# The epidemiology of pathogens with pandemic potential: A review of key parameters and clustering analysis

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## Abstract

### Introduction

In the light of the COVID-19 pandemic many countries are trying to widen their pandemic planning from its traditional focus on influenza. However, it is impossible to draw up detailed plans for every pathogen with epidemic potential. We set out to try to simplify this process by reviewing the epidemiology of a range of pathogens with pandemic potential and seeing whether they fall into groups with shared epidemiological traits.

### Methods

We reviewed the epidemiological characteristics of 19 different pathogens with pandemic potential (those on the WHO priority list of pathogens, different strains of influenza and Mpox). We extracted data on the proportion of presymptomatic transmission, incubation period, serial interval and basic reproduction number ($R_0$) for the targeted pathogens. We applied unsupervised machine learning (specifically K-means and hierarchical clustering) to categorise these pathogens based on these characteristics. .

### Results

Fom 154 articles we extracted 306 epidemiological parameter estimates. The clustering algorithms categorise these pathogens into five archetypes (1) airborne pathogens with high transmission potential, (2) respiratory zoonoses characterized by high case fatality risk, (3) contact zoonoses with high fatality rates, (4) contact zoonoses exhibiting presymptomatic transmission, and (5) vector-borne pathogens capable of secondary human-to-human transmission.

### Conclusion

Unsupervised learning on epidemiological data can be used to predict distinct pathogen archetypes. This method offers a valuable framework to allocate emerging and novel pathogens into defined groups to evaluate common approaches for their control.

## 1. Introduction

Recent global epidemics of COVID-19 and Mpox have illustrated that we remain vulnerable to global biological incidents. Historically, pandemic preparedness strategies have been limited in scope. For instance, prior to COVID-19, the UK government's sole pandemic plan was the 2011 Influenza Pandemic Preparedness Strategy [1,2]. This narrow focus left critical gaps in threat readiness that have been exploited by non-influenza pathogens such as SARS-CoV-2 and Mpox virus (MPV).

Given the potential health and economic impacts of pandemics, the way in which we plan for such risks needs to be revised. There are 26 viral families known to infect humans [3], but only a fraction of these viruses will possess the ability for widespread transmission in the community [4]. Historically, this fraction has been listed, based on historical outbreaks and ranked to inform policy makers on which pathogens possess the highest pandemic potential. A list based approach, while useful, is inflexible and is rooted in responding to yesterday's pandemic rather than proactively planning.

Categorising pathogens based on shared epidemiological traits rather than using historical lists offers a more flexible and inclusive framework for pandemic planning [4]. A trait based approach would facilitate proactive planning for emerging threats by categorising pathogens by characteristics, allowing planners to assess a wider breadth of scenarios and control measures rather than specific historical examples [4].

To address these gaps, we propose classifying pathogens into archetypes based on epidemiological traits. Utilising data collected from reviews, we implement two unsupervised machine-learning models, K-means clustering and hierarchical clustering, to identify relevant pathogen archetypes. By categorising pathogens by their reproduction number, serial interval, case fatality ratio, proportion of presymptomatic transmission and transmission route, we show how pathogens can be grouped by shared characteristics which may point to common approaches for their control.

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## 2. Methods

### 2.1 Review of epidemiological parameters

We reviewed the human epidemiology of the World Health Organisation's (WHO) blueprint pathogens (as of June 2024) [5]. Including SARS-COV-2 (Wild type, Alpha, Delta & Omicron variants), Crimean–Congo hemorrhagic fever orthonairovirus (CCHFV), Ebola virus (EBOV), Marburg virus (MARV), Lassa virus (LASV), MERS-CoV, SARS-CoV-1, Nipah virus (NiV), Rift Valley fever virus (RVFV) and Zika virus (ZIKV) [5]. In addition, we reviewed; pandemic

influenza A virus (H1N1, H2N2, H3N2 & H1N1pdm09), influenza A virus subtype H5N1 (A/H5N1) and Mpox virus (MPV).

Standard search terms were developed based on the review objectives to collect information on epidemiological parameters of pathogens with pandemic potential. We reviewed these pathogens in terms of transmission route and epidemiological characteristics, including the basic reproduction number ($R_0$) and its associated dispersion parameter ($k$), incubation period, latent period, infectious period, serial interval, presymptomatic transmission, case fatality risk (CFR) and infection fatality risk (IFR).

Initial searches were conducted in PubMed to identify existing systematic reviews. Search terms used are listed in **Supplementary Table S1**. Studies were included if they provided quantitative estimates based on primary epidemiological data or meta-analyses of such data. Additional relevant parameters not captured during this search were retrieved via other methods (see supplement). Articles were included if they described and provided estimates of the desired epidemiological characteristics, or provided datasets allowing for parameter estimation.

### 2.2 Parameter estimation

We estimated key parameters that were not available from the literature review. Where appropriate, we estimated values for the incubation period, serial interval, $R_0$ and proportion of presymptomatic transmission for selected pathogens. For the incubation period, we used the {EpiLPS} package [6–8] where publicly available data permitted. We estimated serial intervals by fitting lognormal and gamma distributions to the number of onsets for a given day, accounting for double censoring using the R package {primarycensored} [9,10]. For $R_0$, we used the package {epichains} [10,11], to provide an estimate for CCHFV on the basis of data collected by the European Centre for Disease Prevention and Control [11]. We estimated presymptomatic transmission for all pathogens using published or derived incubation and serial interval estimates, assuming transmission occurred before symptom onset if the mean serial interval was shorter than the mean incubation period. Full methodological details are provided in the Supplementary Information.

### 2.3 Clustering of epidemiological parameters

The primary aim was to identify distinct pathogen archetypes which share similar epidemiological characteristics. For the clustering analysis, where possible, we used pooled values from systematic reviews for $R_0$, serial interval and CFR. Values and justifications are listed in supplementary data. In addition, we included the transmission route and the percentage of presymptomatic transmission. These values were selected as they represent key epidemiological quantities and were available for most pathogens.

We applied the unsupervised machine learning algorithm, K-means, to the dataset. The elbow method was used to help inform the optimal number of clusters. With the final K value being selected based on the elbow plot and practical interpretability of the resulting clusters.

In addition, hierarchical clustering was applied to the same dataset using Ward's linkage method. The results were visualised as a dendrogram, with discrete clusters identified by cutting the tree at a predefined level based on elbow plot analysis. Each pathogen was assigned to a cluster according to its hierarchical position, facilitating the identification of subgroups with shared epidemiological traits.

#### 2.3.1 Sensitivity analysis

We conducted sensitivity analyses by modifying the included parameters. Since serial interval estimates are not applicable for pathogens primarily transmitted via vectors, such as RVFV and ZIKV, we performed an alternative clustering analysis where serial interval and the percentage of presymptomatic transmission were excluded. This adjustment allowed us to incorporate RVFV into the clustering framework.

Additionally, we explored whether the clustering approach could be extended to other pathogens by including HIV. The serial interval for HIV is hard to define given that in a large number of cases the serial interval may be negative [12], in addition the CFR is also highly variable due to differences in access to treatment [13]. We conducted a sensitivity analysis in which we removed both CFR and serial interval. This modification allowed us to assess how HIV might be classified within the existing framework and whether this approach could be generalised to other infectious diseases with different transmission dynamics.

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## 3. Results

### 3.1 Parameter review

A total of 154 articles were retrieved (**Supplementary Figure S1**). This included 43 articles retrieved through the initial search of systematic reviews and 69 articles obtained from supplementary sources. Among these, one was a grey literature report published by the WHO.

For the estimation of key epidemiological parameters using the {EpiLPS} package, 28 articles were identified that provided sufficient data for manual parameter calculations. Additionally, 14 articles contributed pre-existing datasets that were incorporated into the analysis.

### 3.2 Epidemiological characteristics

#### 3.2.1 Transmission dynamics

We extracted 63 estimates for the reproduction number, which varied across pathogens and outbreaks due to differences in settings and the implementation of control measures (**Table 1**). One additional estimate was derived, with the median $R_0$ for CCHFV estimated at 0.03 (95% CrI: 0.004–0.09) based on cases reported in the European Union between 2013 and 2014.

A total of 15 estimates for the dispersion parameter (k) were extracted, revealing varying degrees of heterogeneity in transmission. SARS-CoV-1, SARS-CoV-2, MERS-CoV and NiV exhibited particularly low k values, indicating a high potential for superspreading events, whereas influenza displayed greater uniformity in transmission. Pathogens such as EBOV were reported to have a wide range of estimates suggesting the degree of superspreading may be dependent on outbreak setting (**Table 1**).

We also estimated the proportion of pre-symptomatic transmission for pathogens with reported incubation periods and serial intervals. Our analysis suggests that pre-symptomatic transmission was possible for SARS-CoV-2, SARS-CoV-1, pandemic influenza, MPV, and LASV (**Supplementary information**).

### 3.2.2 Time to key events

We extracted 51 estimates for the incubation period and provided 13 additional estimates based on publicly available data. The length of the incubation period varied across pathogens, with pandemic influenza exhibiting the shortest incubation period. In contrast, pathogens primarily transmitted through contact with infected body fluids, such as LASV, EBOV, and CCHF, had the longest incubation periods (**Table 1**).

For the serial interval, we extracted 33 estimates. As with the incubation period, serial intervals were shortest for pandemic influenza and SARS-CoV-2 and longest for contact-transmitted pathogens (**Table 1**). Additionally, we estimated serial intervals for LASV and CCHF, with mean values of 11.5 days (95% CrI: 0.9–34.6) and 12.0 days (95% CrI: 3.0–27.2), respectively.

For the latent and infectious periods, we extracted 27 and 33 estimates, respectively. These durations showed notable variation between pathogens, highlighting differences in disease progression **(Table 1**).

### 3.2.3 Severity and Mortality Risk

We extracted 59 estimates for the case fatality rate (CFR) and 25 for the infection fatality rate (IFR). CFR estimates exhibited a broad range across pathogens, reflecting varying levels of disease severity (**Table 1**). Additionally, CFR varied within pathogens, with substantial heterogeneity between studies, outbreaks and age groups. For instance, NiV outbreaks with implemented control measures reported lower CFR estimates (**Table 1**).

Compared to CFR, fewer IFR estimates were reported. IFR values were consistently lower than CFR estimates for the same pathogen and demonstrated age-dependent variation (**Table 1**)

**See Table 1. for Epidemiological parameters of pandemic potential pathogens. Located after conclusion**

### 3.3 K-means clustering

A different number of clusters were modeled (K=1-10) (**Figure 1a**). The five cluster solution was ultimately considered the most appropriate according to the elbow method (**Figure 1a**) as well as heuristically since it sufficiently separates the high consequence infectious diseases (HCID) by transmission route and presymptomatic transmission **(Figure 1b)**. In the final clustering, CCHFV, MARV, EBOV, and NiV were grouped into cluster 1; H5N1 and MERS-CoV into cluster 2; LASV and MPV into cluster 3; SARS-CoV-1, SARS-CoV-2 (all variants), and all pandemic influenza subtypes (except H5N1) into cluster 4; and ZIKV into cluster 5 (**Figure 1c**). The characteristics of each archetype are detailed in **Table 2**.

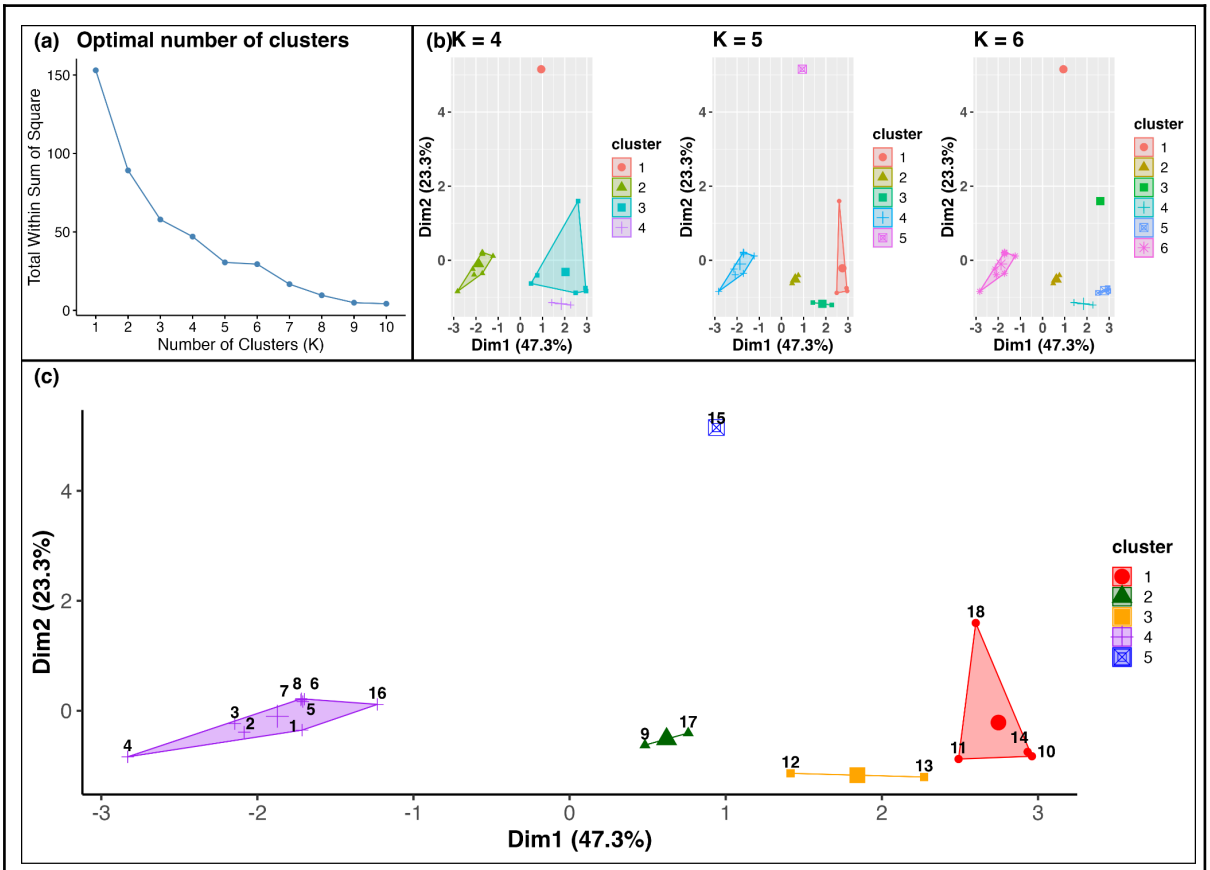


**Figure 1. Clustering results using K-means.**
(a) Elbow plot used to determine the optimal number of clusters. (b) Initial clustering analysis using three K values (K = 4,5,6). (c) Final solution retaining K = 5 clusters.

