

How many Bundibugyo ebolavirus outbreaks are we missing?

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ABSTRACT

The 2026 outbreak of Bundibugyo virus disease (BVD) in the Democratic Republic of the Congo and Uganda highlights critical gaps in global preparedness for emerging infectious diseases. Previously considered rare, the Bundibugyo virus had been linked to only two recognized outbreaks, one in 2007–2008 and another in 2012. However, the current outbreak suggests that its apparent rarity may reflect limitations in diagnostic capabilities and epidemiological surveillance, rather than its true incidence. Non-specific clinical symptoms, genetic divergence from other Ebola virus species, and diagnostic systems designed primarily to detect the Zaire ebolavirus may contribute to delayed identification and underreporting. Conventional surveillance systems may overlook small, localized outbreaks, particularly in regions with limited access to healthcare and laboratory resources. Real-time genome sequencing, decentralized diagnostics, improved laboratory infrastructure, and international data sharing could strengthen the early detection and characterization of such outbreaks. Although the true incidence of BVD remains unknown, the current outbreak challenges the assumption that a low number of recognized outbreaks indicates that the pathogen is genuinely rare.

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1. INTRODUCTION

The declaration of the Bundibugyo virus disease (BVD) epidemic in the Democratic Republic of the Congo (DRC) and Uganda in May 2026 as a Public Health Emergency of International Concern (PHEIC) refocused the world's attention on the Ebola virus threat [1]. Discussions focused on diagnostics, epidemiological surveillance, vaccine availability, and the preparedness of healthcare systems to respond to new outbreaks. However, perhaps the most important question raised by the current epidemic is different: how many Bundibugyo virus outbreaks remain undetected?

Since its identification, Bundibugyo virus (BDBV) has been considered one of the rarest species of the Orthoebolavirus genus. Before 2026, only two recognized outbreaks had been described, the first in Uganda in 2007–2008 and the second in the Democratic Republic of the Congo in 2012 [2]. Unlike Zaire ebolavirus or Sudan ebolavirus, which have caused numerous and well-documented outbreaks, BDBV has remained marginalized by researchers, research funding agencies, and vaccine manufacturers. However, the current epidemic challenges the assumption that BDBV is truly a rare pathogen. A growing body of epidemiological, diagnostic, and genomic data indicates that this virus may be much more common than previously thought, yet it remains invisible to surveillance systems designed primarily for other Ebola virus species.

THE "RARE" VIRUS PARADOX

In epidemiology, we often equate the rarity of a pathogen with a small number of detected cases or epidemics. However, this approach is seriously flawed. The number of recognized outbreaks does not reflect the true incidence of infections, but rather the ability of the healthcare system to detect them. The history of infectious diseases has repeatedly shown that pathogens considered rare suddenly became "common" after the introduction of more effective diagnostic methods. This didn't mean they began to appear more frequently. It simply meant that we began to notice them.

This problem is particularly acute in the case of Ebola virus. Initial symptoms of infection are nonspecific and include fever, weakness, muscle pain, headaches, nausea, and diarrhea [3]. These symptoms are virtually indistinguishable from many other diseases common in sub-Saharan Africa, such as malaria, typhoid fever, leptospirosis, viral diseases, and severe bacterial infections. In regions with limited access to laboratory diagnostics, most patients never undergo testing to identify the specific pathogen. As a result, small outbreaks of infection can subside spontaneously, remaining undetected by national and international epidemiological surveillance systems. Factors underlying the underdiagnosis of Bundibugyo virus disease and approaches to improving its detection are presented in Table 1.

Table 1. Key factors contributing to the underdetection of Bundibugyo virus disease and potential strategies for improvement.

