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Estimation of the size of the Ebola outbreak caused by Bundibugyo virus in the Democratic Republic of the Congo: May 20, 2026 update

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Update 20th May:

- Analysis updated to reflect the number of deaths as reported 20th May 2026 (131 instead of 88).
- The CFR bounds have been corrected to reflect the estimates from previous outbreaks (now 26%, 33%, 40%, rather than 24%, 30%, 40%).

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Executive summary

As of 20 May 2026, a total of 516 suspected cases of Bundibugyo virus disease (BVD) - a form of Ebola virus disease caused by Bundibugyo virus - had been reported in the Democratic Republic of the Congo including 131 deaths. Eight cases were laboratory-confirmed in the Ituri Province from 13 samples, and two cases were confirmed in Kampala, Uganda, among individuals travelling from Ituri Province, Democratic Republic of the Congo. Together, this suggests that the epidemic is larger than currently ascertained; however, the true magnitude remains uncertain.

To estimate the size of the epidemic in the Democratic Republic of the Congo, we applied two independent approaches. The first approach uses population movement data in conjunction with evidence of the two exported cases detected in Uganda. The second approach relies on reported suspected deaths (assumed to be more completely captured than cases) combined with estimates of the case fatality ratio and time from symptom onset to death derived from previous Bundibugyo virus outbreaks, as well as assumptions about how fast the epidemic has been growing.

Both methods yield broadly consistent results, suggesting that as of 20 May 2026, approximately 400 to 900 cases of BVD may have occurred in the Democratic Republic of the Congo. However, there is considerable uncertainty around these estimates, with values of over 1000 not being able to be excluded given current data. Despite this uncertainty, the convergence of findings from two independent methods strengthens confidence in the conclusion of substantial under-detection and the potential for wider transmission.

These estimates rely on a number of key assumptions: that transmission is largely concentrated in Ituri and Nord Kivu provinces, estimates of the scale and patterns of population movement from these areas to Uganda, and values of epidemiological parameters derived from past Bundibugyo virus outbreaks, including the case fatality ratio (CFR) and time between symptom onset and death. Each of these assumptions is subject to uncertainty and may influence the resulting estimates.

Methods overview

We used two independent analyses to estimate the outbreak size; the first relies on the number of confirmed cases reported outside the Democratic Republic of the Congo and population movement information; the second relies on the total number of suspected BVD deaths reported and estimates of the CFR and time between symptom onset and death.

Method 1: geographic spread

The first analysis uses the same approach as Imai et al. (2020): https://www.imperial.ac.uk/media/imperial-college/medicine/mrc-gida/2020-01-17-COVID19-Report-1.pdf.

We estimate the number of BVD cases in the Democratic Republic of the Congo using information on:

- the reported number of confirmed BVD cases in Uganda (two as of 20 May 2026);
- the estimated daily number of international travellers from the Ituri and Nord Kivu Provinces, in the Democratic Republic of the Congo to Uganda;
- assumptions about how long after infection individuals are being detected.

Method 2: backcalculation from deaths

The second analysis backcalculates the number of BVD cases from the total number of suspected BVD deaths reported (131 as of 20 May 2026), using previously published estimates of the distribution of time from symptom onset to death in BVD cases. It examines the sensitivity of estimates to:

- the assumed doubling time and start date of the epidemic
- estimates of the case fatality ratio (CFR, proportion of cases who die as a result of their infection) for Bundibugyo virus;

Both methods are described in greater detail in the appendix.

Results

Table 1: Estimated outbreak size estimated by method 1 (geographic spread), under the 2 source populations (main assumption: source population = Ituri, sensitivity analysis: source population = Ituri + Nord Kivu) and 3 detection windows (defined below) considered. Confidence intervals (CIs) were calculated as exact negative binomial CIs.

Source population	Daily outbound travellers from source population	Source population size	**Estimated number of cases: Mean (95%CI)**		
			Detection window* = 10 days	Detection window* = 15 days	Detection window* = 20 days
Main scenario: Ituri	1,871	4,392,200	**470 (58 –1,306)**	**313 (39–870)**	**235 (29–652)**
Sensitivity analysis: Ituri + Nord Kivu	4,339	13,392,200	**617 (76–1,718)**	**412 (51–1,145)**	**309 (38–858)**

* Here, the detection window is defined approximately as the incubation period + onset to detection period.

