Supplementary File 1

Shortening outbreak-response delays: a multi-source synthesis of six lessons from Sierra Leone's 2025 clade IIb mpox response

Evidence sources, definitions, and implementation methods

This supplement documents the evidence used in the operational synthesis and defines the proposed monitoring package. Reference numbers correspond to the manuscript. Published findings are attributed to their primary reports. Practitioner experience and operational review material informed the informal expert synthesis. No new participant study or genomic analysis was conducted. The Sierra Leone Ethics and Scientific Review Committee (SLESRC) determined the work to be analysis of routine public documents and approved it on May 7, 2026 (SLESRC-099-0111-2026).

Table S1. National counts, analytical populations, and key dates

Quantity	Period / definition	Interpretation and source
44	January 10–March 5, 2025. PCR-confirmed cases in the early analysis.	Early analytic cohort, not the national year-end denominator [1].
5,096	Laboratory-confirmed comparator used in the genomic reconstruction. Its exact enumeration date is not specified in the reported comparison.	Use with the modeled 10,400 estimate only. Do not assign the final outbreak cutoff or infer the comparator date from the last sequencing date [4].
10,400 (95% HPD, 7,000–15,200)	JUNIPER estimate based on the genomic study's sampled epidemic.	Model-based infections, including unsequenced transmission. Not a direct count, identifiable missing-case list, or final national census [4].
5,328 and 56 deaths	September 26, 2025. Confirmed cases and deaths reported in the genomic article's outbreak context.	Interim national figures [4].
5,442 and 60 deaths	Reconciled national confirmed-case dataset through December 14, 2025. Situation Report 335 and Ministry of Health declaration also report 60 deaths and 5,382 recoveries.	Final national total used for Figure 1. The declaration occurred on December 15 and was announced online on December 16 [2,3].
October 25 and December 15	October 25: last case's positive laboratory diagnosis, not onset or notification. December 15: outbreak declared over.	The declaration followed 51 days after laboratory confirmation. The cited 42-day interval is a minimum criterion. All districts passed it [2,3].

HPD means highest posterior density interval. Source-specific periods and case definitions determine the denominators shown in Table S1. PCR means polymerase chain reaction.

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S1. Qualitative evidence and its scope

Design, selection, and eligibility

The source qualitative study used purposive maximum-variation recruitment in Western Area Urban, Western Area Rural, Bo, and Kenema from March 10 to August 28, 2025. Survivor eligibility required a laboratory or clinical mpox diagnosis, completed isolation, age at least 18 years, capacity to consent, and willingness to discuss the experience. Health workers were directly involved in care, laboratories, or infection prevention. Community participants lived in affected communities. Contact tracers were currently or recently involved in surveillance. People outside these eligibility groups were not included [5].

Recruitment used treatment facilities, community health workers, district teams, and community structures. It could therefore underrepresent people who avoided these settings. Published participant categories were 42 survivors, 38 health workers, 36 community members, and 24 contact tracers/surveillance officers. "Caregivers" were not a separately enumerated recruitment stratum. Among survivors, 26 were male and 16 female. Mean age was 28.4 years, range 18–52. Survivor district counts were 25 in Western Area Urban, nine in Western Area Rural, five in Bo, and three in Kenema [5].

Collection and interpretation

Eight Sierra Leonean research assistants received five days of training. Interviews used English, Krio, Mende, or Temne. Sessions were audio-recorded with permission, transcribed in the original language, and translated into English. The source reports checks through back-translation of selected transcript segments. The 94 interviews and 12 focus groups are session counts. They should not be added to, or substituted for, the 140 recruited participants [5].

The Framework Method combined Social Ecological Model and Health Stigma and Discrimination Framework concepts with emergent codes. Two analysts initially coded independently and discussed differences. Separate stakeholder matrices preceded cross-group comparison. Recruitment stopped when additional interviews did not produce new codes or meaningfully extend themes within the iterative group/district review. Weekly debriefings and reflexive memos addressed researchers' operational positions. 20 participants contributed member-checking feedback. These procedures belong to the underlying qualitative study, not to a newly conducted interview or coding exercise for this synthesis [5].

The published study provides its demographic table, COREQ checklist, interview and focus-group guides, coding framework, and extended quotations. We use its findings as reported experiences rather than quantitative estimates of how often stigma, fatigue, or isolation barriers occurred in the national population [5].

