ASSESSMENT

Estimation of the importation risk of Bundibugyo virus into the EU/EEA in June 2026

15 June 2026

Key findings

- The ongoing outbreak of the Bundibugyo virus (BDBV) in the Democratic Republic of the Congo (DRC) has raised some concerns about the BDBV importation risk into the European Union/European Economic Area (EU/EEA).
- Based on mathematical modelling, we estimate approximately one importation per 24 000 travellers (90% Uncertainty Interval, UI: 13 000–54 000) from the main outbreak region (North Kivu and Ituri, DRC) to the EU/EEA.
- We estimate the probability of at least one BDBV importation into the EU/EEA from 11–25 June 2026 to be 0.45% (90% UI: 0.20%–0.85%), under the hypothetical assumption that 100 people travel from the outbreak region to the EU/EEA during this period. We consider 100 travellers to be a conservative upper estimate based on available historical flight data and the closure of multiple airports in the proximity of the outbreak region. The true probability of importation is therefore likely to be lower.
- These estimates apply to travellers from the general population in the outbreak region. The risk of importation associated with returning healthcare workers deployed to support the outbreak response is beyond the scope of this report.

Conclusions:

- While sporadic BDBV importations into the EU/EEA cannot be ruled out, mathematical modelling suggests that the probability of importation from 11 to 25 June is very low. These results apply to importation of BDBV from the general population of Ituri and North Kivu. Humanitarian aid workers or healthcare care personnel returning from the outbreak region to the EU/EEA, who we assume would be medically evacuated from the affected areas with application of appropriate infection prevention and control measures, need to be considered separately.
- As one BDBV importation is expected per 24 000 travellers from the outbreak region, the vast majority of travellers will not be infected. However, since early symptoms of BDBV infections overlap with many other conditions, a potentially large number of travellers will show similar symptoms as BDBV infections without being infected with BDBV (i.e. false positives). Therefore, entry screening strategies based solely on symptom detection are likely to have low specificity, which will lead to unnecessary isolation, testing, and follow-up of a potentially large number of individuals per true case.
- The presented importation probabilities are model estimates, which are subject to several limitations and are based on currently observed trends of BDBV infections in DRC. If there are substantial changes in the epidemiological situation, such as spread to other regions, then the results of this output need to be reassessed.

Suggested citation: European Centre for Disease Prevention and Control. Estimation of the importation risk of Bundibugyo virus into the EU/EEA in June 2026. ECDC: Stockholm; 2026.

ISBN 978-92-9498-892-8; doi: 10.2900/8330190; Catalogue number TQ-01-26-041-EN-N

Introduction

The outbreak of Ebola disease caused by Bundibugyo virus (BDBV), first reported on 15 May 2026 in the Democratic Republic of Congo (DRC) [1], was designated a Public Health Emergency of International Concern by the World Health Organization (WHO) on 17 May 2026 [2] and a Public Health Emergency of Continental Security by the Africa Centres for Disease Control and Prevention (Africa CDC) on 18 May 2026 [3]. As of 9 June, 635 confirmed cases had been reported in DRC [4], mostly in the province of Ituri, and as of 11 June, 19 confirmed cases had been reported in Uganda [5]. The true scale of the outbreak is likely underestimated due to challenges related to surveillance capacity, insecurity, and the broader humanitarian situation. Information on airport operations and the implementation of travel-related public health measures in the affected areas is limited and rapidly evolving.

In this report, we present estimates of the probability of importation of BDBV into EU/EEA countries for the period 11–25 June 2026 under different assumptions of travel volumes from the areas where most cases were reported from. In addition, we estimate the volume of air travel passengers from this region that would be expected to result in one BDBV importation.

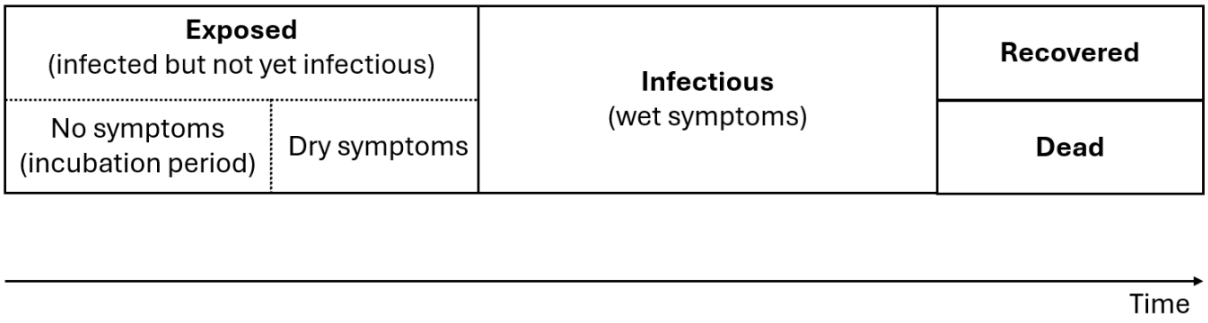
The risk of importation associated with healthcare workers deployed to support the outbreak response is outside the scope of this report and would require a different modelling approach. Presumably, healthcare workers would be medically evacuated from the affected areas while appropriate infection prevention and control measures are applied.

