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Research Article

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Uncovering the Drivers of Ebola Virus Disease Resurgence in DRC: A Root Cause Analysis of the 16th Outbreak in Mwaka, Kasai Province (2025)

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Abstract

Background: *The Democratic Republic of the Congo (DRC) experienced its 16th Ebola Virus Disease (EVD) outbreak in 2025, centered in the Bulape Health Zone of Kasai Province. This outbreak occurred amid multiple concurrent epidemics and in a region with limited health infrastructure. Genomic sequencing revealed a new zoonotic spillover, genetically related to the 1976 Yambuku strain.*

Methods: *A Root Cause Analysis (RCA) was conducted using the "5 Whys" framework, integrating epidemiological data, genomic analysis, and surveillance reports. Key contributing factors to delayed detection and response were identified. Comparative insights were drawn from the 2018–2020 North Kivu EVD outbreak.*

Results: *The outbreak resulted in 28 confirmed, probable, or suspected cases and 15 deaths, including four healthcare workers. Root causes included inadequate ecological surveillance, weak community alert systems, diagnostic delays due to reliance on centralized laboratories, health system overload from concurrent outbreaks, and structural underfunding of preparedness and coordination. These factors contrast with the North Kivu outbreak, where security issues primarily drove response delays.*

Conclusions: *The 2025 Mwaka outbreak highlights how ecological and systemic vulnerabilities facilitate novel Ebola spillovers and their escalation. Effective future preparedness requires sustained investment in One Health surveillance, decentralized diagnostics, and resilient public health governance to strengthen outbreak response capacities.*

Abbreviations

DRC: *Democratic Republic of the Congo*
EVD: *Ebola Virus Disease*
INRB: *Institut National de Recherche Biomédicale*
PCR: *Polymerase Chain Reaction*
RCA: *Root Cause Analysis*

Keywords: Ebola Virus Disease, Zoonotic Spillover, Surveillance, Democratic Republic of Congo, Diagnostics, Health Systems, Outbreak Response

1. Background

Ebola Virus Disease (EVD) remains a significant threat to global public health. Although its outbreaks are mostly localized to Africa, the 2014–2016 West African epidemic highlighted EVD's potential to cause international crises. Its high mortality rate, risk of international spread, and requirement for high-level containment have made it a WHO priority disease for research and response [1]. In North America, significant investments have been made into EVD vaccine research and deployment, such as the development and use of the rVSV-ZEBOV vaccine. Agencies like the U.S. Centers for Disease Control and Prevention (CDC) and the Public Health Agency of Canada (PHAC) have also contributed expert teams and resources during major outbreaks in Africa [1]. Australia has played a role primarily through funding and interna-

tional health deployments, supporting WHO emergency response missions and vaccine development [2]. In Asia, countries like China and India have extended logistical and technical support, and engaged in research collaboration and construction of healthcare infrastructure in EVD-affected regions [3].

Europe's response includes field deployments by Médecins Sans Frontières (MSF), genomic surveillance by the European Centre for Disease Prevention and Control (ECDC), and major sequencing and bioinformatics contributions from institutions such as the Institute of Tropical Medicine (ITM) in Antwerp. Africa remains the epicenter of EVD, with the Democratic Republic of the Congo (DRC) reporting 16 outbreaks since the virus was first discovered in 1976. Despite this history, the country continues to face challenges in surveillance, diagnostics, and health system resilience. The 16th outbreak in Mwaka (2025) occurred in the context of simultaneous public health emergencies—namely, mpox, cholera, and malaria—highlighting gaps in multioutbreak management capacity [4,5].

1.1. Aim

This Root Cause Analysis (RCA) aims to systematically identify and understand the upstream factors and operational failures that led to the resurgence of EVD in Mwaka, Kasai Province (2025). The findings are intended to inform sustainable health systems strengthening, outbreak preparedness, and response strategies in DRC and comparable settings.

2. Methods

2.1. Design and Framework

The RCA was conducted using the "5 Whys" method integrated with systems thinking to investigate upstream and system-level drivers of the outbreak. Data sources included Ministry of Health reports, laboratory data from the Institut National de Recherche Biomédicale (INRB), WHO bulletins, and peer-reviewed genomic and epidemiological publications [4,6,7].

2.2. Laboratory and Bioinformatics Approaches

Laboratory confirmation involved molecular diagnostics using GeneXpert, the BioFire Global Fever Panel, and the Altona RealStar Filovirus RT-PCR Kit [4]. Positive samples were sequenced on an Oxford Nanopore GridION system using R10.4.1 flow cells. The sequencing produced a 99.97% complete genome, with a 99.52% match to the 1976 Yambuku-Mayinga strain [4]. Bioinformatics tools included iVar for consensus genome generation, MAFFT for multiple sequence alignment, and IQTREE for phylogenetic inference [6,7].