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S2. Evidence-to-lesson synthesis

Design and analytical scope

The authors developed the six lessons through informal expert consensus informed by source findings and field experience. They organized the lessons around three response intervals. After grouping the lessons, the synthesis examined source support, implementation conditions, and counter-examples. These secondary interpretive procedures adapted the approach in reference 7. They did not determine lesson selection through prespecified construct coding.

Source selection and analytical roles

We purposively selected material concerning response delays, implementation constraints, or the chronology of actions during the 2025 mpox response. The evidence groups comprised the early case analysis, national surveillance aggregates and operational documentation, the qualitative study, and genomic reconstruction [1,2,4,5]. Authors also drew on field observations, recollections, and participation in intra- and after-action reviews. Table S8 identifies named operational sources and their access routes separately from this experiential input.

Repeated situation reports form one longitudinal monitoring series. Updated cumulative counts for the same indicator and cutoff supersede earlier counts without adding independent observations. The reconciled national notification series supplies Figure 1. The early case analysis reached response leadership in March 2025. Later publications informed retrospective interpretation and were not available for early response decisions. General guidance and the implementation precedent inform methods or proposed actions, rather than national case counts.

Extraction, framework mapping, and consensus

The extraction unit is a source-supported finding relevant to a lesson. The matrix records source identity, type, period, population, finding, response interval, implementation condition, proposed action, and limits. Findings are distinguished as measured observations, reported experiences, documented activities, or model estimates. We recorded proposed safeguards separately from enabling conditions documented during the response. The synthesis used reported findings without recoding transcripts or pooling unlike participant outcomes.

The secondary CFIR mapping followed the grouping of lessons and examined five domains [9]. Innovation refers to the response practice, Inner Setting to service organizations, and Outer Setting to community and wider system conditions. Individuals covers recipients and personnel. Implementation Process covers delivery and coordination. Table S6 links these domains to the six lessons. Cross-domain connections express interpretation without statistical interaction estimates or coded co-occurrence counts.

All five authors reviewed the evidence and used field expertise to discuss differing interpretations. Informal expert consensus grouped candidate lessons into six categories, with none excluded. Each category required at least two supporting sources, a practical district responsibility, and potential relevance beyond mpox. National and regional

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dependencies remained explicit. Agreement concerned the scope and wording of lessons, while uncertainty remained attached to source findings.

Qualitative source appraisal

Table S5 applies AACODS dimensions qualitatively to the sources' evidentiary contributions [8]. Authority concerns provenance and expertise. Accuracy concerns definitions, measurement, and analytical transparency. Coverage concerns populations, places, and reporting periods. Objectivity concerns institutional and interpretive interests. Date distinguishes event, observation, and publication timing. Significance concerns relevance to the operational question. This appraisal followed lesson development and describes fitness for use without numerical scores or independent verification of source records.

Triangulation and negative-case analysis

We compared source findings for agreement, complementary explanations, and disagreement. Different evidence categories can inform the same concern while sharing some underlying observations. The early analysis, national records, and genomic publication draw partly on the same surveillance system. Findings supported by one contribution retain that scope, even when several sources inform the broader lesson. Missing documentation was distinguished from documented non-implementation.

Negative-case analysis examined findings inconsistent with simple interpretations of success or failure. Table S7 checks the decline before enhanced isolation and unmeasured diagnostic timeliness despite laboratory expansion. It also examines incomplete genomic representation and workforce strain alongside the reported tracing workload. These comparisons refine interpretation without adding intervention-effect estimates. Tables 1 and S5–S7 record the source-linked reasoning.

Reflexivity and limits

Field expertise supplied contextual knowledge of delivery conditions and feasible actions. Shared operational roles can also favour institutional explanations. The synthesis distinguishes practitioner observations, participant accounts, measured findings, model estimates, and recommendations. Counter-examples challenge simple interpretations. The work used informal consensus without independent dual coding, numerical AACODS scores, document-frequency rankings, or inter-rater statistics. It did not involve a systematic search, construct-level CFIR coding, or prospective testing of the district package.

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S3. Weekly data and reproducibility

Figure 1 uses weekly aggregates from the reconciled national mpox dataset, totaling 5,442 confirmed cases through December 14, 2025. Situation Report 335 confirms the national total on page 1 [2]. National case classifications and counts enter the analysis without additional author-level reclassification, exclusion, or duplicate removal. Cases are grouped by Monday–Sunday week of district notification, with a peak of 606 in week 19.