Methods

We used a two-step approach to estimate the risk of importation of BDBV into the EU/EEA. First, we developed a compartmental model for the BDBV transmission (see Annex 1 for detailed description of the model). The model concentrates in the Ituri and North Kivu provinces in DRC (hereafter described as the outbreak region), where most BDBV infections have been reported from. The study period was defined as 11–25 June 2026. The estimated population size of the outbreak region is $N = 13{,}392{,}200$ [6]. Throughout this work, when we refer to the general population, we do not include healthcare workers or volunteers deployed to assist in the outbreak.

The mathematical model in this first step partitions the population of the outbreak region into six compartments or disease states: those not infected (susceptible); those who are exposed, which we defined as those who are infected but not yet infectious (latently infected); those who are infectious and will recover; those who are infectious and will die; those who recovered; and the deceased. Figure 1 provides an overview of the disease states and their associated symptoms: exposed individuals do not present any symptoms at first, but after the incubation period, they present dry symptoms. People who are infectious present wet symptoms (regardless of whether they will recover or die); hence, only individuals who present wet symptoms are considered to transmit BVBD in our model. While individuals displaying dry symptoms might already be able to transmit disease, we assume that their contribution to the overall infection pressure is minimal. A list of dry and wet symptoms can be found in the United States Centers for Disease Control and Prevention's 'Signs and Symptoms of Ebola Disease' [7]. The model is initialised using the estimated number of BDBV infections and deaths provided by DRC's Institut National de Santé Publique (INSP) [8] and McCabe et al. [6]. The uncertainty of the parameters in the model is incorporated through Monte Carlo simulation, where key epidemiological inputs are sampled from predefined distributions and propagated through repeated model runs to generate uncertainty intervals for the estimates. The output of the model is compared to reported suspected deaths from 18 to 26 May according to INSP [8] to ensure consistency with the size of the outbreak so far. Rather than accurately predicting the disease dynamics in the outbreak region, the objective of the mathematical model is to provide *approximate* ranges of people who are exposed and infectious, acknowledging the rapidly evolving outbreak and the limited data quality.

Figure 1. Overview of disease states used in our model, and the associated symptoms



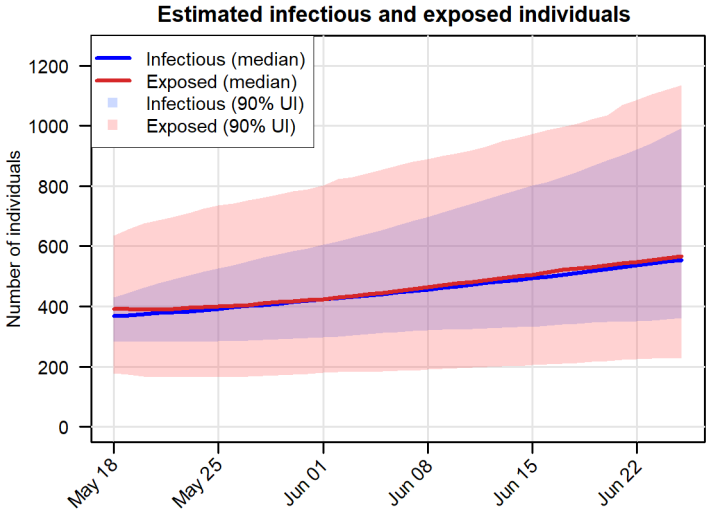
In the second step, we build on the output of the mathematical model to estimate the probability of at least one BDBV importation into the EU/EEA (see Annex 2 for details). An importation occurs when a person who is exposed or infectious travels with destination to any country in the EU/EEA. We assume individuals in the same class of symptoms (no symptoms, dry symptoms, or wet symptoms) share the same probability of travelling, and travels of different individuals are stochastically independent. Compared to susceptible individuals, exposed individuals with no symptoms have the same probability of travelling; symptomatic people who are exposed and infectious are considered to have a lower probability; people who are exposed with dry symptoms are assumed to have 10% lower probability of travelling than a susceptible individual; and those who are infectious with wet symptoms have a 90% lower probability. We consider these assumptions pessimistic, in that they can be considered as a lower bound to the actual impact of symptoms on the travel probability.