Table 2: Outbreak sizes derived by method 2 (backcalculation from deaths), under 3 assumptions for the epidemic growth rate (a main scenario with a 14-day doubling time, and two sensitivity analyses with 7- and 21- day doubling times) and 3 estimates of the CFR. 95% confidence intervals derived assuming Poisson variation shown.

Scenario	Doubling time (days)	Corresponding growth rate (per day)	**Number of cases**		
			CFR = 26%	CFR = 33%	CFR = 40%
Main scenario: Moderate growth, intermediate emergence	14	0.050	**860 (721-1,015)**	**678(568-800)**	**559 (469-660)**
Sensitivity analysis 1: Fast growth, recent emergence	7	0.100	**1,386(1,160-1,636)**	**1,092(914-1,289)**	**901 (754-1,062)**
Sensitivity analysis 2: Slow growth, older emergence	21	0.034	**730(612-862)**	**575(482-679)**	**474(398-560)**

Caveats

- There is high uncertainty in method 1 estimates as these are based on only two exported cases, which travelled specifically for the purposes of seeking care.
- Method 2 uses a simple deterministic epidemic model to explore the relationship epidemic growth rate and epidemic size to date; it does not fully capture stochasticity or overdispersion (super-spreading) in the underlying processes and therefore underestimates true uncertainty.
- The data on border crossing is not comprehensive and may miss informal crossings. If so, the epidemic size might be lower than the estimates presented here. Moreover, the PoE numbers we are using covers other social service seeking including educational, family, religious. It also includes border community movements which may introduce bias.
- Method 1 relies on characterising the detection window which is challenging for Bundibugyo: the mean incubation period has been estimated to be 6–11 days (https://pubmed.ncbi.nlm.nih.gov/20587179/; https://pubmed.ncbi.nlm.nih.gov/26107529/; https://pubmed.ncbi.nlm.nih.gov/21122234/) but the onset to detection is not well characterised for this species (https://pubmed.ncbi.nlm.nih.gov/39127058/).

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- In the absence of data on the timing of cases or deaths, the growth rate and date of origin of the current epidemic cannot be estimated. In Method 2, we therefore explore a range of plausible assumptions for both. These could be refined as more detailed data become available, either to better constrain the likely start of the epidemic or to estimate growth rates from time series of clinical outcomes.
- Estimates of the CFR and time from symptom onset to death for BVD are scarce - we are using the limited available evidence from previous outbreaks and did not account for uncertainty in the estimated distribution of the onset to death delay.
- Method 2 relies on the reported number of suspected BVD deaths detected through syndromic surveillance, which is imperfect. These figures could both be an over- or under-estimate of deaths actually attributable to BVD.

Appendix: Methods

Method 1: geographic spread

We calculate the total number of cases in the Democratic Republic of the Congo as:

$$Total\ cases\ = \frac{cases\ detected\ overseas}{probability\ (p)\ that\ a\ case\ will\ be\ detected\ in\ Uganda}$$

where:

- $p\ =\ daily\ probability\ of\ travel\ to\ Uganda\ \times mean\ detection\ window$
- $daily\ probability\ of\ travel\ to\ Uganda\ = \frac{daily\ outbound\ international\ travellers\ from\ source\ population}{source\ population\ size}$ (see below)
- $Cases\ detected\ overseas\ =\ 2$

We consider a total of 6 scenarios where we assume:

- One of 2 different travel probabilities derived for two sets of source populations: (1) Ituri, (2) Ituri and Nord Kivu (see below).
- One of 3 mean detection windows: (a) 10 days, (b) 15 days and (c) 20 days (approximately corresponding to incubation period + onset to detection period).

Probability of travel:

- This is estimated from point of entry (PoE) data shared by WHO on 16 May 2026. Among these PoEs for which traveller screening data are available in the epi bulletins: PoEs along Uganda-Democratic Republic of the Congo border: Busanza, Busunga, Goli, Mpondwe, Ntoroko Main, Odramacaku, Vurra.
- We received data from 4 sitreps, each covering a one week period. Some PoEs were not covered in all sitreps (see Table 3). The data covered the periods of epiweek 10 (2–8 March 2026); epiweek 11 (9–15 March 2026); epiweek 15 (6–12 April 2026); epiweek 18 (27 April–3 May 2026).
- We further split the Uganda-Democratic Republic of the Congo border points into whether the corresponding province on the Democratic Republic of the Congo side was Ituri or Nord Kivu.
- The data used in our analyses is reproduced in Table 3 below.