1) SARS-CoV-2 (WT). 2) SARS-CoV-2 (Alpha). 3) SARS-CoV-2 (Delta). 4) SARS-CoV-2

(Omicron). 5) A/H5N1. 6) A/H2N2. 7) A/H3N2. 8) A/H1N1pdm09. 9) A/H5N1. 10) EBOV. 11) MARV. 12) MPV. 13) LASV. 14) NiV. 15) ZIKV. 16) SARS-CoV-1. 17) MERS-CoV. 18) CCHFV. Larger unlabeled central points represent cluster centroids. The ZIKV cluster is a cluster of one therefore there is no central point.

**Table 2. K-means archetype characterisation.**

| Archetype | Pathogens | Range of estimates | | | | Transmission route |
|---|---|---|---|---|---|---|
| | | $R_0$ | Serial interval (d) | CFR (%) | Proportion of presymptomatic transmission (%) | |
| **1** | CCHFV, MARV, EBOV, NIV | 0.03–1.95 | 9.20–15.40 | 11.70–61.90 | 0–0 | Direct contact (n=4)<br>Animal to human (n=4)<br>Vector (n=1) |
| **2** | H5N1, MERS-CoV | 0.18–0.95 | 6.80–12.60 | 39.10–53.50 | 0–0 | Respiratory (n=2)<br>Animal to human (n=2) |
| **3** | LASV, MPV | 0.73–1.80 | 8.50–11.80 | 8.70–33.10 | 36.0–38.0 | Direct contact (n=2)<br>Animal to human (n=2) |
| **4** | SARS-CoV-1, SARS-CoV-2 (all variants), Pandemic influenza (all subtypes, except H5N1) | 1.46–9.50 | 3.08–8.32 | 0.02–9.60 | 0.1–25.0 | Respiratory (n=9) |
| **5** | ZIKV | 0.15 | 12.0 | 0.02 | 0 | Vector (n=1) |

### 3.4 Hierarchical clustering

A series of cluster numbers were modelled (K=1-10) (**Figure 2a**)**.** Hierarchical clustering into five clusters was deemed the most appropriate segmentation of pathogens following the elbow method (**Figure 2a**) and considering the division of pathogens (**Figure 2b).** The five-cluster algorithm classified SARS-CoV-2 (all variants), and pandemic influenza (all subtypes) into cluster 1; MARV, EBOV and NiV, into cluster 2; LASV, and MPV, into cluster 3; ZIKV and CCHFV into cluster 4; and A/H5N1, MERS-CoV and SARS-CoV-1, into cluster 5 (**Figure 2c**). **Table 3** summaries the characteristics of each archetype.

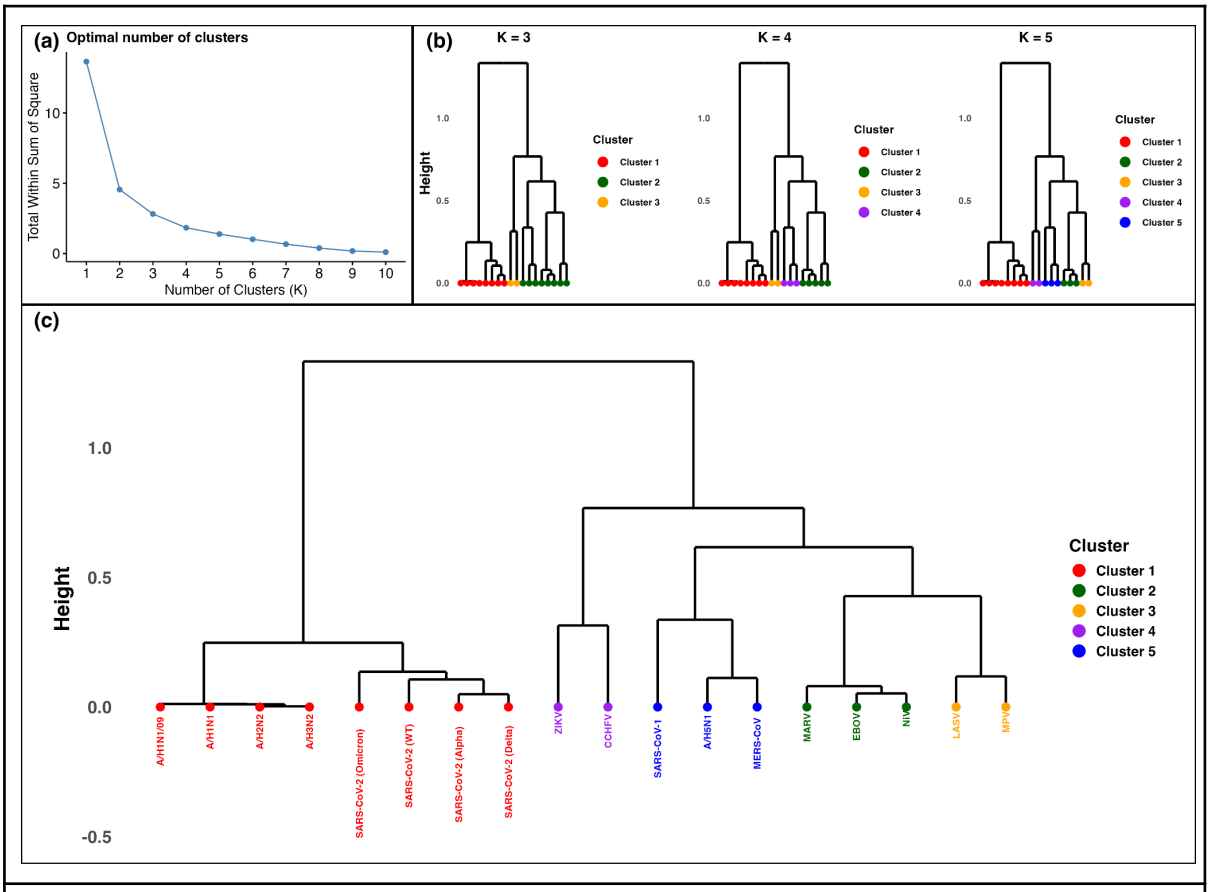


**Figure 2. Hierarchical clustering results.**
(a) Elbow plot used to determine the optimal number of clusters. (b) Initial clustering analysis using three K values (K = 3,4,5) (c) Final solution retaining five clusters.

| Table 3. Hierarchical clustering archetype characterisation. | | | | | | |
|---|---|---|---|---|---|---|
| **Archetype** | **Pathogens** | **Range of estimates** | | | | Transmission route |
| | | $R_0$ | Serial interval (d) | CFR (%) | Proportion of presymptomatic transmission (%) | |
| 1 | SARS-CoV-2 (all variants), Pandemic influenza (all subtypes) | 1.46–9.5 | 3.08–4.82 | 0.02–2.67 | 0.3–25 | Respiratory (n=8) |
| 2 | MARV, EBOV, NIV | 0.33–1.95 | 9.2–15.4 | 61– 61.9 | 0–0 | Direct contact (n=3)<br>Animal to human (n=3) |
| 3 | LASV, MPV | 0.73–1.80 | 8.50–11.80 | 8.70–33.10 | 36.0–38.0 | Direct contact (n=2)<br>Animal to human (n=2) |
| 4 | ZIKV, CCHFV | 0.03–0.15 | 12–12 | 0.02–11.7 | 0–0 | Vector (n=2)<br>Sexual contact (n=1)<br>Direct contact (n=1)<br>Animal to human (n=1) |
| 5 | H5N1, MERS-CoV, SARS-CoV-1 | 0.18– 2.9 | 6.8–12.6 | 9.6–53.5 | 0–0.1 | Respiratory (n=3)<br>Animal to human (n=2) |

### 3.5 Archetype characterisation

#### 3.5.1 Airborne, High Transmission Pathogens

SARS-CoV-2 (all variants), and pandemic influenza are consistently grouped together. This group is characterised by a high $R_0$, short serial intervals, and variable presymptomatic transmission. These pathogens share an airborne transmission route (**Table 2 and 3**). Notably, SARS-CoV-1 was grouped with this archetype in the K-means clustering method but classified separately when using hierarchical clustering. When SARS-CoV-1 is classified with this group it broadens the range of serial intervals and CFR's (**Table 2**).

#### 3.5.2 Respiratory Zoonoses with High CFR

A/H5N1 and MERS-CoV likewise are consistently clustered together, characterised by a low $R_0$ and moderate serial intervals , but high CFRs. Unlike the other respiratory archetype, this group has no evidence for presymptomatic transmission. This archetype contains pathogens

that are primarily transmitted from animals to humans, with limited human-to-human transmission (low $R_0$).

When hierarchical clustering is used, SARS-CoV-1 was included in this category, suggesting that this pathogen may reasonably be grouped with either archetype. When grouped together, the range of $R_0$, CFR and proportion of presymptomatic transmission are widened (**Table 3**)

### 3.5.3 Contact Zoonoses with High CFR

Both clustering approaches consistently grouped MARV, EBOV, and NiV together as high-CFR, contact-transmitted pathogens. This archetype exhibit low $R_0$ values, long serial intervals, and high CFRs (**Table 2**). This archetype is transmitted via direct contact with infected bodily fluids or animal-to-human spillover.

Although MARV, EBOV, and NiV remained stable in their clustering, the classification of CCHFV varied between methods. This led to differences in the characteristics of the corresponding archetypes (**Tables 2 and 3**).

### 3.5.4 Contact Zoonoses with Evidence of Presymptomatic Transmission

LASV and MPV were consistently grouped together, forming an archetype characterised by low to moderate $R_0$ values , long serial intervals, and moderate CFRs. These pathogens may exhibit some degree of presymptomatic transmission (**Table 2 and 3**).

### 3.5.5 Vector-Borne Pathogens with Secondary Transmission Routes

ZIKV was identified as a distinct archetype in K-means clustering but was grouped with CCHFV in hierarchical clustering. CCHFV was alternatively classified either with vector-borne pathogens alongside ZIKV or with contact-transmitted pathogens, depending on the clustering method.

Despite these differences in grouping, both approaches consistently identified low $R_0$ values and long serial intervals for human-to-human transmission. However, when CCHFV is included, the CFR range expands (**Table 2 and 3**).

### 3.5.6 Excluded Pathogens

No human to human transmission has been documented [14] for RVFV, therefore its serial interval is undefined (indeed, it is also difficult to define a serial interval for vector-borne Zika infections) and was not included in the main clustering analysis. When clustering was performed without serial interval and presymptomatic transmission data, and using $R_0$ values from vector-borne transmission, RVFV was grouped with CCHFV (**Supplementary Figure S4**) or appeared as an independent branch close to the HCIDs (**Supplementary Figure S5**).

HIV was not included within the parameter review, however using $R_0$ and proportion of presymptomatic values from Fraser et al. 2004 [15]. HIV will form its own archetype (**Supplementary figure S6 and 7)**

## 4. Discussion

We reviewed key epidemiological parameters for 19 pathogens with pandemic potential and applied two clustering algorithms to identify distinct pathogen archetypes that share similar characteristics. Our findings suggest that grouping pathogens based on transmission traits—such as $R_0$, serial interval, CFR, presymptomatic transmission, and transmission route— could provide a pragmatic approach to pandemic preparedness.