The importation probability strongly depends on the passenger numbers travelling from the affected area to the EU/EEA. However, the actual number of passengers travelling to EU/EEA that can be expected from 11–25 June is unknown; the volatile situation in the region including closure of airports and disruption of travel makes it even more difficult to estimate. Thus, in view of the lack of knowledge on the traveller numbers, we explore different hypothetical scenarios on the number of travellers. The code used for this report is available online [9].

Results

The simulated trajectories for the number of people who are exposed and infectious over the study period are shown in Figure 2. In our model, the number of people who are exposed and infectious increases gradually between 11 and 25 June 2026. These projections are associated with substantial uncertainty both in the initial conditions and in key disease parameters.

Figure 2. Modelled outbreak dynamics (number of people who are exposed and infectious) in Ituri and North Kivu, 11–25 June 2026

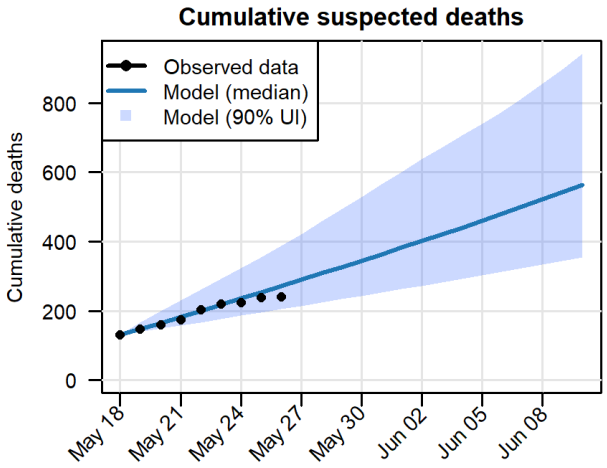


The solid lines correspond to the median and shaded areas indicate 90% uncertainty interval. The results were obtained by running 500 Monte Carlo simulations.

The modelled cumulative deaths align well with observed suspected deaths [8], as shown in Figure 3. In particular, the median model trajectory closely follows the increasing trend in the observed data over the reporting period, and the observed data points are within the 90% uncertainty interval (UI), indicating that the model is consistent with the reported data.

This agreement provides support that the model is able to reproduce recent outbreak dynamics, even though it is not explicitly fitted to the mortality data. At the same time, the widening uncertainty bounds in the forward projections reflect increasing variability in possible epidemic trajectories.

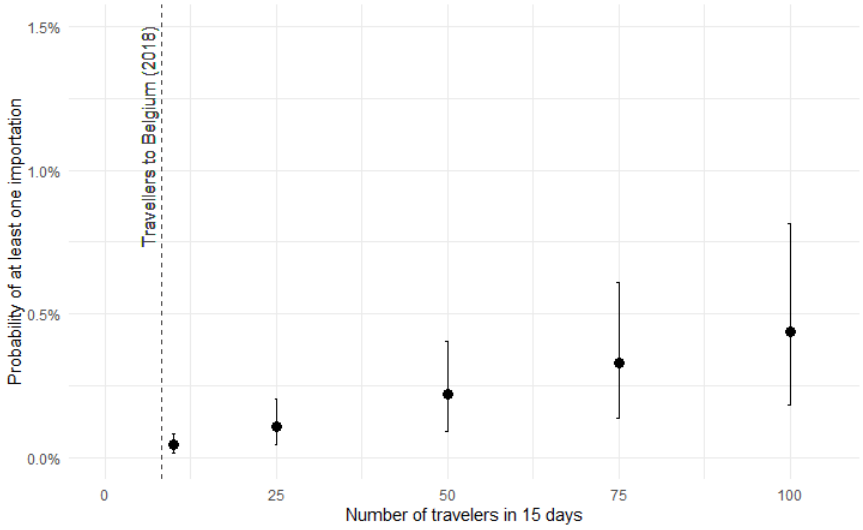
Figure 3. Comparison of modelled and observed cumulative (suspected) deaths



Black points represent observed data, the blue line shows the median model estimate, and the shaded region indicates the 90% uncertainty interval (UI). The results were obtained by running $n_{sim} = 500$ Monte Carlo simulations.

Combining the number of people who are exposed and those who are infectious with the relative probability to travel per disease stage, we find that for every 24 000 (90% UI: 13 000–54 000) travellers from the outbreak area to the EU/EEA, we could expect one importation of BDBV by a person with the infection.