Table 3: Summary of passenger data underpinning estimates.

Location	Point of Entry (PoE)	Number of sitreps with an observation	Mean reported weekly passengers entering Uganda through this PoE	Mean daily passengers*	Total mean daily passengers**
Ituri	Goli	4	4,150	593	1,871
	Ntoroko Main	4	1,846	264	
	Odramacaku	2	3,137	448	
	Vurra	4	3,964	566	
Nord Kivu	Busanza	1	919	131	2,468
	Busunga	3	9,158	1,308	
	Mpondwe	4	7,326	1,047	

*Daily numbers derived by dividing raw weekly passenger numbers by 7 and then taking mean.
** Rounded to nearest integer at the final analysis step.

Method 2: backcalculation from deaths

We estimate the total epidemic size using an analytical formulation that links the cumulative number of cases (counted by date of symptom onset) to the cumulative number of deaths under the simplifying assumptions that

A. the outbreak was seeded T days ago with a single zoonotic case in the human population;
B. the outbreak has been growing exponentially since that first case, with doubling time τ_2;
C. the delay from symptom onset to death is gamma distributed with mean 11.37 days and standard deviation 5.41 days, as estimated by Rosello et al. (https://elifesciences.org/articles/09015) in the 2012 Bundibugyo outbreak in Isiro, Democratic Republic of the Congo. These values for mean and standard deviation imply shape and rate parameters for the gamma distribution of $\alpha = 4.42$ and $\beta = 0.388$/day, respectively.

Under these assumptions, the cumulative incidence of cases by time T after the outbreak start is $C_T = e^{rT}$, where $r = ln(2)/\tau_2$ is the growth rate of the epidemic. Note that the daily incidence then also grows exponentially at the same rate r. If $f(u)$ is the probability density function of the distribution of the delay from symptom onset to death, u, then it can be shown that the expected cumulative number of deaths by time T after the start of the outbreak is given by $D_T = CFR \times \int_0^T e^{rs} f(T-s)ds$. Assuming a gamma distribution for $f(u)$ with shape and rate parameters α and β respectively, this integral can be evaluated to give $D_T = CFR \times C_T(1+r/\beta)^{-\alpha}\gamma(\alpha, (\beta+r)T)/\Gamma(\alpha)$, where $\Gamma()$ is the gamma function, and $\gamma()$ is the lower incomplete gamma function. For the values of α and β assumed here, this equation can be very well approximated by $D_T = CFR \times C_T(1+r/\beta)^{-\alpha}$ for $T \gtrsim 12/(\beta+r)$ days, an inequality which holds for all the scenarios examined here. Re-arranging this equation we obtain $C_T = D_T(1+r/\beta)^{\alpha}/CFR$ as an estimator of the cumulative number of cases by time T after the start of the outbreak given the observed cumulative number of deaths by the same time D_T.

The scaling by $1/CFR$ is to be expected: for the same number of cumulative deaths, one would expect proportionally fewer cases as the CFR increases. The term $(1+r/\beta)^{\alpha}$ represents the effect of epidemic phase bias - that in a growing epidemic, a disproportionate number of cases will have been infected recently, and therefore will not have yet died (or recovered).

We examine three values of the CFR, of 26%, 33% and 40%, spanning the central estimate and 95% confidence bands of published estimates of the two previous outbreak BVD outbreaks according to the United States Centers for Disease Control and Prevention (55 deaths, 169 cases) (https://www.cdc.gov/ebola/outbreaks/index.html).

We note that the assumed duration of the outbreak, T, constrains what doubling time (or equivalently, epidemic growth rate, r) is consistent with the observed epidemic, since $C_T = e^{rT}$, meaning $T = ln(C_T)/r$. Hence choosing a particular doubling time (and thus growth rate) determines ***both*** the total number of cases C_T and the duration of the epidemic T, under our assumption of exponential growth from a single initial case.

In deriving confidence intervals for Table 2 we assume a Poisson likelihood for D_T and calculate the likelihood profile for T for the three assumed values of r.

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