Factor	Implications for outbreak detection	Potential strategies
Nonspecific clinical symptoms	Misdiagnosis as malaria, typhoid fever, or other infections	Increased clinical awareness and broader differential diagnosis
Limited diagnostic capacity	Delayed or missed identification of BVD cases	Improved access to molecular diagnostic testing
Genetic divergence from other Ebola virus species	Potential limitations of tests targeting other ebolaviruses	Development and validation of species-specific diagnostic assays
Weak epidemiological surveillance	Failure to detect small or localized outbreaks	Strengthened community-based and event-based surveillance
Limited genomic surveillance	Difficulty identifying transmission chains and independent spillover events	Real-time genomic sequencing and international data sharing
Limited healthcare infrastructure	Delayed reporting and restricted access to testing	Investment in laboratory infrastructure and local workforce training

The current BDBV epidemic demonstrates how easily this can occur. According to available data, virus transmission may have continued for weeks before official recognition. By the time the pathogen was identified, hundreds of suspected cases and numerous deaths had already been reported [4]. If such a large epidemic could have developed for such a long time undetected, one must ask how many smaller outbreaks were never identified.

PREPARED FOR EBOLA, BUT NOT FOR BUNDIBUGYO

The global strategy to combat Ebola viruses was significantly shaped by the experience of the Ebola Zaire epidemic in West Africa between 2014 and 2016. The tragic consequences of that epidemic led to unprecedented investments in the development of vaccines, antiviral therapies, diagnostic tests, and infection monitoring systems [5]. These investments undoubtedly improved the world's preparedness to respond to future epidemics. However, they also created a trap of preparedness focused on a single pathogen. A significant portion of available molecular tests were developed primarily to detect the Ebola Zaire virus. However, the BDBV differs genetically from it by approximately 30% [6]. Such a significant difference can impact the effectiveness of diagnostic tests, particularly those used in the field.

During the current epidemic, initial tests performed using routinely used diagnostic systems failed to quickly identify the pathogen. Only the use of more advanced molecular methods and genomic sequencing allowed for the confirmation of BDBV infections. This problem goes beyond technical issues. It demonstrates that global epidemic preparedness is often based on the assumption that the next epidemic will resemble the previous one. However, the history of infectious diseases teaches the opposite: subsequent health crises almost always reveal the weaknesses of the systems prepared to combat the previous threat.

ARE SPILLOVERS MORE COMMON THAN WE THINK?

An even more intriguing question concerns the zoonotic origin of BDBV. Despite nearly two decades of research, a natural reservoir for this pathogen has not been clearly identified. As with other filoviruses, fruit bats are suspected, but definitive evidence supporting this hypothesis is lacking. Genomic analyses of viruses isolated during the current epidemic indicate that the strains circulating in 2026 differ from those responsible for the 2007 and 2012 epidemics [2]. This suggests the possibility of new, independent spillover events. If this interpretation proves correct, it could mean that virus transmission from animals to humans occurs more frequently than previously thought. Most such events could go undetected due to limited epidemiological surveillance, insufficient diagnostics, and nonspecific clinical presentation.

Similar phenomena have been observed with other zoonotic pathogens. Studies have shown that human contact with new viruses may occur much more frequently than the number of recognized epidemics suggests [7]. Only a small fraction of such events lead to large chains of transmission that attract the attention of public health authorities. In this sense, recognized epidemics represent only the tip of the iceberg, and the true number of infections remains unknown.

SURVEILLANCE SYSTEMS LOOK FOR FALSE SIGNALS

Modern epidemiological surveillance systems are primarily designed to detect large clusters of disease, sudden increases in mortality, or unusual clinical events. This approach works well for rapid epidemics with high mortality rates. However, it performs significantly less well for pathogens causing diffuse, small, or moderately severe outbreaks. An additional complication in the case of BDBV is that the infection mortality rate appears to be lower than that of Ebola Zaire. Current data indicate a mortality rate of 25–40%, while some Ebola Zaire epidemics have reached significantly higher rates. Furthermore, hemorrhagic symptoms, traditionally associated with hemorrhagic fevers, are less frequent and appear later [3,8]. This can lead to decreased diagnostic vigilance among both medical personnel and epidemiological services. Armed conflicts, population migration, and limited access to healthcare in regions where infections occur pose additional challenges. All these factors reduce the effectiveness of epidemiological surveillance. As a result, public health systems may prioritize the most dramatic epidemics, while smaller outbreaks remain undetected.