Figure 4. Probability of at least one BDBV importation for different travel volumes from the outbreak region (North Kivu and Ituri, DRC) to the EU/EEA from 11 to 25 June 2026



Note that the y-axis is capped, since the depicted probabilities and ranges are all small (not exceeding 1%). The dashed line indicates the number of travellers reported from the region to Belgium in Tuite et al. [10], the country in the EU/EEA with the highest travel volume from the region in 2018, scaling the four-month figure of 66 travellers down to 15 days – the number of travellers to the whole the EU/EEA was larger, and might have increased since 2018.

The actual number of individuals who will travel from the outbreak area to the EU/EEA is unknown, and recent travel data are limited. To understand the impact of travellers on the probability of importation from 11 to 25 June 2026, we explore hypothetical scenarios where the number of travellers over this time period ranges from 10 to 100. Figure 4 shows the probability of at least one BDBV importation for different scenarios on the traveller numbers. For the hypothetical scenarios with 10 and 100 travellers from the outbreak areas from 11 to 25 June 2026, we obtain a probability of at least one importation during that time period between 0.05% (0.02%,0.09%) and 0.45% (90% UI: 0.20–0.85%), respectively.

Assessment and conclusions

In this work, we modelled the risk of a BDBV importation into the EU/EEA from 11 to 25 June 2026. Overall, our results indicate a small probability (below 1%) of a BDBV importation for scenarios of up to 100 travellers from the outbreak region to the EU/EEA. These estimates should be interpreted as a short-term risk assessment. Thus, the results suggest that the direct threat of the BDBV outbreak to public health in the EU/EEA is currently very low, subject to several limitations listed further below. Providing a narrower estimate of the importation probability would require estimates of the traveller numbers from the affected region to the EU/EEA, which is challenging given the disruption of mobility patterns, including closure of airports and border controls.

We expect one importation into the EU/EEA per 24 000 (90% UI: 13 000–54 000) passengers. Since we expect substantially fewer passengers from the outbreak region to the EU/EEA from 11 to 25 June 2026, these results are reassuring as they suggest that the BDBV importation risk into the EU/EEA is very small. While we present these results as importation risk for the EU/EEA, the underlying per-traveller probabilities are independent of the destination and the number of importations per travellers therefore also applies to individual countries or airports. Since BDBV infection among travellers is expected to be very low, unspecific symptoms among travellers are likely to have other causes. Hence, screening methods based solely on unspecific symptom detection are likely to have low positive predictive value, which can lead to unnecessary isolation, testing, and follow-up of a large number of individuals per true case.

If there was reason to expect more than 100 travellers from the outbreak region into the EU/EEA, the probability of an importation might increase. However, the expected ratio of about 24 000 (90% UI: 13 000–54 000) travellers per importation remains valid, regardless of the absolute number of travellers. Thus, increased travel volume raises the chance of at least one importation, but does not change the average number of travellers expected to result in one importation.

The strength of the proposed mathematical modelling and probabilistic approach is that it provides a quantitative framework for assessing the probability of importing BDBV in the EU/EEA combining data and insights from various sources. While the modelling and risk calculation are based on several simplifying assumptions, the applied methods form a basis for further adjustments as the outbreak and public health questions evolve.

This work is subject to several limitations:

- Due to lack of data, we made assumptions on the reduction in travel probability due to dry and wet symptoms as compared to susceptible individuals in the outbreak region, which we set to 10% and 90%, respectively, to reflect a pessimistic scenario. These probabilities may change over time and depend on various factors, including the stringency of and adherence to exit screening, ability and willingness to travel despite symptoms, and public awareness. If estimates of these probabilities became available, the values in the modelling approach can be adjusted accordingly.
- This work focusses only on the general population of the Ituri and North Kivu provinces in DRC. Specifically, it does not consider travel of healthcare workers (HCW) of non-governmental organisations to the EU/EEA.
- The mathematical model assumes a continuation of BDBV infections in line with observed trends. If the number of infections increases/decreases markedly in size (e.g. due to superspreading events or laboratory backlog clearing) estimates should be updated.
- The considered outbreak region in the model is defined as Ituri and North Kivu provinces in DRC. The results need to be adjusted if significant community transmission is established in other regions or if the outbreak spreads to other countries, in particular, if the outbreak spreads to areas with international or well-connected airports.
- There are several well-known simplifications of the suggested compartmental model, including homogeneous mixing, deterministic description of a stochastic process (mean-field approximation), exponential sojourn times in the compartments (Markov property), absence of population structure, no adaptive behaviour to the epidemic, no interventions, and no transmission from recovered individuals.

Acknowledgements

ECDC thanks external expert Alessandro Vespignani (Institute for Scientific Interchange Foundation, Turin, Italy; Laboratory for the Modeling of Biological and Socio-technical Systems, Northeastern University, Boston, US) for his peer-review of this document and is grateful for input by the Center for Advanced Epidemic Analytics and Predictive Modeling Technology at Northeastern University, Boston, US.