The most frequently reported parameters were the incubation period, reproduction number, and CFR. However, data availability was uneven, with SARS-CoV-2 and influenza accounting for nearly half of all estimates. Parameter estimates varied both across pathogens and within studies of the same pathogen, aligning with previous reviews [16]. Notably, $R_0$, serial interval, and CFR estimates were highly context-dependent. For example, MERS-CoV $R_0$ estimates ranged from 5.4 (95% CI: 4.61-6.19) in an uncontrolled hospital outbreak to 0.14 (95% CI: 0.04-0.26) with control measures in place (Park et al. 2018). Similarly, influenza A/H1N1 $R_0$ estimates were higher in confined settings compared to overall estimates [18]. Likewise EBOV estimates varied by country during the 2013-2016 epidemic [19]. Serial interval estimates also decreased when control measures were implemented, with the serial interval of SARS-CoV-2 decreasing post epidemic peak in China correlating with decreased time to isolation (Xu et al. 2023).

There were considerable differences in CFR estimates between outbreaks of the same pathogen. Influenza A/H5N1 varies by clade [21]. MPV varies when hospital care is available [22] or when comparing outcomes from outbreaks in Africa to outbreaks in the United States (Bunge et al. 2022). Varying estimates for NiV highlights how CFR can vary depending on country, strain and the control measures implemented, with the CFR being lower in Singapore (1999) compared to Malaysia (1998-1999) [25]. These examples illustrate that parameter estimates are generated across a wide range of contexts and the importance of contextualising parameter estimates when applying them to modeling efforts.

Our clustering analysis identified five pathogen archetypes, each with shared characteristics that could inform group-based control strategies rather than a pathogen-specific approach. With the effectiveness of interventions such as contact tracing and case isolation being influenced by $R_0$ and presymptomatic transmission [15], as well as the serial interval [26].

The limitations of this approach include the potential for the grouping of pathogens which may not display similar characteristics in reality. This is particularly seen in the archetype containing LASV and MPV. Presymptomatic spread has been documented for Mpox [27], it however remains uncertain for Lassa fever. Discrepancies in symptom onset reporting in source datasets may have led to an overestimation of presymptomatic transmission for LASV. Additionally, the $R_0$ estimate for LASV is derived from a hospital outbreak [28] and

will not reflect community-level transmission. The clustering of LASV and MPV may imply a higher risk of sustained human-to-human LASV transmission than observed in endemic communities, where transmission is primarily zoonotic with occasional nosocomial outbreaks [29]. These potential discrepancies highlight the need to continually update the parameter estimates used in this framework once they become available.

These findings highlight the potential for this framework to serve as an adaptable tool for classifying and assessing pathogens beyond those included in this study. The inclusion of HIV in our sensitivity analysis illustrates how this clustering approach could extend to a wide spectrum of infectious diseases with different transmission dynamics. Moreover, the framework could be continuously updated as new epidemiological data emerge, refining clustering methods and integrating additional pathogens, including both novel and emerging threats.

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## 5. Conclusion

Documenting epidemiological parameters is crucial for effective outbreak risk analysis. We provide 342 parameter estimates for 19 pathogens, offering a valuable foundation for modeling their spread and containment. However, key transmission parameters—such as the dispersion parameter and latent period—remain underreported, highlighting the need for further research to strengthen outbreak preparedness. Our clustering approach demonstrates a practical framework for evaluating control strategies across groups of similar pathogens. By maintaining a dynamic classification system, public health preparedness efforts can shift away from a reactive, pathogen-specific focus toward a more anticipatory, trait-based strategy for managing future infectious disease risks.

**Table 1. Epidemiological parameters of pandemic potential pathogens**

| Pathogen | Parameter | Description | Value | Reference |
|---|---|---|---|---|
| A/H1N1 | Basic reproduction number | Systematic review of the reproduction number for pandemic influenza. Combined estimates for the basic and effective reproductive numbers and presenting median estimates. All waves | Median: 1.8 (IQR: 1.47-2.27) | Biggerstaff et al. 2014 [18] |
| | | Systematic review of the reproduction number for pandemic influenza. Combined estimates for the basic and effective reproductive numbers | Median: 3.82 (IQR: 2.68-4.84) | Biggerstaff et al. 2014 [18] |

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|---|---|---|---|---|
| | | and presenting median estimates. Confined settings | | |
| | | Systematic review of the reproduction number for pandemic influenza. Combined estimates for the basic and effective reproductive numbers and presenting median estimates. 1st wave | Median: 1.81 (IQR: 1.50-2.28) | Biggerstaff et al. 2014 [18] |
| | | Systematic review of the reproduction number for pandemic influenza. Combined estimates for the basic and effective reproductive numbers and presenting median estimates. 2nd wave | Median:1.73 (IQR: 1.39-2.33) | Biggerstaff et al. 2014 [18] |
| | | Systematic review of the reproduction number for pandemic influenza. Combined estimates for the basic and effective reproductive numbers and presenting median estimates. 3rd wave | Median:1.70 (IQR: 1.55-1.76) | Biggerstaff et al. 2014 [18] |
| | Dispersion parameter | Modelling, estimated using time series analysis, using a large household survey dataset conducted in Maryland late 1918 | 0.94 (95% CI: 0.59-1.72) | Fraser et al. 2011 [30] |
| | Serial interval (d) | Median of the mean generation time or serial interval used to estimate reproduction number. | Median: 3.3 (range: 1.5-6.0) | Biggerstaff et al. 2014 [18] |
| | | Systematic review for serial interval estimates for influenza up to 2013. | 6 studies with a range of 1.9 to 8.28 days | Vink et al. 2014 [36] |
| | Incubation period (d) | Modelling study, estimated through the re-analysis of daily incidence data of cases on ships departing Australia in 1919 | Lognormal distribution with mean of 1.34 | Nishiura 2007 [31] |
| | Latent period (d) | Modelling study, viral excretion profile over time used directly to estimate latent period. (H1N1/H3N2) | Weibull distribution with mean of 1.60 (95% CI: 1.50-1.70) | Cori et al. 2012 [32] |
| | Infectious period (d) | Modelling study, viral excretion profile over time used directly to estimate infectious period. (H1N1/H3N2) | Weibull distribution with mean of 1.0 (95% CI: 0.50-1.70) | Cori et al. 2012 [32] |

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|---|---|---|---|---|
| | Case fatality risk (%) | Modelling, referenced range of CFR's for H1N1 pandemic. | 1-4 | Carrat et al. 2006 [33] |
| | | Pandemic Influenza Risk Management<br>WHO Guidance. Estimated value (for 1918 pandemic) | 2-3 | WHO 2017 [34] |
| A/H1N1pdm09 | Basic reproduction number | Systematic review of the reproduction number for pandemic influenza. Combined estimates for the basic and effective reproductive numbers and presenting median estimates. | Median: 1.46 (IQR: 1.30-1.70) | Biggerstaff et al. 2014 [18] |
| | | Systematic review of the reproduction number for pandemic influenza. Combined estimates for the basic and effective reproductive numbers and presenting median estimates. Confined settings | Median: 1.96 (IQR: 1.50-2.23) | Biggerstaff et al. 2014 [18] |
| | | Systematic review of the reproduction number for pandemic influenza. Combined estimates for the basic and effective reproductive numbers and presenting median estimates. 1st wave | Median:1.47 (IQR: 1.31-1.71) | Biggerstaff et al. 2014 [18] |
| | | Systematic review of the reproduction number for pandemic influenza. Combined estimates for the basic and effective reproductive numbers and presenting median estimates. 2nd wave | Median: 1.48 (IQR: 1.30-1.66) | Biggerstaff et al. 2014 [18] |
| | Dispersion parameter | Review. Pooled estimate of k (based on studies describing community transmission). | 0.91 | Chen et al. 2021 [35] |
| | Serial interval (d) | Median of the mean generation time or serial interval used to estimate reproduction number. | Median: 2.8. (range: 1.90-7.0) | Biggerstaff et al. 2014 [18] |
| | | Systematic review for serial interval estimates for influenza up to 2013. | 36 studies ranging from 1.9 to 5 days | Vink et al. 2014 [36] |
| | | Estimates from household datasets with information on symptom onset dates. | Mean ranged from 1.7 to 3.7 days, with a pooled mean of 2.8 | Vink et al. 2014 [36] |

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|---|---|---|---|---|
| | | Serial interval estimated from model fit of the serial interval to index case–to–case interval data | Normal distribution with mean of 2.1 | Vink et al. 2014 [36] |
| | Incubation period (d) | Modeling study, estimated using laboratory-confirmed swine influenza case-information in the UK 2009 | Weibull distribution with mean of 1.66 (95% CI: 1.42-1.90) | Tom et al. 2010 [37] |
| | | Modeling study, estimated using laboratory-confirmed swine influenza case-information in the UK 2009 | Gamma distribution with mean of 1.65 (95% CI: 1.41-1.89) | Tom et al. 2010 [37] |
| | | EpiLPS - Dataset from Lessler et al. 2009 [38] | Semipar. Distribution with mean of 2.0 (95% CI:1.80-2.10) | Estimated |
| | | Modelling study - Outbreak of 2009 Pandemic Influenza A (H1N1) at a New York City School | Median: 1.4 days (95% CI: 1.0–1.8) | Lessler et al. 2009 [39] |
| | Latent period (d) | Modelling study, estimated using data on laboratory-confirmed cases of pandemic H1N1 influenza reported in Ontario, Canada, between Apr. 13 and June 20, 2009 | Mean: 2.62 (95% CI: 2.28-3.12) | Tuite et al. 2010 [40] |
| | Infectious period (d) | Modelling study, estimated using data on laboratory-confirmed cases of pandemic H1N1 influenza reported in Ontario, Canada, between Apr. 13 and June 20, 2009 | Mean: 3.38 (95% CI: 2.06-4.69) | Tuite et al. 2010 [40] |
| | Case fatality risk (%) | Pandemic Influenza Risk Management<br>WHO Guidance. Estimated value. 2009 pandemic | 0.02 | WHO 2017 [34] |
| | | Sero-epidemiological study. Prevalence of cross‐reactive antibodies to H1N1pdm virus and rates of H1N1pdm infection | 0.02 | Van Kerkhove et al. 2013 [41] |
| | Infection fatality risk | Systematic review of published estimates of the case fatality risk of | Point estimates 0–13,500 deaths per | Wong et al. 2013 (Wong et al. 2013) |

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|---|---|---|---|---|
| | | H1N1pdm09 up to 2013. Laboratory-confirmed cases | 100,000 cases | |
| | | Symptomatic cases | Point estimates 0–1,200 per 100,000 cases | Wong et al. 2013 (Wong et al. 2013) |
| | | Infections | Point estimates 1–10 per 100,000 infections | Wong et al. 2013 (Wong et al. 2013) |
| | | Symptomatic cases in children | One death per 100,000 symptomatic cases in children | Wong et al. 2013 (Wong et al. 2013) |
| | | Symptomatic cases in the elderly | Approximately 1,000 deaths per 100,000 symptomatic cases in the elderly, | Wong et al. 2013 (Wong et al. 2013) |
| A/H2N2 | Basic reproduction number | Systematic review of the reproduction number for pandemic influenza. Combined estimates for the basic and effective reproductive numbers and presenting median estimates. | Median: 1.65 (IQR: 1.53-1.70) | Biggerstaff et al. 2014 [18] |
| | Serial interval (d) | Median of the mean generation time or serial interval used to estimate reproduction number. | Median: 3.5 (Range: 2.60-4.10) | Biggerstaff et al. 2014 [18] |
| | Incubation period (d) | Systematic review of volunteer challenge studies | Median: 2 (IQR: 2.00-2.50) | Carrat et al. 2008 [43] |
| | Latent period (d) | Modelling study, assumed value | Mean: 1.9 | Elveback et al. 1976 [44] |
| | Infectious period (d) | Modelling study, assumed value | Mean: 4.1 | Elveback et al. 1976 [44] |
| | Case fatality risk (%) | Pandemic Influenza Risk Management<br>WHO Guidance. Estimated value. (1957 pandemic) | 0.2 | WHO 2017 [34] |

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| A/H3N2 | Basic reproduction number | Systematic review of the reproduction number for pandemic influenza. Combined estimates for the basic and effective reproductive numbers and presenting median estimates. | Median: 1.80 (IQR: 1.56-1.85) | Biggerstaff et al. 2014 [18] |
| | | Systematic review of the reproduction number for pandemic influenza. Combined estimates for the basic and effective reproductive numbers and presenting median estimates. Confined settings | Median: 1.39 | Biggerstaff et al. 2014 [18] |
| | | Systematic review of the reproduction number for pandemic influenza. Combined estimates for the basic and effective reproductive numbers and presenting median estimates. 1st wave | Median: 1.56 | Biggerstaff et al. 2014 [18] |
| | | Systematic review of the reproduction number for pandemic influenza. Combined estimates for the basic and effective reproductive numbers and presenting median estimates. 2nd wave | Median: 1.68 | Biggerstaff et al. 2014 [18] |
| | Serial interval (d) | Median of the mean generation time or serial interval used to estimate reproduction number. | Median: 4.0 (Range: 2.95-4.10) | Biggerstaff et al. 2014 [18] |
| | | Systematic review for serial interval estimates for influenza up to 2013. | Mean values of 3.1 and 3.4 | Vink et al. 2014 [36] |
| | | Estimates from household datasets with information on symptom onset dates. | Normal distribution with mean of 2.2 | Vink et al. 2014 [36] |
| | Incubation period (d) | Modelling study, estimated through analysis of an outbreak of influenza aboard a commercial airliner | Weibull distribution with mean of 1.48 | Ferguson et al. 2005 [46] |
| | Latent period (d) | Modelling. Assumed value. Assumed to be same length as incubation period | Weibull distribution with mean of 1.48 | Ferguson et al. 2005 [46] |
| | Infectious period (d) | Modelling. Transmission model to estimate the main characteristics of influenza transmission in households | Gamma distribution with mean of | Cauchemez et al. 2004 [47] |