The notification series comes from the reconciled dataset, rather than transcription of the situation report's epidemic curve. Report 335, page 2, Figure 2, uses symptom-onset weeks and displays confirmed, probable, and suspected cases [2]. Its page 2, Figure 3, records days since the last confirmed case. Page 3 reports the nine functional testing sites. The aggregate analysis does not reconstruct the source custodian's record-level reconciliation.

For week t, the centered mean is $(N[t-1] + N[t] + N[t+1])/3$, using three complete displayed weeks. Boundary averages are omitted, and later weeks do not provide zero padding. No onset or confirmation dates are imputed. October 25 denotes the last case's positive laboratory diagnosis, separately from district notification. Supplementary File 2 supplies the weekly counts, formulas, and milestone definitions without individual records.

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Table S2. Genomic methods, uncertainty, and interpretation

Component	Reported method or result	Interpretive boundary
Sampling	338 new genomes, January 10–August 3. 14 districts. Ct ≤30 prioritized. >60% genome coverage, mean depth ≥25× [4].	Service-based selection. Neither equal district sampling nor complete coverage of the outbreak's final months.
Additional sequences	Two previously generated Sierra Leone genomes were added, giving 340. 339 were clade IIb and one clade IIa [4].	The predominant G.1 epidemic does not imply every national case was sequenced or clade IIb.
Common ancestor	BEAST nested exponential-growth model: September 27, 2024. 95% HPD August 12–November 11, 2024 [4].	Ancestor timing is not a known first patient, exact importation date, or operational 7-1-7 detection trigger.
Growth	G.1 doubling time approximately 3 weeks. 95% HPD 2.4–3.9 weeks [4].	Estimated lineage growth under the model. Not a uniform district-specific doubling time.
Time-varying reproduction	EpiFilter/Smooth on national reported case counts, serial interval 11.4 days: Rt 4.4 in early March, 95% CI 3.1–5.9 [4].	A time-specific national estimate during growth, not a whole-outbreak average or a separate estimate for every district.
Unobserved transmission	JUNIPER. Fixed mutation rate. Generation interval 11.4 days. Sojourn interval 15 days. 30,000 total iterations across two runs, 20% burn-in [4].	Inferred sampling and transmission depend on model assumptions and selected genomic observations. HPD limits do not eliminate sampling bias.
Sampling proportion	JUNIPER estimated 3.3%, 95% HPD 2.3–4.8% [4].	This is the inferred sequenced fraction of the modeled epidemic, not sequencing coverage among reported confirmed cases.
Within-country movements	Discrete phylogeography and Markov-jump reconstruction: 71 movements originating in Western Area Urban, 95% HPD 56–88 [4].	Inferred lineage transitions between districts, not individually verified journeys or independent introductions into Sierra Leone.

All genomic quantities come from Campbell and colleagues [4]. No model was refitted. Ct means cycle threshold, HPD means highest posterior density, and CI means confidence interval. The reported 6.9% differs from 338/5,328 (6.34%), and the study also describes a 340-genome analysis. Sampling dates, dataset counts, and the modeled sampling proportion are therefore reported separately. Rt denotes the time-varying reproduction number.

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Table S3. District distribution of the 338 newly generated genomes

District	Genomes
Western Area Urban	129
Kenema	46
Port Loko	39
Bo	32
Bonthe	18
Bombali	16
Tonkolili	16
Western Area Rural	15
Koinadugu	12
Kailahun	5
Kambia	4
Falaba	3
Pujehun	2
Kono	1
Total	338

Source: Campbell et al. [4], sequencing methods. Sample collection spanned January 10–August 3, 2025. Counts describe the newly generated dataset, not the two additional genomes. Geographic coverage was unequal. Month-specific counts are not reconstructed from the overall sampling period.

External sequence interpretation

The source described United States and German sequences with documented travel links to Sierra Leone for some cases. Guinea sequences were phylogenetically linked, but their travel histories were not confirmed [4]. A phylogenetic association, an inferred district transition, and a verified travel-associated infection are different kinds of evidence.