References

1. European Centre for Disease Prevention and Control (ECDC). Threat assessment brief: Ebola disease outbreak caused by Bundibugyo virus – Democratic Republic of the Congo and Uganda – 2026. Stockholm: ECDC; 2026. Available at: https://www.ecdc.europa.eu/en/publications-data/threat-assessment-brief-ebola-disease-outbreak-caused-bundibugyo-virus-democratic
2. World Health Organization (WHO). Epidemic of Ebola Disease caused by Bundibugyo virus in the Democratic Republic of the Congo and Uganda determined a public health emergency of international concern. Geneva: World Health Organization; 2026. Available at: https://www.who.int/news/item/17-05-2026-epidemic-of-ebola-disease-in-the-democratic-republic-of-the-congo-and-uganda-determined-a-public-health-emergency-of-international-concern
3. Africa CDC. Africa CDC Declares the Ongoing Bundibugyo Ebola Outbreak a Public Health Emergency of Continental Security. Addis Ababa: Africa CDC; 2026. Available at: https://africacdc.org/news-item/africa-cdc-declares-the-ongoing-bundibugyo-ebola-outbreak-a-public-health-emergency-of-continental-security
4. Institut National de Santé Publique (INSP) de la République Démocratique du Congo. SitRep N°020/MVB_02/06/2026. Kinshasa: INSP; 2026. Available at: https://insp.cd/sitrep-n020-mvb_02-06-2026
5. Ministry of Health, Uganda. Ebola update - 2 June 2026. 2026. Kampala: Ministry of Health, Uganda; 2026. Available at: https://health.go.ug/download/ebola-update-2nd-june-2026
6. McCabe R, Ebbarnezh L, Okware S, Fotsing R, Koua E, Mbaka P, et al. Estimation of the size of the Ebola outbreak caused by Bundibugyo virus in the Democratic Republic of the Congo. London: Imperial College London; 2026. Available at: https://www.imperial.ac.uk/media/imperial-college/medicine/mrc-gida/Report-ebola-18-05-2026.pdf
7. United States Centers for Disease Control and Prevention (US CDC). Signs and Symptoms of Ebola Disease. Atlanta: US CDC; 2024. Available at: https://www.cdc.gov/ebola/signs-symptoms/index.html
8. Institut National de Santé Publique (INSP) de la République Démocratique du Congo. Bundibugyo Ebola virus outbreak 2026: Epidemiological & operational data. Kinshasa: INSP; 2026. Available at: https://github.com/INRB-UMIE/BDBV2026-Data/tree/main/data/insp_sitrep
9. European Centre for Disease Prevention and Control (ECDC). Ebola Importation Risk – GitLab. Stockholm: ECDC; 2026. Available at: https://code.europa.eu/ecdc/ebola_importation_risk
10. Tuite AR, Watts AG, Khan K, Bogoch, II. Ebola virus outbreak in North Kivu and Ituri provinces, Democratic Republic of Congo, and the potential for further transmission through commercial air travel. J Travel Med. 2019 Oct 14;26(7). Available at: https://www.ncbi.nlm.nih.gov/pubmed/31414699
11. Chowell G, Hengartner NW, Castillo-Chavez C, Fenimore PW, Hyman JM. The basic reproductive number of Ebola and the effects of public health measures: the cases of Congo and Uganda. J Theor Biol. 2004 Jul 7;229(1):119-26. Available at: https://www.ncbi.nlm.nih.gov/pubmed/15178190
12. Althaus CL. Estimating the reproduction number of Ebola virus (EBOV) during the 2014 outbreak in West Africa. PLoS Currents Outbreaks. 2014 Sep 2. Edition 1. Available at: https://currents.plos.org/outbreaks/article/estimating-the-reproduction-number-of-zaire-ebolavirus-ebov-during-the-2014-outbreak-in-west-africa
13. Area I, Ndairou F, Nieto JJ, Silva CJ, Torres DF. Ebola model and optimal control with vaccination constraints. arXiv preprint arXiv:170301368. 2017. Available at: https://arxiv.org/abs/1703.01368
14. Velasquez GE, Aibana O, Ling EJ, Diakite I, Mooring EQ, Murray MB. Time From Infection to Disease and Infectiousness for Ebola Virus Disease, a Systematic Review. Clin Infect Dis. 2015 Oct 1;61(7):1135-40. Available at: https://www.ncbi.nlm.nih.gov/pubmed/26129757
15. US Centers for Disease Control and Prevention (US CDC). Ebola Disease Basics. Atlanta: US CDC; 2026. Available at: https://www.cdc.gov/ebola/about/index.html
16. Choi B, Busch S, Kazadi D, Ilunga B, Okitolonda E, Dai Y, et al. Modeling outbreak data: Analysis of a 2012 Ebola virus disease epidemic in DRC. Biomath (Sofia, Bulgaria). 2019;8(2):1910037. Available at: https://pmc.ncbi.nlm.nih.gov/articles/PMC7665115
17. MacNeil A, Farnon EC, Morgan OW, Gould P, Boehmer TK, Blaney DD, et al. Filovirus outbreak detection and surveillance: lessons from Bundibugyo. J Infect Dis. 2011 Nov;204 Suppl 3:S761-7. Available at: https://www.ncbi.nlm.nih.gov/pubmed/21987748
18. Rosello A, Mossoko M, Flasche S, Van Hoek AJ, Mbala P, Camacho A, et al. Ebola virus disease in the Democratic Republic of the Congo, 1976-2014. Elife. 2015 Nov 3;4:e09015. Available at: https://www.ncbi.nlm.nih.gov/pubmed/26525597
19. Wamala JF, Lukwago L, Malimbo M, Nguku P, Yoti Z, Musenero M, et al. Ebola hemorrhagic fever associated with novel virus strain, Uganda, 2007-2008. Emerg Infect Dis. 2010 Jul;16(7):1087-92. Available at: https://www.ncbi.nlm.nih.gov/pubmed/20587179