2.3. Ethics Statement

This Root Cause Analysis was based on data collected through routine public health surveillance activities during an officially declared outbreak. All genomic sequencing and clinical data were anonymized in compliance with DRC national health policies and reviewed by the INRB and the Ministry of Public Health. The analysis was conducted under ethical guidelines provided by the DRC National Health Ethics Committee. No personally identifiable information was used, and genomic data are shared under pre-publication agreements [4].

3. Results

A detailed root cause analysis (see **Table 1**) identifies several critical weaknesses that contributed to the 16th Ebola Virus Disease (EVD) outbreak in the Democratic Republic of Congo (DRC). The outbreak likely originated from a zoonotic spillover event, evidenced by a 99.52% genetic similarity to the 1976 Yambuku strain and no linkage to recent human cases, highlighting an unmanaged wildlife-human interface. Surveillance systems failed to detect the outbreak early, with cases only identified after deaths—including among healthcare workers reflecting a lack of community-based surveillance. Diagnostic confirmation was delayed due to reliance on centralized laboratories in Kinshasa and the absence of regional lab capacity and cold chain logistics. Concurrent epidemics of mpox, cholera, and malaria further strained health system resources and weakened infection prevention and control (IPC) practices. Structural gaps such as fragmented preparedness and poor multisectoral coordination perpetuate the vulnerability of affected zones to repeated outbreaks.

Root Cause	Evidence	Key Weakness Identified
Zoonotic Spillover	99.52% similarity to 1976 strain; no linkage to recent cases [4]	Wildlife-human interface unmanaged
Surveillance Failure	Detected only after deaths, including healthcare workers [4]	No community-based surveillance system
Diagnostic Delay	Samples shipped to Kinshasa for confirmation [4]	No regional lab capacity or cold chain logistics
Health System Overload	Ongoing mpox, cholera, malaria outbreaks [1,8,9]	Competing resource demands, weak IPC systems

Structural Gaps	Recurrent outbreaks in the same zones [4]	Fragmented

Table 1: Root Cause Summary Table

The outbreak, officially declared on 4 September 2025, centred in Bulape Health Zone, Kasai Province, with a single suspected spillover case in the neighbouring Mweka Health Zone (see **Table 2**). The causative virus was confirmed as Zaire ebolavirus, genetically like the 1976 strain, supporting the zoonotic spillover hypothesis. A total of 28 suspected, probable, or confirmed cases were reported, with 15 deaths, resulting in a provincial case fatality rate of 53.6%. The index case, a 34-year-old pregnant woman presenting with haemorrhagic symptoms, died rapidly, triggering further transmission, including nosocomial infections. Bulape experienced a high case fatality rate of 62%, while Mweka reported one fatal suspected case, raising concerns about surveillance and containment capabilities in this isolated zone.

Metric	**Value**
Outbreak Declaration Date	4 September 2025
Virus Strain	Zaire ebolavirus
Total Cases	28 (confirmed, probable, suspected)
Total Deaths	15
Case Fatality Rate (CFR)	53.6%
Geographic Spread	Bulape (14 deaths), Mweka (1)
Healthcare Worker Deaths	4
Index Case	Pregnant woman, 34 yrs, died 25 Aug
Genomic Similarity	99.52% to 1976 Yambuku-Mayinga
Diagnostic Timeline	Samples shipped to Kinshasa for PCR and WGS

Table 2: Summary of Mwaka (Kasai, 2025) Ebola Outbreak

When compared to the much larger North Kivu outbreak of 2018–2020 (see Table 3), the Kasai outbreak was smaller in scale but similarly exposed underlying systemic weaknesses. North Kivu's outbreak was exacerbated by armed conflict and community mistrust, while Kasai's challenges were primarily geographic isolation, weak logistics, and ecological risk. Importantly, North Kivu benefited from decentralized laboratory networks and digital surveillance tools, enabling faster diagnostics and contact tracing. In contrast, Kasai relied on centralized confirmation in Kinshasa and lacked rapid detection mechanisms. Both outbreaks highlight the urgent need to strengthen multi-sectoral preparedness, including local laboratory capacity, community-based surveillance, rapid response logistics, and effective cross-zone coordination to mitigate future Ebola emergence in known hotspots.