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Table S4. Prospective indicator definitions

Proposed measure	Definition and denominator	Use and caution
Onset to presentation	First encounter for the illness minus reported symptom onset. Report median/IQR and n with valid paired dates / all eligible cases.	Record recall uncertainty and care sought outside facilities. Do not infer stigma from this interval alone.
Presentation to actionable diagnosis	Acknowledgment of the diagnostic decision/result by responsible clinical and surveillance officers minus first presentation. Record both acknowledgment times.	Also report specimen collection, laboratory receipt, result authorization, and communication separately. Do not substitute confirmation date for acknowledgment.
Diagnosis to supported measures	Record each component's actual start time minus actionable diagnosis: placement, required support, and contact investigation. Preserve negative differences when measures began before diagnosis.	Classify each component as already underway, started afterward, still pending, not required, or not documented. Report components separately and time until all required components are underway.
Timely case interview	Cases interviewed within the locally specified maximum / cases requiring interview with an assessable due date.	Report missing times and refusals separately. Do not treat a refusal as a staff failure without review.
Contact follow-up completion	Contacts completing required follow-up / contacts whose follow-up was due to finish in the reporting period.	Do not use all cumulative contacts as the denominator when some remain under follow-up.
Tracing workload	Active assigned cases and contacts per available tracer, alongside staff numbers and deployment duration.	No universal caseload threshold is derived here. Adjust for travel, complexity, supervision, and work time.
Allowance payment delay	Payment date minus due date. Unresolved payments measured through the review date.	Administrative measure distinct from fatigue or burnout. Verify due dates and funding arrangements.
Genomic representation	Eligible, forwarded, sequenced, and reported specimens by district and week. Report the specific denominator at each stage.	Avoid one national percentage that conceals geographic or temporal gaps. Regional comparisons require comparable selection criteria.

The indicators are proposed for prospective evaluation. Report the eligible, assessable, and missing counts, together with the reporting period for each measure. Calculate observed intervals from paired individual timestamps. Keep missing values separate from zero, not required, and measures already underway before diagnosis. No threshold is presented as empirically validated. IQR means interquartile range.

A negative component interval denotes action before actionable diagnosis and is not automatically a data error. Preserve the signed interval and actual timestamps. For a post-diagnosis waiting measure, assign zero only when the required component was already underway, and report that status separately. Calculate waiting time until all required components are underway from the latest required start time, with zero when all were already underway. Missing start times remain missing.

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S4. Suggested implementation sequence

Assign responsibility

The district medical officer identifies the existing incident-management function responsible for each action. The health information officer maintains the analytical register and a surveillance officer serves as backup. Named staff, deputies, escalation contacts, and decision deadlines should be written into the district plan.

Establish a usable baseline

Confirm which timestamps and denominators can be recorded reliably. Begin prospective recording and review data completeness with clinical, laboratory, surveillance, logistics, and community representatives. Use the baseline to locate bottlenecks, not to legitimize unsafe delays.

Set targets and triggers

Use national standards when available. Otherwise, agree provisional performance targets and maximum acceptable intervals based on clinical urgency, travel time, and service capacity. Record the rationale and review it after initial use. A target is desired performance. A maximum is the upper acceptable delay. A trigger specifies when corrective review begins.

Cost and fund the minimum package

List staff time, communication, transport, specimen materials, household support, beds, and sequencing dependencies. Existing staff time is not cost-free. Identify the budget holder and funding source for each recurrent item. Escalate unfunded clinical or laboratory requirements through national coordination rather than assigning impossible targets to districts.

Review and evaluate

District teams should review each problem, responsible officer, action, deadline, resource requirement, and completion status weekly. Review frequency can increase during surges. Evaluate feasibility, staff burden, completeness, acceptability, and timeliness before wider adoption. A later outcome evaluation should account for concurrent interventions.

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S5. Analytical matrices

Table S5. Source roles and AACODS-informed qualitative appraisal

The qualitative appraisal examines the evidentiary contributions described in the source methods. It uses no numerical scores or independent source-record verification.