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| | | | 3.80 (95% CI: 3.10-4.60) | |
| | | Modelling. Transmission model to estimate the main characteristics of influenza transmission in households (Children) | Gamma distribution with mean of 3.60 (95% CI: 2.30-5.20) | Cauchemez et al. 2004 [47] |
| | | Modelling. Transmission model to estimate the main characteristics of influenza transmission in households (Adults) | Gamma distribution with mean of 3.9 (95% CI: 3.20-4.90) | Cauchemez et al. 2004 [47] |
| | Case fatality risk (%) | Pandemic Influenza Risk Management<br>WHO Guidance. Estimated value. (1964 pandemic) | 0.2 | WHO 2017 [34] |
| A/H5N1 | Basic reproduction number | Modelling study, estimated Re in Vietnam 2004–2006. | 0.0 (95% CI: 0.0-0.42) | Bettencourt and Ribeiro 2008 [48] |
| | | Modelling study, estimated Re in Indonesia 2004–2006. | 0.0 (95% CI: 0.0-0.0) | Bettencourt and Ribeiro 2008 [48] |
| | | Modelling study, estimated Re in Indonesia 2005–2009. | 0.1-0.25 (95% CI: 0.0-0.40) | Aditama et al. 2012 [49] |
| | | Modelling study, estimated lower limit on the local R0 in a household outbreak in Indonesia 2006. | 1.14 (95% CI: 0.61-2.14) | Yang et al. 2007 [50] |
| | | Modelling. Estimated from previous human to human cases. | 0.06 (95% CI: 0.01-0.2) | Ferguson et al. 2004 [51] |
| | Serial interval (d) | Median of the mean value of generation time or serial interval used to estimate reproduction number. | Mean: 7.8 (range: 6.0-9.5) | Biggerstaff et al. 2014 [18] |
| | | Modelling. Estimated by fitting case data from Aditama et al. 2012. Preprint | Median: 6.80 (95% CrI: 0.3–13.3) | Ward et al. 2024 [52] |
| | Incubation period (d) | Review, median value from outbreaks in Thailand and Vietnam 2004 | Median: 4.0 (range: 2.0-8.0) | Beigel et al. 2005 [53] |
| | | Estimated value. Retrospective descriptive study of 24 human cases in China 1997-2008 | Median: 5.0 (range: 2.0-9.50) | Huai et al. 2008 [54] |

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| | | Estimated value, using survival analysis techniques. 43 human cases in China | Weibull distribution with mean of 3.30 (95% CI: 2.70-3.90) | Cowling et al. 2013 [55] |
| | | Estimated value, 8 human cases in Eastern Turkey in 2006 | Mean: 5 (Range: 4.0-7.0) | Oner et al 2006 [56] |
| | Infectious period (d) | Modelling. Assumed value. Family Cluster, Indonesia 2006 | Uniform distribution with mean of 9 (range 5-13) | Yang et al. 2007 [50] |
| | Case fatality risk (%) | Systematic Review. Crude CFR 1997-2009 | Median: 56.3% (IQR: 32.5–77.8) | Van Kerkhove et al. 2011 [57] |
| | | Systematic review of individual case data. 1997-2015 (Overall) | 53.5 | Lai et al. 2016 [21] |
| | | Systematic review of individual case data. 1997-2015 (Clade 0) | 31.6 | Lai et al. 2016 [21] |
| | | Systematic review of individual case data. 1997-2015 (Clade 1) | 58.6 | Lai et al. 2016 [21] |
| | | Systematic review of individual case data. 1997-2015 (Clade 2.1) | 84.6 | Lai et al. 2016 [21] |
| | | Systematic review of individual case data. 1997-2015 (Clade 2.2) | 33.2 | Lai et al. 2016 [21] |
| | | Systematic review of individual case data. 1997-2015 (Clade 2.3) | 61.8 | Lai et al. 2016 [21] |
| | | Systematic review of individual case data. 1997-2015 (Clade 7) | 100 | Lai et al. 2016 [21] |
| | Infection fatality risk (%) | Adjusted CFR based on surveillance and seroprevalence studies | 14-33 | Li et al. 2008 [58] |
| CCHFV | Basic reproduction number | Estimated using epichains. Using data from cases of CCHFV infected in the European union/European | Median: 0.03 (95% CrI: 0.004–0.09) | Estimated |

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| | | Economic Area from 2013–2024. | | |
| | Serial interval (d) | Estimated from fitting outbreak data reporting the interval between the onset of illness in successive cases. | Gamma distribution with mean of 12.0 days (95% CrI: 3.0–27.2) | Estimated |
| | Incubation period (d) | EpiLPS – Dataset collected from review. | Gamma distribution with mean of 5.70 (95% CI: 5.30-6.00) | Estimated |
| | Case fatality risk (%) | Review of published reports of CCHF in Europe, Asia, middle east and Africa. 1944-2010 | Mean: 30.6 | Bente et al. 2013 [59] |
| | | Systematic review, CFR worldwide of confirmed cases 1948-2018 | Mean: 19.9 (IQR: 8-32) | Belhadi et al. 2022 [60] |
| | | Systematic review, Overall CFR (%) with ongoing CCHF infection up to 2020 | 11.7% (95% CI: 9.1-14.5) | Belobo et al. 2021 [61] |
| | | Systematic review, fatality rate in the Arab world 1978 to 2021 | Mean: 29 (range: 24-61) | Perveen and Gulfaraz Khan 2022 [62] |
| | | Systematic review, CFR calculated from annual cases from 1944 to 2017 | Mean: 32.2 | Nasirian 2020 [63] |
| EBOV | Basic reproduction number | Systematic review. R0 reported as a range of central estimates, from database inception up to July 2023 | 0.05-12.00 | Nash et al. 2024 [16] |
| | | Systematic review. Pooled mean of Ebola R0 in African countries from 1976 to February 2023. | Mean: 1.95 (95% CI: 1.74-2.15) | Muzembo et al. 2024 [19] |
| | | Transmission in hospitals and funeral rites during the 2013–2016 Ebola epidemic in West Africa (overall basic reproductive number) | Mean: 1.8 (range: 1.5-2) | Muzembo et al. 2024 [19] |
| | | Systematic review, Zaire ebolavirus,2013-2016 epidemic in Nigeria (pooled mean). | Mean: 9.38 (95% CI: 4.16-14.59) | Muzembo et al. 2024 [19] |

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| | | Systematic review, Zaire ebolavirus,2013-2016 epidemic in DRC (pooled mean) | Mean: 3.31 (95% CI: 2.3-4.32) | Muzembo et al. 2024 [19] |
| | | Systematic review, Sudan ebolavirus, 2000 outbreak in Uganda (pooled mean Ebola). | Mean: 2.0 (95% CI: 1.25-2.76) | Muzembo et al. 2024 [19] |
| | | Systematic review, Zaire ebolavirus, 2013-2016 epidemic in Liberia (pooled mean) | Mean: 1.83 (95% CI: 1.61-2.05) | Muzembo et al. 2024 [19] |
| | | Systematic review, Zaire ebolavirus,2013-2016 epidemic in Sierra Leonne (pooled mean) | Mean: 1.73 (95% CI: 1.47-2.0) | Muzembo et al. 2024 [19] |
| | | Systematic review, Zaire ebolavirus,2013-2016 epidemic in Guinea (pooled mean | Mean: 1.44 (95% CI: 1.29-1.6) | Muzembo et al. 2024 [19] |
| | | Systematic review of early modelling studies. 2013-2016 Epidemic in four West African countries. median of the R0 means reported. | Median: 1.78 (IQR: 1.44-1.78) | Wong et al. 2017 [65] |
| | Dispersion parameter | Systematic review. K reported as a range of central estimates, up to July 2023 | 0.02-2.20 | Nash et al. 2024 [16] |
| | Serial interval (d) | Systematic review, up to July 2023 (Pooled value). | Mean: 15.4 (95% CI: 13.20-17.50) | Nash et al. 2024 [16] |
| | | Systematic review of early modelling studies. 2013-2016 Epidemics in four West African countries. median of the means reported. | Median: 14.35 (IQR: 12.28-16.35) | Wong et al. 2017 [65] |
| | Incubation period (d) | Systematic review up to July 2023. Pooled random effect | Mean: 8.5 (95% CI: 7.70-9.20) | Nash et al. 2024 [16] |
| | Latent period (d) | Systematic review- 1976 to 2000. Data from individuals with single-day exposures | Mean: 12.27 | Velásquez et al. 2015 [67] |
| | | Systematic review of early modelling studies. 2013-2016 Epidemic in four West African countries. median of the means reported. | Median: 9.7 (IQR: 8.8-10.38) | Wong et al. 2017 [65] |

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| | | Systematic review up to July 2023. Pooled random effect | 0.10-31.20 | Nash et al. 2024 [16] |
| | Infectious period (d) | Systematic review up to July 2023. Pooled random effect and range of central estimates | Mean: 5.0 (95% CI: 3.70-6.30) | Nash et al. 2024 [16] |
| | | Systematic review of early modelling studies. 2013-2016 Epidemic in four West African countries. median of the means reported | Median: 7 (IQR: 4-10) | Wong et al. 2017 [65] |
| | | Systematic review- 1976 to 2000. data from individuals with single-day exposures (Survivors) | Mean:9.4 | Velásquez et al. 2015 [67] |
| | | Systematic review- 1976 to 2000. data from individuals with single-day exposures (fatal infections) | Mean: 5.33 | Velásquez et al. 2015 [67] |
| | Case fatality risk (%) | Systematic review up to July 2023. Mean CFR across all estimates | Mean: 57.8 | Nash et al. 2024 [16] |
| | | Systematic review of Asian and African countries between 1999 and June 2021, estimated pooled case fatality rates | 61.1 (95% CI: 50.26-71.85) | Khan et al. 2022 [69] |
| LASV | Effective reproduction number | Modelling. Estimated from published outbreaks and the number of LF hospitalized patients to Kenema Government Hospital in Sierra Leone. Pure human to human transmission | 0.73 | Lo Iacono et al. 2015 [28] |
| | Serial interval (d) | Estimated using Lo Iacono et al. 2015 [28] data combined with outbreak data. fitted to a lognormal distribution | Lognormal distribution with mean of 11.5 days (95% CrI: 0.9-34.6) | Estimated |
| | | Modelling study, referenced value (Lo Iacono et al. 2015 [28]) | Gamma distribution with mean of 7.8 | Zhao et al. 2020 [72] |
| | Incubation period (d) | Systematic review, range of central estimates reported | Range: 7.0-12.80 | Doohan et al. 2024 [73] |
| | | EpiLPS – Dataset from Akhmetzhanov et al. 2019 [74] | Lognormal distribution with mean of | Estimated |

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| | | | 12.6 (95% CI: 11.8-13.8) | |
| | Latent period (d) | Modelling study, Referenced value | Lognormal distribution with mean of 10.0 (Range: 5-21) | Tuite et al. 2019 [75] |
| | Infectious period (d) | Modelling study, Referenced value | Lognormal distribution with mean of 10.0 (Range: 6-17) | Tuite et al. 2019 [75] |
| | Case fatality risk (%) | Systematic review, CFR for imported Lassa fever cases in non-endemic countries outside West Africa. 1969-2019 | 35.1 | Wolf et al. 2020 [29] |
| | | Systematic review, overall fatality rate in sub-Saharan Africa 1972-2020 | 29.7 (95% CI: 22.3-37.5) | Kenmoe et al. 2020 [76] |
| | | Systematic review, pooled estimate up to 2023 | 33.1 (95% CI: 25.7-41.5) | Doohan et al. 2024 [73] |
| | Infection fatality risk (%) | Crude estimate of the overall case-fatality rate | 1% | Dwalu et al. 2024 [77] |
| MARV | Basic reproduction number | Modelling study, R0 estimated using previous Marburg outbreaks | Median: 0.81 (95% CI: 0.08-1.83) | Qian et al. 2023 [78] |
| | | Modelling study, R0 estimated for the 2005 epidemic in Angola | 1.59 (95% CI: 1.53–1.66) | Ajelli and Merle 2012 [79] |
| | Dispersion parameter | Modelling study, K estimated from 18 chains of transmission from the outbreak in DRC. | negative binomial distribution with a range of 0.52-0.67 | Qian et al. 2023 [78] |
| | Serial interval (d) | Modelling. Estimated using Identified discernible infector-infectee pairs from line list data and obtained the difference between the dates of infection of each pair. | Gamma distribution with mean of 9.2 | Qian et al. 2023 [78] |
| | Incubation period (d) | Modelling study, estimated range of cental values | 5.0-10.0 | Qian et al. 2023 [78] |
| | | EpiLPS - Dataset from Pavlin 2014 [80] | Weibull distribution with mean of | Estimated |