Annex 1. Compartmental model of Bundibugyo virus dynamics in affected areas in the DRC

We formulate an SEIR-type epidemic model to describe the spread of Bundibugyo virus (BDBV) in the outbreak region. Mathematical models following SEIR dynamics have been applied to Ebola outbreaks, capturing the progression of individuals through susceptible, exposed, infectious, recovered, and dead compartments, and enabling estimation of key epidemiological quantities such as the basic reproduction number through fitting to incidence data [11,12]. Extensions further allow incorporation of control measures, such as vaccination or interventions [13]. In line with these approaches, we assume homogeneous mixing within the region and a constant total population over the outbreak; over the modelled period we assume no migration or death due to natural causes.

In this work, the outbreak region is defined as North Kivu and Ituri. The population size of the outbreak region is estimated at $N = 13{,}392{,}200$ [6] and was assumed constant over the simulation.

We partition the population by assigning each person into either one of the six compartments below.

- **People who are susceptible** in compartment S have not been exposed to BDBV and may become infected through contact with the virus (for more details, see the governing equations below), upon which they transition to the exposed compartment E.
- **People who are exposed** (or latently infected) have been infected with BDBV but are not infectious yet. Individuals are exposed for an average duration of 10 days [14], after which they transition to one of the infectious compartments I_R or I_D. Exposed individuals do not have any symptoms for an average duration of 6.22 days [15], the remaining time they have dry symptoms.
- **People who are infectious** in compartments I_R and I_D are infected with BDBV, have wet symptoms, and transmit the virus via contacts with susceptible individuals. The separation into the two compartments I_R and I_D is made to indicate whether the respective individuals are going to recover (I_R) or die (I_D). The transmission of individuals in I_D also captures post-mortem transmission (e.g. through transmissions during funerals).
- **People who have recovered** in compartment R have cured from an infection with BDBV. While transmission from recovered individuals can occur (e.g. via unprotected sex), the model assumes the force of infection mainly depends on the infectious individuals (in I_D and I_R) and makes the approximation that individuals in the compartment R are not infectious. Recovered individuals are considered immune to reinfections with BDBV.
- **Deceased** individuals in compartment D have died as a consequence of an infection with BDBV. These individuals are not considered infectious anymore (as post-mortem transmission is captured via the compartment I_D).

Figure 1A. The compartmental epidemic model to describe the transmission of BDBV in the outbreak areas (Ituri and North Kivu, DRC)

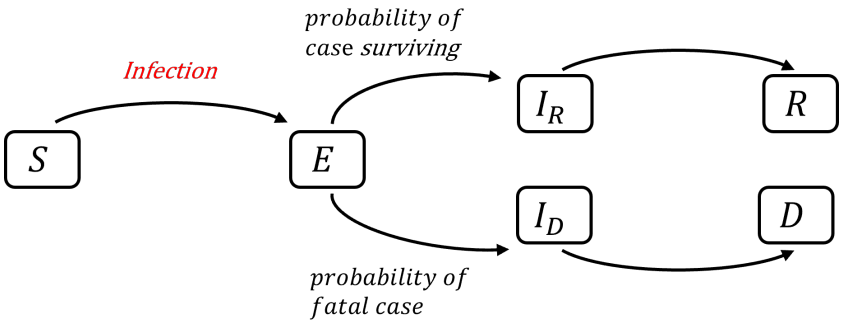


Figure 1A provides a visualisation of the epidemic model and the transitions between the compartments. We define the number of susceptible individuals by $S(t)$ at time t, and the variables $E(t)$, $I_R(t)$, $I_D(t)$, $R(t)$, and $D(t)$ are defined analogously. We assume homogeneous mixing of the population and consider a memoryless, deterministic epidemic model. Specifically, the state of epidemic model evolves according to the set of ordinary differential equations (ODEs), by dropping the time index t for simplicity,