Evidence contribution and role	Authority and Accuracy	Coverage and Date	Objectivity and Significance	Implication for use
Early case analysis [1]	Response-linked epidemiological and laboratory analysis. Reported case definitions and interval summaries.	44 PCR-confirmed cases, January 10–March 5, 2025. An early cohort, not a national year-end sample.	Operationally relevant to presentation, confirmation, and contact investigation. Selection favors detected cases.	Retain observed medians and denominators. Do not infer population prevalence, subtract medians to create a diagnostic interval, or count reused surveillance records as independent evidence.
Reconciled surveillance and situation reports [2,3]	National reporting provides the case total, weekly aggregates, service activity, and declaration chronology. No new record-level validation is undertaken here.	National series through December 14, 2025. Laboratory-confirmation milestone October 25. Declaration December 15.	Implementing-agency records support chronology and workload, but reporting incentives and completeness can affect interpretation.	Treat repeated reports as one longitudinal monitoring series. Use 5,442 reconciled cases. Do not sum updated cumulative totals or equate activity counts with intervention effectiveness.
Qualitative study [5]	Reported purposive recruitment, Framework analysis, translation, and reflexivity support interpretation of participant accounts.	140 participants in four districts, March 10–August 28, 2025. Interview/focus-group sessions are not participant counts.	Multiple perspectives illuminate care seeking, support, and workforce concerns. Service/community recruitment can miss people avoiding both.	Use for reported experiences and explanations, not national frequencies or independent causal effects. Source-study coding procedures are not new procedures in this synthesis.
Genomic reconstruction [4]	Explicit sampling criteria, models, and uncertainty intervals support model-dependent inference.	338 newly generated genomes, January 10–August 3, 2025, from 14 districts. Later publication, incomplete late-outbreak coverage.	Useful for unsampled transmission and geographic uncertainty. Selected specimens and sparse regional data condition conclusions.	Preserve each analytical denominator and uncertainty interval. Distinguish inferred movements from verified travel and later knowledge from real-time evidence.
Operational reviews and practitioner experience	Incident-management documents, intra- and after-action reviews, and response expertise supply contextual accounts. They are not a newly enumerated research sample.	Experience concerns the 2025 response and its review. No item-level corpus count or independent observation schedule is assigned.	Insider knowledge helps interpret implementation and feasibility. Shared institutional positions can favor common explanations.	Use as identified contextual input. Quantitative claims remain tied to cited analyses or the national dataset. Agreement and repeated institutional accounts do not count as independent confirmation.

AACODS means Authority, Accuracy, Coverage, Objectivity, Date, and Significance [8]. Reference 7 provides the adaptation precedent. Appraisal followed lesson development and guides the scope of interpretation. Table S8 identifies named operational records separately from practitioner context.

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Table S6. CFIR-informed interpretation of the six operational lessons

The three response intervals organized the lessons. Subsequent CFIR domain mapping examined implementation conditions [9]. Documented enabling conditions and proposed safeguards remain distinct.

Lesson and interval	CFIR domains used	Reported implementation concern	Enabling condition or proposed safeguard	Cross-domain interpretation and boundary
1. Confidential care seeking Onset to presentation	Outer Setting. Individuals. Inner Setting. Implementation Process	Accounts of concealment, anticipated rejection, income loss, and delayed care. Early interval/contact summaries [1,5].	Confidential interviews, patient feedback, and support-sensitive communication are proposed safeguards, not evaluated facilitators.	Social and economic conditions interact with recipients' decisions and service encounters. Routine delay/contact measures alone do not identify stigma.
2. Sustained recognition Presentation to diagnosis. Early detection	Individuals. Inner Setting. Implementation Process	Diagnostic-journey accounts and ancestor timing raise concern about recognition before testing [1,4,5].	Standing rash-recognition, sampling, referral, and supervision arrangements are proposed.	Recognition needs a functioning route to specimens and testing. The evidence does not locate every missed infection or directly measure clinical suspicion.
3. End-to-end diagnosis Presentation to actionable diagnosis	Innovation. Inner Setting. Implementation Process	Early testing at three laboratories, later expansion to nine sites, and reported coordination constraints [1,2,5].	Expanded laboratory capacity is documented. Linked timestamps, scheduled transport, and result acknowledgment are proposed safeguards.	Testing technology and capacity depend on logistics and communication. Neither laboratory counts nor model-estimated infections measure a national diagnostic interval.
4. Supported isolation Diagnosis to supported measures	Innovation. Outer Setting. Inner Setting. Individuals. Implementation Process	Perceived bed/support barriers and household/close-contact accounts, alongside overlapping response changes [1,2,4,5].	Facility expansion is documented. Feasible placement, household support, transport, and reliable communication are proposed requirements.	A placement policy operates through service capacity and household feasibility. Acceptability accounts and chronology do not establish comparative isolation effectiveness.
5. Workforce sustainability All intervals	Individuals. Inner Setting. Implementation Process	Reported distress and allowance uncertainty alongside the cumulative tracing workload [2,5].	Surge rosters, relief teams, predictable payments, and psychosocial support are proposed safeguards.	Personnel experience depends on workload and organizational support. Fatigue, burnout, workload, and payment delay remain distinct. No independent effect on tracing quality is estimated.
6. Multilevel genomic surveillance Cross-cutting early warning	Outer Setting. Inner Setting. Implementation Process	Uneven district representation and incomplete temporal/regional sampling despite substantial genomic output [1,4].	Sequencing output is documented. Gap-based specimen referral and national/regional feedback arrangements are proposed.	District sampling requires national laboratory and regional coordination. Sequence counts alone do not establish representativeness, lineage origin, or complete transmission histories.