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| | | | 6.90 (95% CI: 6.20-7.60) | |
| | | Modelling study, estimated from pooled data from all Marburg cases between 1967 and 2008 | Median: 7 (range: 2.0-13.0) | Pavlin 2014 [80] |
| | Latent period (d) | Modelling study, latent period estimated using the average viral load in non-human primates | Mean: 3 | Ajelli and Merle 2012 [79] |
| | | Modelling study, estimated by fitting the epidemic curve of MARV cases during the epidemic in Angola (assumes incubation period is same length as latent period) | Mean: 6.50 (95% CI: 6.0-7.0) | Bettencourt 2009 [81] |
| | Infectious period (d) | Modelling study, estimated by fitting the epidemic curve of MARV cases during the epidemic in Angola | Mean: 3.0 (95% CI: 3.0-4.0) | Bettencourt 2009 [81] |
| | Case fatality risk (%) | Systematic review, from database inception to March 2023 (estimated pooled total random) | 61.9 (95% CI: 38.8-80.6) | Cuomo-Dann enburg et al 2024 [82] |
| MERS-CoV | Basic reproduction number | Systematic review, Saudi Arabia or Middle East area data | Range: 0.45-0.98 | Park et al. 2018 [83] |
| | | Systematic review, South Korea data (Early stage) | Range: 2.5–8.09 | Park et al. 2018 [83] |
| | | Modelling. Referenced value derived from Cauchemez et al. 2014 | Median: 0.95 (95% CI: 0.6-1.3) | Peak et al. 2017 [84] |
| | Dispersion parameter | Systematic review, point estimates of k | Range: 0.06 (95% CI: 0.03-0.09) to 2.94 (95% CI: 0.23-infinity) | Wang et al. 2021 [85] |
| | Serial interval (d) | Modelling. Outbreak in a hospital in Saudi Arabia. Estimated using symptom onset times in the patient of infected–infector pairs. Outbreak period covers interventions being introduced | Lognormal distribution with mean of 7.60 (95% CI: 2.50-23.10) | Assiri et al. 2013 [86] |

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| | | Modelling study, Outbreak in two hospitals in South Korea. Estimated using symptom onset times in the patient of infected–infector pairs. Outbreak period covers interventions being introduced | Gamma distribution with median of 14.60 (95% CI: 12.90-16.50) | Park et al. 2016 [87] |
| | | Modelling study, estimated by analysing 119 cases in South Korea | Gamma distribution with mean of 12.60 (95% CI: 12.10-13.10) | Cowling et al. 2015 [88] |
| | Incubation period (d) | EpiLPS – Dataset from Cauchemez et al. 2014 [89] | Lognormal distribution with mean of 5.40 (95% CI: 4.50-6.50) | Estimated |
| | | Systematic review up to 2017 | Range: 4.50-7.80 | Park et al. 2018 [83] |
| | Latent period (d) | Modelling assumed value. Deemed unlikely that a case will cause any subsequent infections prior to 7 days after infection | 7.0 | Lessler et al. 2014 [91] |
| | Infectious period (d) | Modelling study. Assumed value. Maximum duration of infectiousness | Uniform distribution with median of 16.43 (95% CI: 9.59-24.5) | Peak et al. 2017 [84] |
| | Case fatality risk (%) | Systematic review, up to 2017. Mortality rate in south Korea | Range: 14.5–47.8 | Park et al. 2018 [83] |
| | | Systematic review, up to 2017. Mortality rate in Saudi Arabia | Range: 22–69.2 | Park et al. 2018 [83] |
| | | Systematic review, up to 2017. Mortality rate from multiple areas. | Range: 26.6 - 59.4 | Park et al. 2018 [83] |
| Mpox | Basic reproduction number | Systematic review of the 2022 Mpox outbreak. Pooled mean | Mean: 1.8 (95% CI: 1.7-1.9) | Okoli et al. 2024 [93] |
| | | Systematic review. Analysis of active surveillance data | 0.8 | Beer et al. 2019 [24] |

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| | | collected in the DRC between 1980 and 1984. | | |
| | Dispersion parameter | Modelling study, DRC 1980-1984. Estimated by analysing chain size data. | 0.36 (95% CI: 0.14-1.47) | Blumberg and Lloyd-Smith 2013 [94] |
| | | Modelling study 2022 Mpox outbreak. Estimated using genomic and epidemiological metadata. | 0.3 (95% CI: 0.18-0.54) | Paredes et al. 2024 [95] |
| | Serial interval (d) | Systematic review of the 2022 Mpox outbreaks. Pooled mean. | 8.5 (95% CI: 7.3-9.9) | Okoli et al. 2023 [96] |
| | | Modelling study 2022 Mpox outbreak USA. May–August 2022. | Gamma distribution with mean of 8.5 (95% CI: 7.3-9.9) | Madewell et al. 2023 [97] |
| | | Modelling study 2022 Mpox outbreak UK. PCR confirmed cases between 6 May and 1 August 2022. | Gamma distribution with mean of 8.0 (95% CI: 6.5-9.8) | Ward et al. 2022 [27] |
| | Incubation period (d) | Systematic review, analysis of 18,275 Mpox cases during the 2022 outbreak | Median: 7.0 (IQR: 3-21) | Chenchula et al. 2023 [98] |
| | | Systematic review of the 2022 Mpox outbreaks. Pooled mean (up to Dec 2022) | Mean: 7.8 (95% CI: 6.6-9.0) | Okoli et al. 2023 [96] |
| | | Systematic review of the 2022 Mpox outbreaks. Pooled mean (up to May 2022) | Mean: 7.4 (95% CI: 6.4-8.4) | Okoli et al. 2023 [96] |
| | | Systematic review of previous Mpox outbreaks. Pooled mean | Mean: 12.9 (95% CI: 10.4-15.5 ) | Okoli et al. 2023 [96] |
| | | Systematic Review, analysis of outbreaks pre and post 2022 | Mean: 7.9 (Range: 1-21) | Hatami et al. 2023 [99] |
| | | Modelling study 2022 Mpox outbreak USA. May–August 2022 | Lognormal distribution with mean of 5.6 (95% CI: 4.3-7.8) | Madewell et al. 2023 [97] |
| | | EpiLPS – dataset from Miura et al. 2022 [100] | Weibull distribution with mean of 7.6 (95% CI: 6.5-9.9) | Estimated |

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| | | Modelling study 2022 Mpox outbreak UK. PCR confirmed cases between 6 May and 1 August 2022. | Lognormal distribution with mean of 8.9 (95% CI: 7.9-9.9) | Ward et al. 2022 [27] |
| | Latent period (d) | Modelling study, assumed value from viral shedding data (Preprint) | 3.0 | Asakura et al. 2024 [101] |
| | Infectious period (d) | Modelling study, assumed value from documented duration of illness | 21 | Endo et al. 2022 [102] |
| | | Modelling study, May-June 2022 MSM. Estimated infectious period while not refraining from sexual contacts (Netherlands) | 6.0 (95% CI: 4.4-7.8) | Xiridou et al. 2023 [103] |
| | | Modelling study, July 2022 MSM. Estimated infectious period while not refraining from sexual contacts (Netherlands) | 2.6 (95% CI: 2.0-4.3) | Xiridou et al. 2023 [103] |
| | | Modelling study, assumed value based on viral shedding data (Preprint) | 10.0 | Asakura et al. 2024 [101] |
| | Case fatality risk (%) | Systematic review - CFR of outbreaks. From discovery to 2019 | Mean: 8.7 (95% CI: 7.0-10.8) | Bunge et al. 2022 [23] |
| | | Systematic review - CFR of Central African clade outbreaks. From discovery to 2019 | Mean:10.6 (95% CI: 8.4-13.3) | Bunge et al. 2022 [23] |
| | | Systematic review - CFR of West African clade outbreaks. From discovery to 2019 | Mean: 3.6 (95% CI: 1.7-6.8) | Bunge et al. 2022 [23] |
| | | Systematic review - CFR of West African clade, African countries only. From discovery to 2019 | Mean: 4.6 (95% CI: 2.1-8.6) | Bunge et al. 2022 [23] |
| | | Systematic review 1950 to 2022. CFR when hospital care is available | 0.03 (95% CI: 0.0-0.44) | DeWitt et al. 2022 [22] |
| | | Systematic review 1980 to 2022, CFR in hospitalised patients | 4 (95% CI:1-9%) | Benites-Zapata et al. 2022 [104] |
| NiV | Basic reproduction number | Review of hospital-based surveillance and outbreak investigations in Bangladesh from 2001 to 2014. | 0.33 (95% CI: 0.19-0.59) | Nikolay et al. 2019 [105] |

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| | | Hospital-based surveillance implemented in 2007 | | |
| | | Review of hospital-based surveillance and outbreak investigations in Bangladesh. R0 for cases identified 2007-2014. Hospital-based surveillance implemented in 2007 | 0.23 (95% CI: 0.11-0.46) | Nikolay et al. 2019 [105] |
| | | Review of hospital-based surveillance and outbreak investigations in Bagladesh. R0 for primary cases between 2001 and 2014. Hospital-based surveillance implemented in 2007 | 0.30 (95% CI: 0.15-0.61) | Nikolay et al. 2019 [105] |
| | | Review of hospital-based surveillance and outbreak investigations in Bangladesh 2001-2014. R0 for cases hospitalized >7 days since symptom onset or not hospitalised. Hospital-based surveillance implemented in 2007 | 0.60 (95% CI: 0.07-4.97) | Nikolay et al. 2019 [105] |
| | Dispersion parameter | Modelling study, referenced value | 0.06 | Bradbury et al. 2023 [106] |
| | Serial interval (d) | Review of hospital-based surveillance and outbreak investigations in Bangladesh from 2001 to 2014. Serial interval estimated using epidemiologically linked transmission pairs. Bangladesh 2001-2014. Hospital-based surveillance implemented in 2007 | Gamma distribution with mean of 12.7 | Nikolay et al. 2019 [105] |
| | Incubation period (d) | EpiLPS – Dataset from Nikolay et al. 2019 [105] | Gamma distribution with mean of 9.4 (95% CI: 8.7-10.1) | Estimated |
| | | Systematic review up to 30 May 2019. Incubation period in the Philippines 2014 | Median: 8.0 (Range: 4-20) | Hegde et al. 2023 [25] |
| | | Systematic review up to 30 May 2019. Incubation period in Bangladesh | Median: 9.0 (Range: 6-14) | Hegde et al. 2023 [25] |
| | | Systematic review up to 30 May 2019. Incubation period in India | Median: 10.0 (Range: 6-18) | Hegde et al. 2023 [25] |

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| | Infectious period (d) | Review of hospital-based surveillance and outbreak investigations in Bangladesh from 2001 to 2014. Assumed maximum infectious period for contact tracing | 15 | Nikolay et al. 2019 [105] |
| | Case fatality risk (%) | Systematic review, overall random effect meta-analysis. 1999-2014 (Bangladesh, India, Malaysia, Singapore, Philippines) | 61 (95% CI: 45.7-75.4) | Kenmoe et al. 2019 [107] |
| | | Systematic review, Bangladesh random effect meta-analysis from Bangladesh 2001-2014 | 67.9 (95% CI: 47.7-85.4%) | Kenmoe et al. 2019 [107] |
| | | Systematic review, random effect meta-analysis from India 2001 | 71.3 (95% CI: 63.2-78.8) | Kenmoe et al. 2019 [107] |
| | | Systematic review, random effect meta-analysis from Malaysia 1998-1999 | 32.6% (95% CI: 25.8-39.8) | Kenmoe et al. 2019 [107] |
| | | Systematic review, random effect meta-analysis from the Philippines 2014 | 81.8 (95% CI: 52.7-99.5) | Kenmoe et al. 2019 [107] |
| | | Systematic review, random effect meta-analysis from Singapore 1999 | 2.9 (0.0-11.9) | Kenmoe et al. 2019 [107] |
| | | Systematic review, CFR in Singapore 1999. Pig imports from Malaysia banned; abattoirs closed; preventive control measures in hospitals | 8.3 | Hegde et al. 2024 [25] |
| | | Systematic review, CFR in Malaysia 1998-1999. Pig culling and transport ban; active surveillance for encephalitis cases; protective equipment for all persons who have exposure to pigs; education campaign | 40 | Hegde et al. 2024 [25] |
| | | Systematic review, CFR in the Philippines 2014. Contact tracing implemented | 53 | Hegde et al. 2024 [25] |
| | | Systematic review, CFR in Bangladesh 2001-2014 | 78 | Hegde et al. 2024 [25] |
| | | Systematic review, CFR in India 2001-2018 | 93 | Hegde et al. 2024 [25] |

