

Bundibugyo virus and the cognition gap: rethinking epidemic preparedness in the era of regionalised outbreaks



The 2026 emergency caused by the Bundibugyo virus (BDBV)¹ marked a turning point in the history of filovirus preparedness. This emergency represents only the third documented human BDBV outbreak, following those in Uganda in 2007–08 (131 cases, 42 deaths) and in DR Congo in 2012 (38 cases, 13 deaths).² For the first time, BDBV is associated with an outbreak that rapidly reached regional proportions and required the declaration of a public health emergency of international concern. Unlike Ebola virus, which was responsible for the devastating 2018–20 North Kivu epidemic and most previous outbreaks in DR Congo,² BDBV remains characterised by a substantial therapeutic gap in terms of authorised vaccines and validated, specific treatments. Similarly, effective medical countermeasures are absent for the Sudan virus, which caused recurrent outbreaks in Uganda over the past two decades, including the 2022 and 2025 epidemics.³

Two monoclonal antibodies (Inmazeb and Ebanga)⁴ that improved survival during the North Kivu outbreak were developed specifically against Ebola virus glycoproteins, and their activity against BDBV remains unknown. Although historical case-fatality rates for BDBV range from 30% to 50%, the apparent rate observed in the current outbreak might reflect, at least partly, a detection bias towards more severe clinical presentations, rather than greater intrinsic virulence. Our Bayesian phylogenetic analysis (appendix), conducted on all BDBV genome sequences freely available in the Pathoplexus Database as of May 16, 2026, revealed two main clades, corresponding to historical outbreaks in Uganda (UGA clade, 2007) and DR Congo (COD clade, 2012), highlighting clear geographical and temporal segregation of the viral lineages characterised to date and evolutionary continuity with the Congolese lineage. In the absence of evidence supporting independent zoonotic introductions, new genome sequences are likely to fall within or near the historical COD clade.

This phylogenetic uncertainty is compounded by substantial clinical and epidemiological challenges. The initial manifestations of BDBV are indistinguishable from other endemic febrile illnesses in eastern DR Congo, delaying case recognition. The index case, a nurse who presented in

Bunia on April 24, 2026, was not identified for over 3 weeks. By that point, transmission chains had already spread through Ituri's mining, commercial, and displacement networks, reaching Kampala in Uganda and Kinshasa. The imported case in Kampala and the suspected cases in Kinshasa show that transmission outpaced institutional visibility. The ongoing armed conflict in Ituri has further fragmented surveillance and limited access in the field.

Historically, epidemic preparedness has been conceptualised primarily through a biological framework focused on pathogen identification, diagnostics, and contact tracing. The current outbreak challenges this approach. As early as May 15, 2026, reports from the Africa Centres for Disease Control and Prevention suggested the circulation of a non-Zaire orthoebolavirus strain;⁵ however, confirmatory sequencing took an additional 24 h. During this interval, cases continued to accumulate, contacts dispersed across borders, and at least one infected person died outside the country of origin. This diagnostic delay highlights a bottleneck that is not primarily laboratory-based. For example, in previous orthoebolavirus outbreaks in Uganda, delays in identification and fragmented reporting systems slowed decision making. As observed during the 2022 Sudan virus outbreak in Uganda,⁶ the absence of rapidly updated, centrally maintained open access epidemiological repositories can substantially compromise situational awareness, delay the estimation of transmission dynamics, and weaken operational coordination.

We propose that the defining vulnerability of the contemporary epidemic response is fundamentally cognitive: the ability of institutions to reconstruct an operational understanding of an evolving epidemic at the same pace at which the epidemic itself unfolds. During the early stages, decision makers need to simultaneously integrate fragmented reports, evolving case definitions, delayed laboratory data, mobility patterns, health-care accessibility, misinformation, and political constraints. We define this gap between epidemic spread and institutional understanding as a cognition gap: the interval during which the epidemic takes hold at the regional level and becomes progressively more challenging to contain (appendix).

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See [Online](#) for appendix

For more on BDBV genomes in the Pathoplexus Database see <https://pathoplexus.org/ebola-bdbv/search/>

The implications of artificial intelligence for preparedness are considerable, but they require reconceptualisation. The prevailing discourse presents artificial intelligence as primarily a predictive tool. However, prediction alone does not bridge the cognition gap if institutions remain unable to operationally synthesise rapidly evolving realities. A more relevant application of artificial intelligence could be as real-time cognitive infrastructure: systems capable of continuously integrating heterogeneous surveillance streams (genomic sequences,⁷ health reports, mobility indicators, social media, and cross-border alert systems) that reconstruct a coherent operational representation under conditions of uncertainty. Such systems would not replace epidemiologists but could extend their situational awareness.

The current outbreak shows this need. By the time sequencing confirmed BDBV on May 15, 2026, the outbreak had already spread through multiple mobility networks in ways that no single institution could monitor in real time. The 2024 Marburg outbreak in Rwanda⁸ provides a complementary example. Despite scarce resources, Rwanda successfully implemented coordinated surveillance systems, early detection, and rapid data sharing to contain the highly lethal pathogen. This experience shows that strategic investments, even in resource-constrained settings, can substantially mitigate the impact of an outbreak.

The central challenge is not merely to accelerate the development of vaccines and therapies against non-Zaire orthoebolaviruses, although these objectives remain essential. The primary challenge lies equally in building institutional frameworks capable of real-time operational synthesis—systems capable of reconstructing the evolving epidemic reality more rapidly than outbreaks can reorganise themselves through networks of mobility,

conflict, and social disintegration. Preparedness should therefore evolve from a paradigm based on detection alone to one centred on understanding, as understanding is a prerequisite for containment.

We declare no competing interests.

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