GENOMICS AS A NEW TOOL FOR THREAT DETECTION

The development of genomic sequencing technology offers the opportunity to change this situation. One of the most important lessons from the current epidemic is the importance of rapid, real-time virus sequencing [9,10]. Genomic analyses allow not only the identification of a pathogen but also its evolution, reconstructing transmission chains, and determining the number of independent spillover events.

Classical diagnostics answer the question of whether a given pathogen is present. Genomic diagnostics answer the question of which pathogen is present. This difference is fundamental in a world where new zoonotic diseases are increasingly emerging. Portable sequencers, decentralized molecular laboratories, and international data exchange systems could enable the detection of unexpected threats much earlier than

currently possible. However, achieving this goal requires long-term investments in laboratory infrastructure, personnel training, and the development of local scientific competence.

CONCLUSIONS

The 2026 Bundibugyo virus epidemic challenges our current understanding of the epidemiology of this pathogen. Although we currently lack evidence to determine the true incidence of infection, increasing evidence suggests that the number of recognized outbreaks may represent only a small fraction of the true disease burden. The most important lesson from the current epidemic may therefore not be how to combat Bundibugyo virus, but how to spot it. Rarity is not a biological characteristic of the virus. It is the result of observation. And observation is limited by the quality of epidemiological surveillance, the availability of diagnostics, and the capacity of healthcare systems. Until we develop systems capable of detecting unexpected threats, we will continue to confuse invisibility with rarity.

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REFERENCES

1. Abdool Karim S, Faure M. The Bundibugyo Ebolavirus Outbreak: the need for a solidaristic response under the revised International Health Regulations. *Lancet Regional Health - Africa*. 2026;100091. doi:10.1016/j.lanafr.2026.100091
2. Diseases TLI. Key facts about the Bundibugyo virus outbreak. *Lancet Infect Dis*. 2026. doi:10.1016/S1473-3099(26)00293-8
3. Ebola Bundibugyo Virus Disease in the Democratic Republic of the Congo and Uganda - Level 2 - Travel Health Notices. CDC. Accessed 15 June 2026. <https://wwwnc.cdc.gov/travel/notices/level2/ebola-drc-uganda>
4. Bhadelia N, Gikandi I, Lassmann B. Regional Signals Preceding the 2026 Bundibugyo Virus Disease Outbreak. *Int J Infect Dis*. 2026;108862. doi:10.1016/j.ijid.2026.108862
5. Letafati A, Salahi Ardekani O, Karami H, Soleimani M. Ebola virus disease: A narrative review. *Microb Pathog*. 2023;181:106213. doi:10.1016/j.micpath.2023.106213
6. Ontario Agency for Health Protection and Promotion. Genomic epidemiology and molecular characteristics of bundibugyo virus. Published online 2026.
7. Weiss RA, Sankaran N. Emergence of epidemic diseases: zoonoses and other origins. *Fac Rev*. 2022;11:2. doi:10.12703/r/11-2
8. Gupta N, Mora-Rillo M, Gkrania-Klotsas E, Drexler JF, Jokelainen P, Pellejero-Sagastizabal G, et al. Bundibugyo ebolavirus outbreak in the Democratic Republic of the Congo and Uganda: rapid assessment from the ESCMID Emerging Infections Subcommittee. *Clin Microbiol Infect*. 2026;S1198-743X(26)00285-5. doi:10.1016/j.cmi.2026.05.042
9. Houldcroft CJ. 2026 Bundibugyo virus outbreak: the role of genomics in Orthoebolavirus outbreaks. *Microb Genom*. 2026;12(6):001754. doi:10.1099/mgen.0.001754
10. Kupferschmidt K. Scientists play catch-up to startling Ebola outbreak. *Science*. 2026;392(6800):792-793. doi:10.1126/science.aej0202