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| | | Systematic review, CFR in Bangladesh and Malaysia 1999-2016 | 61 (95% CI: 45.7-75.4) | Suman et al. 2024 [108] |
| RVF | Incubation period (d) | Systematic review of incubation periods up to 2011. Pooled estimate | Lognormal distribution with median of 4.0 (95% CI: 3.40-4.90) | Rudolph et al. 2014 [109] |
| | | EpiLPS – Dataset collected from outbreak reports with reported exposure and symptom onset times | Semipar. with mean of 4.0 (95% CI: 3.3-4.5) | Estimated |
| | Case fatality risk (%) | Systematic review, pooled estimate in Africa 1997-2020 | 27.5 (95% CI: 8.0-52.5) | Ebogo‐Belobo et al. 2023 [110] |
| SARS-CoV-1 | Basic reproduction number | Modelling study. Median estimate from study estimated using exponential doubling times of several epidemics in 2003. Without control measures. Data from Lipsitch et al. 2003 [111] | Mean: 2.9 (95% CI: 2.2-3.6) | Peak et al. 2017 [84] |
| | | Modelling, R0 estimate at the start of the epidemic in Hong Kong (excluding superspreading events) | 2.7 (95% C): 2.2 to 3.7) | Riley et al. 2003 [112] |
| | | Modelling. Estimated R0 from outbreak at the National Taiwan University Hospital | Lognormal distribution with mean of 2.65 | Chen et al. 2006 [113] |
| | | Modelling, estimated R0 distribution for SARS | Median 1.1 (IQR: 0.43-2.41) | Chowell et al. 2004 [114] |
| | | Modelling estimated R0 distribution Toronto 2003 (after implementing control measures). 77% of cases exposed in hospital setting | Median:0.58 (IQR: 0.24-1.18) | Chowell et al. 2004 [114] |
| | | Modelling study, estimated R0 distribution Hong Kong 2003 | Median: 1.1 (IQR: 0.44-2.29) | Chowell et al. 2004 [114] |
| | | Modelling study, estimated R0 distribution Singapore 2003 | Median: 1.17 (IQR: 0.47-2.47) | Chowell et al. 2004 [114] |
| | Dispersion parameter | Systematic review, range of k estimates | Range: 0.12 (90% CI: 0.08-0.42) to | Wang et al. 2021 [85] |

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| | | | 0.20 (95% CI: 0.13-0.27) | |
| | Serial interval (d) | Modelling study, estimated by analysing 205 probable cases reported in Singapore (after interventions were implemented) | Weibull distribution with mean of 8.4 | Lipsitch et al. 2003 [111] |
| | | Modelling study, estimated by analysing 205 probable cases reported in Singapore (before full-scale interventions) | Mean 10.0 | Lipsitch et al. 2003 [111] |
| | Incubation period (d) | Systematic review, pooled analysis | Lognormal distribution with median of 4.0 (95% CI: 3.6-4.4) | Lessler et al. 2009 [38] |
| | | EpiLPS – Dataset from Tsang et al. 2003 [115] | Semipar with mean of 4.70 (95% CI: 3.90-5.50) | Estimated |
| | Latent period (d) | Modelling study referenced value. Assumed to be the same as the incubation period and a fixed value | 6.5 | Becker et al. 2005 [116] |
| | | Modelling study. Assumed to be a fixed value. | 6.81 | Klinkenberg et al. 2006 [117] |
| | | Modelling study assumed value. Average time of progression from latent infection to infectious | 5.0 | Lipsitch et al. 2003 [111] |
| | Infectious period (d) | Modelling study. Assumed value. Average duration of infectiousness | Mean: 5.0 (Range: 1-5) | Lipsitch et al. 2003 [111] |
| | | Modelling study referenced value. Symptomatic period assumed to be infectious period | Gamma distribution with mean of 16.3 | Lloyd-Smith et al. 2003 [118] |
| | | Modelling study, estimated value | Gamma distribution with mean of 9.25 | Fraser et al. 2004 [15] |
| | | Modelling study referenced value. Effective infectious period | 9.0 | Becker et al. 2005 [116] |
| | | Modelling study referenced value. Effective infectious period | 3.87 | Klinkenberg et al. 2006 [117] |

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| | Case fatality risk (%) | Epidemiology review article | Mean: 12.5 (Range 0-40) | Hui et al. 2004 [119] |
| SARS-CoV-2 (Wild type) * | Basic reproduction number | Systematic review of R0 values from January 1 to August 31, 2020 (World) | Mean: 2.69 (95% CI: 2.40-2.98) | Ahammed et al. 2021 [120] |
| | | Systematic review of R0 values from January 1 to August 31, 2020 (Asia) | Mean: 2.59 (95% CI: 2.19-2.94) | Ahammed et al. 2021 [120] |
| | | Systematic review of R0 values from January 1 to August 31, 2020 (Europe) | Mean: 2.70 (95% CI: 2.26-3.13) | Ahammed et al. 2021 [120] |
| | | Systematic review of R0 values from January 1 to August 31, 2020 (North America) | Mean: 3.69 (95% CI: 1.46-5.92) | Ahammed et al. 2021 [120] |
| | | Systematic Review of transmission-Dynamic Models in Wuhan. R0 before the lockdown on the 23rd of January 2020 | Median: 3.77 (IQR: 2.78-5.13) | Lin et al. 2020 [121] |
| | | Systematic Review of transmission-Dynamic Models in Wuhan. R0 post lockdown starting on the 23rd of January 2020 | Median: 1.88 (IQR: 1.41-2.24) | Lin et al. 2020 [121] |
| | | Systematic review and meta-analysis of Epidemiologic, clinical, and laboratory findings. 1st December 2019 to 16th July 2020. | Mean: 3.32 (95% CI: 3.24-3.39) | Xie et al 2020 [122] |
| | | Systematic Review and Meta-Analysis December 2019 up to March 2020 | Mean: 2.99 (95% CI: 2.71-3.27) | Izadi et al. 2022 [123] |
| | Dispersion parameter | Systematic review of superspreading in a mix of countries from January to December 2020 | Mean: 0.55 (95% CI: 0.30-0.79) | Du et al. 2022 [124] |
| | Serial interval (d) | Systematic review of serial intervals 2020-2023 | Mean: 4.82 (95% CI: 4.50-5.14) | Xu et al. 2023 [125] |
| | Incubation period (d) | Systematic review of Incubation periods 2020-2023 | Mean: 6.50 (95% CI: 5.88-7.12) | Xu et al. 2023 [125] |

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| | | EpiLPS - Using dataset from Backer et al. 2020 [129] | Lognormal distribution with mean of 4.40 (95% CI: 4.0-4.80) | Estimated |
| | | Modelling study, based on exposure information on COVID-19 cases in China | Weibull distribution with mean of 6.94 | Xin et al. 2022 [130] |
| | | Systematic Review of transmission-Dynamic Models in Wuhan. December 2019 and 21 February 2020 | Median: 5.9 (IQR: 4.78-6.25) | Lin et al. 2020 [121] |
| | Latent period (d) | Modelling, estimated based on exposure information on COVID-19 cases in China | Gamma distribution with mean of 5.48 (95% CI: 5.06-5.86) | Xin et al. 2022 [122] |
| | | Modelling, estimated based on exposure information on COVID-19 cases in China | Lognormal distribution with mean of 5.51 | Xin et al. 2022 [122] |
| | | Modelling, estimated based on exposure information on COVID-19 cases in China (symptomatic cases) | Gamma distribution with mean of 5.53 (95% CI: 5.09-5.99) | Xin et al. 2022 [122] |
| | | Modelling, estimated based on exposure information on COVID-19 cases in China (asymptomatic cases) | Gamma distribution with mean of 5.24 (95% CI: 4.30-6.14) | Xin et al. 2022 [122] |
| | Infectious period (d) | Modelling, estimated from infectiousness profiles from a sample of 77 transmission pairs | Weibull distribution with mean of 9.3 (95% CI: 7.8-10) | He et al. 2020 [131] |
| | | Modelling. Assumed that latent and the infectious period is approximately equal to the incubation period and the length of hospital stay. | 12.53 | Zhu et al. 2021 [132] |
| | | Systematic Review of transmission-Dynamic Models in Wuhan December 2019 and 21 February 2020 | Median: 9.94 (IQR: 3.93-13.5) | Lin et al. 2020 [121] |

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| | Case fatality risk (%) | Systematic review of CFR's worldwide from January 1 to August 31, 202 | Mean: 2.67 (95% CI: 2.25-3.13) | Ahammed et al. 2021 [120] |
| | | Systematic Review and Meta-Analysis December 2019 up to March 2020 | Mean: 3.29 | Izadi et al. 2020 [123] |
| | | Systematic review and meta-analysis of Epidemiologic, clinical, and laboratory findings. 1st December 2019 to 16th July 2020 | 4.4 | Xie et al 2020 [122] |
| | | Systematic Review of transmission-Dynamic Models in Wuhan December 2019 and 21 February 2020 | Median: 2.94 (IQR: 2.25-5.4) | Lin et al. 2020 [121] |
| | Infection fatality risk (%) | IFR from Japanese citizens who were evacuated from Wuhan on 29–31 January 2020 | Range: 0.3-0.6 | Nishiura et al. 2020 [133] |
| | | Crude risk of death among all infected individuals in Wuhan city January-February, 2020 | 0.07 (95% CI: 0.05-0.09) | Mizumoto et al. 2020 [134] |
| | | Estimating infection fatality ratio accounting for seroreversion. During the first wave of COVID-19 across different settings | 0.49–2.53 | Brazeau et al. 2022 [135] |
| SARS-CoV-2 (Alpha) | Basic reproduction number | Modelling, transmissibility model of Alpha variant in the United Kingdom fitted until the 24th of December 2020. | Alpha variant has a 43 to 90% higher reproduction number | Davies et al. 2021 [136] |
| | Serial interval (d) | Systematic review of serial intervals 2020-2023 | Mean: 3.47 (95% CI: 2.52-4.41) | Xu et al. 2023 [125] |
| | | Modelling. Estimated using household clusters from week 12/2021 until 22/2021 in Germany | Gamma distribution with mean of 4.5 (95% CI: 4.46-4.54) | Heiden and Buchholz 2022 [137] |
| | Incubation period (d) | Systematic review of Incubation periods 2020-2023 | Mean: 4.92 (95% CI: 4.53-5.30) | Xu et al. 2023 [125] |
| | Latent period (d) | Epidemiological analysis. Assumed value as the ratio of mean duration of the latent and incubation periods | Median: (95% CI: 0.23 (0.04-0.50) | Hart et al. 2022 [140] |

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| | Infectious period (d) | Epidemiological analysis. Assumed value of symptomatic infectious period | Gamma distribution with a mean of 3.5 (95% CI: 1.9-5.8) | Hart et al. 2022 [140] |
| | Case fatality risk (%) | Systematic review of CFR's worldwide from January 1, 2020, and March 31, 2023 | 2.62 (95% CI: 2.0-3.23) | Xia et al. 2024 [122] |
| | Infection fatality risk (%) | IFR for six epidemic waves in Osaka Japan from February 2020 to January 2022. Elderly partly vaccinated. Ages 20–39 years | 0.03 (95% CI: 0.03-0.1) | Zhang and Nishiura 2023 [141] |
| | | IFR for six epidemic waves in Osaka Japan from February 2020 to January 2022. Elderly partly vaccinated. 40–59 years | 0.37 (95% CI: 0.29-0.56) | Zhang and Nishiura 2023 [141] |
| | | IFR for six epidemic waves in Osaka Japan from February 2020 to January 2022. Elderly partly vaccinated. 60 + years | 6.42 (95% CI: 4.69-7.44) | Zhang and Nishiura 2023 [141] |
| SARS-CoV-2 (Delta) | Basic reproduction number | Review of R0 from May to July 2021 using studies from China and the UK. | Mean: 5.08 (range: 3.20-8.0) | Liu and Rocklöv 2021 [142] |
| | Dispersion parameter | Modelling study. Calculated using 1,344 transmission pairs from the 11th of July to the 24th of July 2021 in South Korea. (Mask mandate, active case finding and immediately isolating laboratory-confirmed COVID-19 patients and exposed persons by using digital QR codes, 4-person limit for gatherings was implemented beginning July 19, 2021) | Negative binomial distribution with mean of 0.64 (95%CI: 0.57–0.72) | Ryu et al. 2022 [143] |
| | | Modelling study. Calculated using 2,384 transmission pairs from the 25th of July to the 15th of August 2021 in South Korea. (Mask mandate, active case finding and immediately isolating laboratory-confirmed COVID-19 patients and exposed persons by using digital QR codes, 4-person limit for gatherings was implemented beginning July 19, 2021) | Negative binomial distribution with mean of 0.85 (95% CI: 0.75–0.98) | Ryu et al. 2022 [143] |