Dimension	**Mwaka (Kasai, 2025)**	**North Kivu (2018–2020)**
Total Cases	28	3,470 confirmed and probable [WHO, CDC]
Total Deaths (CFR)	15 (53.6%)	2,287 (65.9%)
Outbreak Origin	New zoonotic spillover	Linked to the 2014–2016 West Africa strain
Security Context	Stable, remote	Armed conflict, high community mistrust
Surveillance Capacity	Weak, passive case finding	Contact tracing and digital tools used
Diagnostic Access	Centralized (Kinshasa)	Decentralized labs (e.g., Goma, Beni)

Concurrent Outbreaks	Yes – Mpox, cholera,	Minimal during the EVD peak period
Health Worker Infections	4 fatalities	>170 infected [CDC]
Community Trust	Low literacy, moderate engagement	literacy,

Table 3: Comparison: Mwaka vs. North Kivu EVD Outbreaks

4. Discussion

The 2025 outbreak was genetically distinct from recent transmission chains and was most closely related to the 1976 Yambuku-Mayinga strain [4]. This finding supports the conclusion that the outbreak was due to a novel zoonotic spillover event. Deforestation, bushmeat consumption, and increased climate-related displacement of reservoir species—particularly bats—have elevated the risk of such spillovers in forest-edge communities [10]. A One Health framework is essential to address these intersecting environmental and biological drivers. The outbreak in Mwaka was detected only after several fatalities had occurred, including among healthcare workers [4]. This indicates a critical breakdown in local surveillance systems, which failed to detect early warning signs. Traditional, topdown alert systems are not functional in remote zones like Bulape, where community mistrust and limited health education persist. Implementing trusted communication channels, mobile reporting tools, and trained community health workers can significantly improve early detection [11].

Although sequencing was rapidly completed once samples reached Kinshasa, the centralization of diagnostic infrastructure created substantial delays. Geographic remoteness, lack of regional PCR capacity, and weak cold chain logistics contributed to a delayed outbreak confirmation [4]. In contrast to North Kivu, where mobile labs were available, Bulape lacked such decentralization. Prioritizing the deployment of GeneXpert systems and biosafety-level diagnostics in provincial hubs is essential to reduce confirmation timeframes [12]. The outbreak coincided with active epidemics of mpox, cholera, and malaria, all competing for the same personnel, laboratory time, and financial resources [1,8,9]. This multi-outbreak burden overwhelmed the already fragile health system and diluted the response to the Ebola outbreak. Compounded by donor fatigue and fragmented funding, the situation underscores the importance of integrated emergency management systems and consistent funding strategies [13].

4.1. Persistent Structural Weaknesses

Despite multiple EVD outbreaks in the DRC over the past two decades, health system resilience remains weak. The recurrence of outbreaks in similar geographic zones demonstrates the absence of sustained investment in preparedness, poor intersectoral coordination, and limited local ownership [14]. Emergency interventions alone are not sufficient. Long-term solutions require the institutionalization of public health training, the development of regional genomic labs, and governance reform to support decentralized outbreak response.

5. Conclusion

The 2025 Mwaka outbreak of Ebola Virus Disease reveals that zoonotic spillovers remain a pressing threat, particularly in areas marked by ecological fragility and weak public health systems. Although DRC has made strides in genomic surveillance and rapid outbreak declaration, diagnostic centralization, poor surveillance, and inadequate system resilience continue to hinder response efforts. Effective future containment will require localized outbreak detection, decentralized diagnostic capacity, and a coordinated One Health strategy to manage ecological and structural risks sustainably.

Declarations

Ethics approval and consent to participate

This Root Cause Analysis was conducted based on data collected through routine public health surveillance activities during an officially declared outbreak. All genomic sequencing and clinical data were anonymized and handled in accordance with the Democratic Republic of Congo's national health policies. The study was reviewed and approved by the DRC National Health Ethics Committee. Individual informed consent was waived due to the use of de-identified secondary data collected for public health purposes.

Consent for publication

Not applicable. This manuscript does not contain any person's data in any form.

Availability of data and materials

All data generated or analyzed during this study are included in this published article and its supplementary information files. Genomic sequence data are available under pre-publication agreements and can be accessed upon reasonable request to the corresponding author.

Competing interests

The authors declare that they have no competing interests.

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Authors' contributions

MJP conceived the study, conducted the root cause analysis, and drafted the manuscript. MJP contributed to data collection and epidemiological analysis. INRB performed genomic sequencing and bioinformatics analysis. All authors critically reviewed and approved the final manuscript.

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