$$\frac{dS}{dt} = -\beta\frac{S(I_R + I_D)}{N},$$
$$\frac{dE}{dt} = \beta\frac{S(I_R + I_D)}{N} - \sigma E,$$
$$\frac{dI_R}{dt} = (1 - p_{death})\sigma E - \gamma I_R,$$
$$\frac{dI_D}{dt} = p_{death}\sigma E - \mu I_D,$$
$$\frac{dR}{dt} = \gamma I_R\,,$$
$$\frac{dD}{dt} = \mu I_D.$$

The model parameters are given by the infection rate β, the latency rate σ, the infection fatality probability p_{death}, the recovery rate γ, and the rate μ of transitioning from the compartment I_D to D. Provided that $\mu = \gamma$, the basic reproduction number is equal to $\mathcal{R}_0 = \beta/\gamma$, which is used to set the infection rate β given estimates for $\mathcal{R}_0$ and γ. Table A in Annex 1 summarises the values for the parameters that were used in the simulations.

Model initialisation

We initialise the model at time $t = 0$, which corresponds to 18 May 2026. The initial number of deceased individuals (suspected deaths) is obtained from [8] as $D(0) = 131$. The governing equations from our model imply that

$$R(0) = D(0)\frac{1 - p_{death}}{p_{death}}.$$

In [6], the cumulative number of infections as of 22 May 2026 is estimated, based on back-calculations from 204 suspected deaths, to be 1 054 under a main scenario. From this, we derive the ratio of undetected cases per suspected death and use this at t=0, to estimate the number of people who are infected, i.e.

$$x_{\text{init}} = I_R(0) + I_D(0) + D(0) + R(0).$$

This gives $x_{\text{init}} = D(0)\frac{1054}{204} = 677$, which yields that

$$I_R(0) = \big(x_{\text{init}} - D(0) - R(0)\big)(1 - p_{death})$$

and

$$I_D(0) = \big(x_{init} - D(0) - R(0)\big)p_{death}.$$

Finally, the initial number of exposed $E(0)$ is obtained from $I(0) = I_R(0) + I_D(0)$ by linearising the model around the disease-free equilibrium ($S \approx N$) and setting the fraction $E(0)/I(0)$ equal to the ratio of the respective components of the principal eigenvector of the linearised system. We obtain that

$$E(0) = \frac{1}{\frac{(1-p)\sigma}{\gamma + \lambda_1} + \frac{p\sigma}{\mu + \lambda_1}}\ I(0),$$

where λ_1 is the eigenvalue of the system matrix of the linearised system with the largest real part. Since the initial states $E(0)$, $I_R(0)$, $I_D(0)$ and $R(0)$ depend on parameters which are drawn from a prior distribution, the initial states are not deterministic.

Monte Carlo simulations

To capture uncertainty in input parameters, we used a Monte Carlo approach with $n_{sim} = 500$ independent simulations. For each simulation, parameters were randomly drawn from specified distributions:

- The probability of death p_{death} (infection fatality proportion) was sampled from a uniform distribution.
- The incubation period ($1/\sigma$) (time from infection to onset of symptoms) was sampled from a gamma-based distribution with specified mean and bounds.
- The infectious period for individuals who recover ($1/\gamma$) was sampled from a gamma-based distribution.
- The infectious period for individuals who die ($1/\mu$) was sampled from a gamma-based distribution.
- The basic reproduction number R_0 was sampled from a normal distribution. From this, the transmission rate β was derived as $\beta = \frac{R_0}{\frac{(1-p_{death})}{\gamma} + \frac{p_{death}}{\mu}}$, since the basic reproduction number is equal to the transmission rate

β (infected per time unit) times the expected infectious period, $R_0 = \beta\, E[T_{\text{inf}}]$. We have that $E[T_{\text{inf}}] = (1 - p_{death}) \times \frac{1}{\gamma} + p_{death}\frac{1}{\mu}$.

By sampling from the parameters according to the above distributions, we obtain a distribution of the output metrics (i.e. the state of the compartmental model over time and the importation probability). The empirical quantiles of these distributions yield the 90% uncertainty intervals of the output metrics reported in the main text.