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| | | Modelling study. Using a likelihood-based estimating framework based on 126 observations from May to December 2021 in Guangdong, China. Under intense control measures | Negative binomial distribution with mean of 0.26 (95% CI: 0.16, 0.41) | Zhao et al. 2022 [144] |
| | Serial interval (d) | Systematic review of serial intervals 2020-2023 | Mean: 3.59 (95% CI: 3.26-3.92) | Xu et al. 2023 [125] |
| | | Modelling. Estimated value using household clusters from week 27/2021 until 49/2021 in Germany | Gamma distribution with mean of 4.19 (95% CI: 4.16-4.22) | Heiden and Buchholz 2022 [137] |
| | Incubation period (d) | Systematic review of Incubation periods 2020-2023 | Mean: 4.63 (95% CI: 4.11-5.15) | Xu et al. 2023 [125] |
| | | EpiLPS- Data set from Backer et al. 2022 [146] | Lognormal distribution with mean of 4.30 (95% CI: 4.10-4.50) | Estimated |
| | | Modelling, estimated from infected individuals with clear transmission chains and infectors from epidemiological survey reports in China | Gamma distribution with mean of 5.04 (95% CI: 4.83-5.33) | Li et al. 2024 [147] |
| | Latent period (d) | Modelling, estimated from infected individuals with clear transmission chains and infectors from epidemiological survey reports in China | Gamma distribution with mean of 4.40 (95% CI: 4.24-4.63) | Li et al. 2024 [147] |
| | Infectious period (d) | Viral shedding dynamics in fully vaccinated adults in the USA | Median: 6.0 (IQR: 5.0-8.0) | Garcia-Knight et a. 2022 [148] |
| | Case fatality risk (%) | Systematic review of CFR's worldwide from January 1, 2020, and March 31, 2023 | 2.01 (95% CI: 1.88-2.14) | Xia et al. 2024 [149] |
| | | Systematic review of confirmed case-fatality risk. 18 January 2021 to December 2021 | 0.46 (95% CI: 0.2-0.73) | Yuan et al. 2023 [150] |
| | Infection fatality risk (%) | IFR for six epidemic waves in Osaka Japan from February 2020 to January 2022. Elderly was prioritised for vaccination and were fully vaccinated | 0.01 (95% CI: 0.01-0.01) | Zhang and Nishiura 2023 [141] |

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| | | before the end of July 2021. Ages 20–39 years | | |
| | | IFR for six epidemic waves in Osaka Japan from February 2020 to January 2022. Elderly was prioritised for vaccination and were fully vaccinated before the end of July 2021. Ages 40–59 years | 0.12 (95% CI: 0.1-0.16) | Zhang and Nishiura 2023 [141] |
| | | IFR for six epidemic waves in Osaka Japan from February 2020 to January 2022. Elderly was prioritised for vaccination and were fully vaccinated before the end of July 2021. Ages 60 + years | 0.95 (95% CI: 0.7-1.1) | Zhang and Nishiura 2023 [141] |
| | | Infection fatality risk in England at the end of the Delta period (November 2021) | 0.11 (95% CI: 0.08-0.15) | Ward et al. 2024 [151] |
| SARS-CoV-2 (Omicron) | Basic reproduction number | Rapid review of R0 from November 2021 to December 2021 (Mix of countries) | Mean: 9.5 (IQR: 7.25-11.88) | Liu and Rocklöv 2022 [152] |
| | Effective reproduction number | Rapid review of RE from November 2021 to January 2022 (Mix of countries). | Mean: 3.4 (IQR: 0.88-9.40) | Liu and Rocklöv 2022 [152] |
| | Dispersion parameter | Modelling. 427 laboratory-confirmed cases from 25 November to 31 December 2021 in South Korea. (BA.1) | 0.10 (95% CI: 0.08–0.13) | Guo et al. 2022 [153] |
| | | Modelling. 67 epidemiologic linked cases from 2 to 21 January 2022 in Hong Kong (border control, physical distancing and contact tracing in place) (BA.1,2) | 0.33 (95% CI: 0.17–0.62) | Guo et al. 2022 [153] |
| | Serial interval (d) | Systematic review of serial intervals 2020-2023 | Mean: 3.21 (95% CI: 2.94-3.48) | Xu et al. 2023 [125] |
| | Incubation period (d) | Systematic review of Incubation periods. (BA.1) | Mean: 3.49 (95% CI: 3.13-4.86) | Xu et al. 2023 [125] |
| | | Modelling, estimated from infected individuals with clear transmission chains and infectors from epidemiological survey reports in China | Gamma distribution with mean of 3.41 (95% CI: 3.27-3.58) | Li et al. 2024 [147] |

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| | | Modelling, estimated from infected individuals with clear transmission chains and infectors from epidemiological survey reports in China. (BA.1) | Gamma distribution with mean of 3.42 (95% CI: 3.00-3.89) | Li et al. 2024 [147] |
| | | Modelling, estimated from infected individuals with clear transmission chains and infectors from epidemiological survey reports in China. (BA.2) | Gamma distribution with mean of 3.39 (95% CI: 3.24-3.55) | Li et al. 2024 [147] |
| | | EpiLPS - Dataset from Backer et al. 2022 [146] | Lognormal distribution with mean of 3.30 (95% CI: 3.20-3.50) | Estimated |
| | Latent period (d) | Cross-sectional study in China, with 114 cases with COVID-19 Omicron variant BA.1.1 between January 2022 and February 2022 | Gamma distribution with mean of 3.13 (95% CI: 2.82-3.48) | Xin et al. 2023 [130] |
| | | Modelling, esitmated from infected individuals with clear transmission chains and infectors from epidemiological survey reports in China | Gamma distribution with mean of 2.58 (95% CI: 2.48-2.68) | Li et al. 2024 [147] |
| | | Modelling, estimated from infected individuals with clear transmission chains and infectors from epidemiological survey reports in China. (BA.1) | Gamma distribution with mean of 2.50 (95% CI: 2.27-2.76) | Li et al. 2024 [147] |
| | | Modelling, estimated from infected individuals with clear transmission chains and infectors from epidemiological survey reports in China. (BA.2) | Gamma distribution with mean of 2.58 (95% CI: 2.48-2.69) | Li et al. 2024 [147] |
| | Infectious period (d) | Transmission period after symptom onset date (Spain). BA.1 | Mean: 0.5 (IQR: -1.0-2.0) | Águila-Mejía et al. 2022 [156] |
| | | Time to first negative viral culture (USA). (BA.2, 5, XBB) | Median: 4.0 (IQR: 3.0-4.0) | Edelstein et al. 2023 [157] |
| | Case fatality risk (%) | Systematic review of CFR's worldwide from January 1, 2020, and March 31, 2023 | 0.7 (95% CI: 0.67-0.73) | Xia et al. 2024 [149] |
| | | Systematic review confirmed case-fatality risk. 18 January 2021 to December 2021 | 0.04 (95% CI: 0-0.61) | Yuan et al. 2023 [150] |

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| | | Systematic review, patient deaths/omicron patients. From 14/11/2021 to 07/03/2022 | 0.21 | Ahmad et al. 2024 [158] |
| | Infection fatality risk (%) | IFR for six epidemic waves in Osaka Japan from February 2020 to January 2022. Elderly fully vaccinated. Ages 20–39 years | 0 (95% CI: 0-0) | Zhang and Nishiura 2023 [141] |
| | | IFR for six epidemic waves in Osaka Japan from February 2020 to January 2022. Elderly fully vaccinated. Ages 40–59 years | 0.02 (95% CI: 0.01-0.04) | Zhang and Nishiura 2023 [141] |
| | | IFR for six epidemic waves in Osaka Japan from February 2020 to January 2022. Elderly fully vaccinated. Ages 60+ years | 1.26 (95% CI: 0.9-2.54) | Zhang and Nishiura 2023 [141] |
| | | Infection fatality risk in England at the end of the Omicron BA.1 and Omicron BA.2 period (April 2022) | 0.06 (95% CI: 0.04-0.08) | Ward et al. 2024 [151] |
| ZIKV | Basic reproduction number | Review of R0 across global climate zones (1980-2018) | Mean: 3.02 (range: 0.16-9.40) | Liu et al. 2020 [159] |
| | | Estimated R0 values for the outbreak in Miami 2016 | Lognormal distribution with mean of 1.88 (95% CI: 1.53-2.32) | Liu et al. 2020 [159] |
| | | Reproduction number for ZIKV sexual transmission | Median: 0.136 (95% CI: 0.009–0.521) | Gao et al. 2016 [160] |
| | Serial interval (d) | Systematic review, serial symptom onset interval in 15 couples via sexual transmission | Median: 12.0 (IQR:10.0-14. 50) | Counotte et al 2018 [161] |
| | Incubation period (d) | Systematic review up to 2016. Pooled analysis | Lognormal distribution with median of 5.90 (95% CI: 4.40-7.60) | Lessler et al. 2016 [162] |
| | | EpiLPS - Dataset from lessler et al. 2016 [162] | Semipar. with mean of 6.7 (95% CI: 5.8-7.6) | Estimated |
| | Latent period (d) | Modelling study. Referenced value. Assumed that human latent period is equivalent to | 6.8 | Agudelo et al. 2022 [163] |

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| | | the intrinsic incubation period and is a constant value | | |
| | | Modelling study Referenced value. Assumed that latent period is equivalent to the incubation period | Gamma distribution with mean of 3.9 | Kucharski et al. 2016 [164] |
| | Infectious period (d) | Systematic review up to 2016. Time period that Zika virus is detectable in blood | Mean: 9.9 | Lessler et al. 2016 [162] |
| | | Modelling study. Referenced value | Gamma distribution with mean of 5.0 | Kucharski et al. 2016 [164] |
| | | Systematic review, range of zika virus shedding in male genital tract | Range: 3-69 | Moreira et al. 2017 [165] |
| | Case fatality risk (%) | Systematic review, CFR in the Americas up to 2018 | Median: 0.02 (range: 0.002-0.324) | Cardona-Ospina et al. 2019 [166] |
| * SARS-CoV-2 wild type is defined as articles published regarding the first wave of COVID-19 prior to the emergence of the Alpha variant. | | | | |

## 6. References


[1] Rietveld J, Hobson T, Mani L, Avin S, Sundaram L. The UK's pandemic preparedness and early response to the COVID-19 pandemic. Glob Public Health 2024;19:2415499.
[2] Rt Hon the Baroness Hallett DBE. UK Covid-19 Inquiry. House of Commons; 2024.
[3] Looi M-K. What could the next pandemic be? BMJ 2023;381:909.
[4] Adalja AA, Watson M, Toner ES, Cicero A, Inglesby TV. Characteristics of microbes most likely to cause pandemics and global catastrophes. Curr Top Microbiol Immunol 2019;424:1–20.
[5] Prioritizing diseases for research and development in emergency contexts n.d. https://www.who.int/activities/prioritizing-diseases-for-research-and-development-in-emergency-contexts (accessed June 24, 2024).
[6] Gressani O. EpiLPS: A Fast and Flexible Bayesian Tool for Estimating Epidemiological Parameters. 2021.
[7] Gressani O, Torneri A, Hens N, Faes C. Flexible Bayesian estimation of incubation times. Am J Epidemiol 2025;194:490–501.
[8] Gressani O, Wallinga J, Althaus CL, Hens N, Faes C. EpiLPS: A fast and flexible Bayesian tool for estimation of the time-varying reproduction number. PLoS Comput Biol 2022;18:e1010618.
[9] Charniga K, Park SW, Akhmetzhanov AR, Cori A, Dushoff J, Funk S, et al. Best practices for estimating and reporting epidemiological delay distributions of infectious diseases. PLoS Comput Biol 2024;20:e1012520.
[10] Abbott S, Brand S. primarycensored: Primary Event Censored Distributions 2024. https://doi.org/10.5281/zenodo.13632839.
[11] Cases of Crimean–Congo haemorrhagic fever infected in the EU/EEA, 2013–present. European Centre for Disease Prevention and Control 2021.

