from the NCBI Nucleotide database, and ecological data were derived from the CHIRPS dataset. Country-level indicators of surveillance capacity, policy, and governance were compiled from peer-reviewed publications. The processed country-level dataset, qualitative coding sheet, and analysis scripts are available from the corresponding author upon reasonable request.

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