Annex 2. Estimating the importation probability

In the following, we calculate the importation risk of BDBV into the EU/EEA. Specifically, we estimate the probability that at least one person who is exposed or infected (i.e. in compartment E, I_R or I_D) travels via plane from the outbreak region to the EU/EEA. Thus, we obtain the probability $p_{\text{imp}}(t)$ of importation on day t as

$$p_{\text{imp}}(t) = P(\text{at least one traveller in } E \text{ or } I) = 1 - P(\text{no traveller in } E \text{ or } I).$$

We define the probability $p(t)$ that a single traveller from the outbreak region to the EU/EEA is infected or exposed at time t, and we assume that infections of different travellers are stochastically independent. We model the probability $p(t)$ as

$$p(t) = \frac{E(t)}{N}(1 - \alpha p_E) + \frac{I(t)}{N}(1 - p_I).$$

Here, the parameters $p_E = 0.1$ and $p_I = 0.9$ are the travel reduction of an individual due to having dry symptoms and wet symptoms, respectively. In other words, the probability of a traveller to be exposed and infected is proportional to the fraction of the exposed and infected, respectively, individuals from the outbreak region times a travel reduction factor. The parameter α equals the fraction of the incubation period during which dry symptoms occur, i.e. $\alpha = \frac{10-6.22}{10} = 0.378$ using the parameters [14].

Let $N_{\text{out}}(t)$ be the number of travellers from the outbreak region to the EU/EEA at time t. Then, the probability that none of the $N_{\text{out}}(t)$ travellers is infected or exposed follows as

$$P(\text{no traveller in } E \text{ or } I) = P(\text{single passenger not in } E \text{ or } I)^{N_{\text{out}}(t)} = (1 - p(t))^{N_{\text{out}}(t)}.$$

This yields the probability of importation on day t as

$$p_{\text{imp}}(t) = 1 - \big(1 - p(t)\big)^{N_{\text{out}}(t)}.$$

Finally, as we are interested in the probability p_{imp} on any (at least one) from 11–25 June 2026, we obtain that

$$p_{\text{imp}} = 1 - \prod_{t=1}^{15} \Big(1 - p_{\text{imp}}(t)\Big),$$

where the time index $t = 1, \ldots, 15$ refers to 11–25 June 2026.

As an alternative metric to the importation probability p_{imp}, we calculate the expected number of travellers per importation. With the probability $p(t)$ of a passenger being exposed or infected on day t, the expected number of importations at time t equals

$$E[\text{number of importations}] = p(t) N_{\text{out}}(t).$$

By setting $E[\text{number of importations}] = 1$, the travellers per importation on day t equals $N_{\text{out,pI}} = 1/p(t)$.

Annex 3. Parameters

Table A. Parameters used in the mathematical model

Parameter	Description	Value/range	Reference/source
Population size	Total population of the outbreak area (Ituri and North Kivu)	13 392 200	McCabe et al. [6]
$\mathbf{R_0}$	Basic reproduction number	1.24	Mean of the estimates in Choi et al. [16]
CFR	Case-fatality ratio	0.32-0.54	Lower bound: MacNeil et al. [17] Upper bound: Rosello et al. [18] (lowest and highest values on grEPI)
Incubation period	Time from getting infected to becoming infectious	10 (2-21)	CDC [15]
Presymptomatic period	Time until first symptoms ('dry symptoms') appear	6.22	Velasquez et al. [14]
Infectious period when recovering	Time from first 'wet' symptoms/becoming infectious to recovery	10 (2-26)	Wamala et al. [19]
Infectious period when dying	Time from first 'wet' symptoms/becoming infectious to death	10 (3-21)	Wamala et al. [19]
Reported deaths	Deaths reported (suspected) at 22 May 2026	204	INSP [8] and McCabe et al. [6]
Total infections	Estimated total infections by 22 May 2026	1054	McCabe et al. [6]
Dark factor deaths	Factor of under-ascertainment (a fraction dark factor of deaths is not reported)	0.806	Estimated from suspected deaths and total cases as of May 22, 2026.
Travel probability reduction p_E given dry symptoms	Reduction in probability of travel for individuals suffering from mild ('dry') symptoms, due to symptoms, screening etc	0.1	ECDC expert opinion (estimate based on assumption that mild symptoms are unspecific and easy to treat)
Travel probability reduction p_D given wet symptoms	Reduction in probability of travel for symptomatic infectious individuals ('wet' symptoms), due to symptoms, screening etc	0.9	ECDC expert opinion (estimate based on assumption that most people who are infectious will be too sick to travel)