CFIR means Consolidated Framework for Implementation Research [9]. Reference 7 supplies the adaptation precedent. Multiple domains indicate interpretive connections, without statistical interaction estimates or document-frequency results.

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Table S7. Counter-examples and limits tested in the interpretation

Negative-case analysis examined reported chronology, observations, and gaps after the lessons were grouped. Unmeasured outcomes remain evidence gaps rather than demonstrated failures.

Interpretation examined	Discordant or qualifying evidence	Interpretation retained	Inference not supported
Enhanced facility isolation explains the decline.	Notifications declined after the week 19 peak, before the enhanced phase in week 26. Vaccination began earlier and response components overlapped [2,4].	Supported, feasible placement remains an operational concern informed by access and household accounts [1,5].	No independent effect of facility isolation, home care, vaccination, or another component is estimated. This is a chronology-based counter-example, not a comparative trial.
More laboratories establish faster actionable diagnosis.	The number of functional sites increased, but the aggregate data do not link presentation, specimen transport, laboratory result, and communication timestamps [1,2,5].	Capacity expansion and end-to-end diagnostic timeliness are different questions. Linked timestamps are needed.	The absence of linked data is an evidence gap, not proof that expansion failed or delays persisted unchanged.
A substantial genomic dataset ensures representative early warning.	338 new genomes covered 14 districts unevenly and sampling ended August 3, before outbreak closure. Regional sampling was sparse [4].	Genomic inference is informative while conditional on which places and periods were sampled.	The dataset does not establish the lineage's country of origin or complete late-outbreak/regional transmission.
A large tracing programme demonstrates a sustainable workforce.	National records show 22,536 cumulative contacts, while workers described distress and allowance uncertainty [2,5].	Operational scale and personnel experience are complementary, not interchangeable, indicators.	Cumulative contacts cannot validate staffing adequacy or quantify a causal effect of fatigue or payment delay on tracing completeness.

These checks define the limits of the lessons without introducing new participant outcomes, intervention effects, or retrospective 7-1-7 scores.

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Table S8. Operational source register for the 2025 mpox response

Named operational records are listed separately from field observations, recollections, and participation in response reviews. The latter supplied contextual knowledge without a separately enumerated document corpus.

Source / identifier	Date and custodian	Use in the synthesis	Access and provenance
Reconciled national mpox surveillance dataset. Weekly Figure 1 aggregates.	Through December 14, 2025. National Public Health Agency and Ministry of Health.	Notification-week counts, total 5,442, peak 606 in week 19. National context and Figure 1 chronology.	Weekly aggregate data accompany the article as Supplementary File 2. Individual records remain under institutional control.
Mpox Situational Report 335 [2].	December 14, 2025. National Public Health Agency.	Page 1: cases, outcomes, and contact workload. Page 2: last-case counters. Page 3: testing capacity. Lessons 3 and 5, national context.	National report. Its symptom-onset curve is separate from the district-notification series in Supplementary File 2.
In a defining moment for public health response in Sierra Leone, Health Minister declares the mpox outbreak over [3].	Declaration: December 15, 2025. Online publication: December 16. Ministry of Health.	Outbreak closure, the minimum 42-day criterion, and response context. Figure 1 chronology.	Public Ministry of Health announcement. Source URL appears in reference 3.
Sierra Leone hosts national and regional intra-action review to strengthen mpox response [6].	Published August 11, 2025. Review scheduled August 11–12 in Freetown. National Public Health Agency.	Documents review context and reported concerns about logistics, data harmonization, and surge capacity. Lessons 3 and 5.	Public agency account, used in retrospective source mapping. It is distinct from the full review report or meeting minutes.

The register identifies the national dataset and named public records. Author experience from other incident-management, intra-action, and after-action reviews remains contextual input. No count of independent written field notes or internal review documents is assigned.

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