https://www.ecdc.europa.eu/en/crimean-congo-haemorrhagic-fever/surveillance/cases-eu-since-2013 (accessed February 4, 2025).
[12] Fine PEM. The interval between successive cases of an infectious disease. Am J Epidemiol 2003;158:1039–47.
[13] Lin MW, Pei YX, Chen QF, Liu R, Sun C, Dou ZH. A retrospective cohort study of case fatality rate of HIV/AIDS cases and influencing factors in Jingzhou, Hubei Province, 1996-2021. Zhonghua Liu Xing Bing Xue Za Zhi 2023;44:1369–75.
[14] Rift valley fever n.d. https://www.who.int/health-topics/rift-valley-fever (accessed June 26, 2024).
[15] Fraser C, Riley S, Anderson RM, Ferguson NM. Factors that make an infectious disease outbreak controllable. Proc Natl Acad Sci U S A 2004;101:6146–51.
[16] Nash RK, Bhatia S, Morgenstern C, Doohan P, Jorgensen D, McCain K, et al. Ebola virus disease mathematical models and epidemiological parameters: a systematic review. Lancet Infect Dis 2024;24:e762–73.
[17] Kim Y, Lee S, Chu C, Choe S, Hong S, Shin Y. The characteristics of Middle Eastern respiratory syndrome Coronavirus transmission dynamics in South Korea. Osong Public Health Res Perspect 2016;7:49–55.
[18] Biggerstaff M, Cauchemez S, Reed C, Gambhir M, Finelli L. Estimates of the reproduction number for seasonal, pandemic, and zoonotic influenza: a systematic review of the literature. BMC Infect Dis 2014;14:480.
[19] Muzembo BA, Kitahara K, Mitra D, Ntontolo NP, Ngatu NR, Ohno A, et al. The basic reproduction number (R0) of ebola virus disease: A systematic review and meta-analysis. Travel Med Infect Dis 2024;57:102685.
[20] Ali ST, Yeung A, Shan S, Wang L, Gao H, Du Z, et al. Serial Intervals and Case Isolation Delays for Coronavirus Disease 2019: A Systematic Review and Meta-Analysis. Clin Infect Dis 2022;74:685–94.
[21] Lai S, Qin Y, Cowling BJ, Ren X, Wardrop NA, Gilbert M, et al. Global epidemiology of avian influenza A H5N1 virus infection in humans, 1997-2015: a systematic review of individual case data. Lancet Infect Dis 2016;16:e108–18.
[22] DeWitt ME, Polk C, Williamson J, Shetty AK, Passaretti CL, McNeil CJ, et al. Global monkeypox case hospitalisation rates: A rapid systematic review and meta-analysis. EClinicalMedicine 2022;54:101710.
[23] Bunge EM, Hoet B, Chen L, Lienert F, Weidenthaler H, Baer LR, et al. The changing epidemiology of human monkeypox-A potential threat? A systematic review. PLoS Negl Trop Dis 2022;16:e0010141.
[24] Beer EM, Rao VB. A systematic review of the epidemiology of human monkeypox outbreaks and implications for outbreak strategy. PLoS Negl Trop Dis 2019;13:e0007791.
[25] Hegde ST, Lee KH, Styczynski A, Jones FK, Gomes I, Das P, et al. Potential for person-to-person transmission of henipaviruses: A systematic review of the literature. J Infect Dis 2024;229:733–42.
[26] Nishiura H, Linton NM, Akhmetzhanov AR. Serial interval of novel coronavirus (COVID-19) infections. Int J Infect Dis 2020;93:284–6.
[27] Ward T, Christie R, Paton RS, Cumming F, Overton CE. Transmission dynamics of monkeypox in the United Kingdom: contact tracing study. BMJ 2022;379:e073153.
[28] Lo Iacono G, Cunningham AA, Fichet-Calvet E, Garry RF, Grant DS, Khan SH, et al. Using modelling to disentangle the relative contributions of zoonotic and anthroponotic transmission: the case of lassa fever. PLoS Negl Trop Dis 2015;9:e3398.
[29] Wolf T, Ellwanger R, Goetsch U, Wetzstein N, Gottschalk R. Fifty years of imported Lassa fever: a systematic review of primary and secondary cases. J Travel Med 2020;27. https://doi.org/10.1093/jtm/taaa035.
[30] Fraser C, Cummings DAT, Klinkenberg D, Burke DS, Ferguson NM. Influenza transmission in households during the 1918 pandemic. Am J Epidemiol 2011;174:505–14.
[31] Nishiura H. Early efforts in modeling the incubation period of infectious diseases with an

acute course of illness. Emerg Themes Epidemiol 2007;4:2.
[32] Cori A, Valleron AJ, Carrat F, Scalia Tomba G, Thomas G, Boëlle PY. Estimating influenza latency and infectious period durations using viral excretion data. Epidemics 2012;4:132–8.
[33] Carrat F, Luong J, Lao H, Sallé A-V, Lajaunie C, Wackernagel H. A “small-world-like” model for comparing interventions aimed at preventing and controlling influenza pandemics. BMC Med 2006;4:26.
[34] WHO. Pandemic Influenza Risk Management. 2017.
[35] Chen PZ, Bobrovitz N, Premji Z, Koopmans M, Fisman DN, Gu FX. Heterogeneity in transmissibility and shedding SARS-CoV-2 via droplets and aerosols. Elife 2021;10. https://doi.org/10.7554/eLife.65774.
[36] Vink MA, Bootsma MCJ, Wallinga J. Serial intervals of respiratory infectious diseases: a systematic review and analysis. Am J Epidemiol 2014;180:865–75.
[37] Tom BDM, Van Hoek AJ, Pebody R, McMenamin J, Robertson C, Catchpole M, et al. Estimating time to onset of swine influenza symptoms after initial novel A(H1N1v) viral infection. Epidemiol Infect 2011;139:1418–24.
[38] Lessler J, Reich NG, Brookmeyer R, Perl TM, Nelson KE, Cummings DAT. Incubation periods of acute respiratory viral infections: a systematic review. Lancet Infect Dis 2009;9:291–300.
[39] Lessler J, Reich NG, Cummings DAT, New York City Department of Health and Mental Hygiene Swine Influenza Investigation Team, Nair HP, Jordan HT, et al. Outbreak of 2009 pandemic influenza A (H1N1) at a New York City school. N Engl J Med 2009;361:2628–36.
[40] Tuite AR, Greer AL, Whelan M, Winter A-L, Lee B, Yan P, et al. Estimated epidemiologic parameters and morbidity associated with pandemic H1N1 influenza. CMAJ 2010;182:131–6.
[41] Van Kerkhove MD, Hirve S, Koukounari A, Mounts AW, H1N1pdm serology working group. Estimating age-specific cumulative incidence for the 2009 influenza pandemic: a meta-analysis of A(H1N1)pdm09 serological studies from 19 countries. Influenza Other Respi Viruses 2013;7:872–86.
[42] Wong JY, Wu P, Nishiura H, Goldstein E, Lau EHY, Yang L, et al. Infection fatality risk of the pandemic A(H1N1)2009 virus in Hong Kong. Am J Epidemiol 2013;177:834–40.
[43] Carrat F, Vergu E, Ferguson NM, Lemaitre M, Cauchemez S, Leach S, et al. Time lines of infection and disease in human influenza: a review of volunteer challenge studies. Am J Epidemiol 2008;167:775–85.
[44] Elveback LR, Fox JP, Ackerman E, Langworthy A, Boyd M, Gatewood L. An influenza simulation model for immunization studies. Am J Epidemiol 1976;103:152–65.
[45] Cowling BJ, Fang VJ, Riley S, Malik Peiris JS, Leung GM. Estimation of the serial interval of influenza. Epidemiology 2009;20:344–7.
[46] Ferguson NM, Cummings DAT, Cauchemez S, Fraser C, Riley S, Meeyai A, et al. Strategies for containing an emerging influenza pandemic in Southeast Asia. Nature 2005;437:209–14.
[47] Cauchemez S, Carrat F, Viboud C, Valleron AJ, Boëlle PY. A Bayesian MCMC approach to study transmission of influenza: application to household longitudinal data. Stat Med 2004;23:3469–87.
[48] Bettencourt LMA, Ribeiro RM. Real time bayesian estimation of the epidemic potential of emerging infectious diseases. PLoS One 2008;3:e2185.
[49] Aditama TY, Samaan G, Kusriastuti R, Sampurno OD, Purba W, Misriyah, et al. Avian influenza H5N1 transmission in households, Indonesia. PLoS One 2012;7:e29971.
[50] Yang Y, Halloran ME, Sugimoto JD, Longini IM Jr. Detecting human-to-human transmission of avian influenza A (H5N1). Emerg Infect Dis 2007;13:1348–53.
[51] Ferguson NM, Fraser C, Donnelly CA, Ghani AC, Anderson RM. Public health. Public health risk from the avian H5N1 influenza epidemic. Science 2004;304:968–9.
[52] Ward J, Lambert JW, Russell TW, Azam JM, Kucharski AJ, Funk S, et al. Estimates of epidemiological parameters for H5N1 influenza in humans: a rapid review. medRxiv

2024:2024.12.11.24318702. https://doi.org/10.1101/2024.12.11.24318702.
[53] Beigel JH, Farrar J, Han AM, Hayden FG, Hyer R, de Jong MD, et al. Avian Influenza A (H5N1) Infection in Humans. N Engl J Med 2005;353:1374–85.
[54] Huai Y, Xiang N, Zhou L, Feng L, Peng Z, Chapman RS, et al. Incubation period for human cases of avian influenza A (H5N1) infection, China. Emerg Infect Dis 2008;14:1819–21.
[55] Cowling BJ, Jin L, Lau EHY, Liao Q, Wu P, Jiang H, et al. Comparative epidemiology of human infections with avian influenza A H7N9 and H5N1 viruses in China: a population-based study of laboratory-confirmed cases. Lancet 2013;382:129–37.
[56] Oner AF, Bay A, Arslan S, Akdeniz H, Sahin HA, Cesur Y, et al. Avian influenza A (H5N1) infection in eastern Turkey in 2006. N Engl J Med 2006;355:2179–85.
[57] Van Kerkhove MD, Mumford E, Mounts AW, Bresee J, Ly S, Bridges CB, et al. Highly pathogenic avian influenza (H5N1): pathways of exposure at the animal-human interface, a systematic review. PLoS One 2011;6:e14582.
[58] Li FCK, Choi BCK, Sly T, Pak AWP. Evidence-based public health policy and practice: Finding the real case-fatality rate of H5N1 avian influenza. Journal of Epidemiology and Community Health (1979-) 2008;62:555–9.
[59] Bente DA, Forrester NL, Watts DM, McAuley AJ, Whitehouse CA, Bray M. Crimean-Congo hemorrhagic fever: history, epidemiology, pathogenesis, clinical syndrome and genetic diversity. Antiviral Res 2013;100:159–89.
[60] Belhadi D, El Baied M, Mulier G, Malvy D, Mentré F, Laouénan C. The number of cases, mortality and treatments of viral hemorrhagic fevers: A systematic review. PLoS Negl Trop Dis 2022;16:e0010889.
[61] Belobo JTE, Kenmoe S, Kengne-Nde C, Emoh CPD, Bowo-Ngandji A, Tchatchouang S, et al. Worldwide epidemiology of Crimean-Congo Hemorrhagic Fever Virus in humans, ticks and other animal species, a systematic review and meta-analysis. PLoS Negl Trop Dis 2021;15:e0009299.
[62] Perveen N, Khan G. Crimean-Congo hemorrhagic fever in the Arab world: A systematic review. Front Vet Sci 2022;9:938601.
[63] Nasirian H. New aspects about Crimean-Congo hemorrhagic fever (CCHF) cases and associated fatality trends: A global systematic review and meta-analysis. Comp Immunol Microbiol Infect Dis 2020;69:101429.
[64] Camacho A, Kucharski AJ, Funk S, Breman J, Piot P, Edmunds WJ. Potential for large outbreaks of Ebola virus disease. Epidemics 2014;9:70–8.
[65] Wong ZSY, Bui CM, Chughtai AA, Macintyre CR. A systematic review of early modelling studies of Ebola virus disease in West Africa. Epidemiol Infect 2017;145:1069–94.
[66] WHO Ebola Response Team, Agua-Agum J, Ariyarajah A, Aylward B, Blake IM, Brennan R, et al. West African Ebola epidemic after one year--slowing but not yet under control. N Engl J Med 2015;372:584–7.
[67] Velásquez 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;61:1135–40.
[68] Nyakarahuka L, Kankya C, Krontveit R, Mayer B, Mwiine FN, Lutwama J, et al. How severe and prevalent are Ebola and Marburg viruses? A systematic review and meta-analysis of the case fatality rates and seroprevalence. BMC Infect Dis 2016;16:708.
[69] Khan SA, Imtiaz MA, Islam MM, Tanzin AZ, Islam A, Hassan MM. Major bat-borne zoonotic viral epidemics in Asia and Africa: A systematic review and meta-analysis. Vet Med Sci 2022;8:1787–801.
[70] Kawuki J, Musa TH, Yu X. Impact of recurrent outbreaks of Ebola virus disease in Africa: a meta-analysis of case fatality rates. Public Health 2021;195:89–97.
[71] Rojek AM, Salam A, Ragotte RJ, Liddiard E, Elhussain A, Carlqvist A, et al. A systematic review and meta-analysis of patient data from the West Africa (2013-16) Ebola virus disease epidemic. Clin Microbiol Infect 2019;25:1307–14.
[72] Zhao S, Musa SS, Fu H, He D, Qin J. Large-scale Lassa fever outbreaks in Nigeria:

quantifying the association between disease reproduction number and local rainfall. Epidemiol Infect 2020;148:e4.
[73] Doohan P, Jorgensen D, Naidoo TM, McCain K, Hicks JT, McCabe R, et al. Lassa fever outbreaks, mathematical models, and disease parameters: a systematic review and meta-analysis. Lancet Glob Health 2024;12:e1962–72.
[74] Akhmetzhanov AR, Asai Y, Nishiura H. Quantifying the seasonal drivers of transmission for Lassa fever in Nigeria. Philos Trans R Soc Lond B Biol Sci 2019;374:20180268.
[75] Tuite AR, Watts AG, Kraemer MUG, Khan K, Bogoch II. Potential for Seasonal Lassa Fever Case Exportation from Nigeria. Am J Trop Med Hyg 2019;100:647–51.
[76] Kenmoe S, Tchatchouang S, Ebogo-Belobo JT, Ka'e AC, Mahamat G, Guiamdjo Simo RE, et al. Systematic review and meta-analysis of the epidemiology of Lassa virus in humans, rodents and other mammals in sub-Saharan Africa. PLoS Negl Trop Dis 2020;14:e0008589.
[77] Dwalu E, Jetoh RW, Shobayo BI, Pewu I, Taweh F, Wilson-Sesay HW, et al. Trend of Lassa fever cases and factors associated with mortality in Liberia, 2016 - 2021: a secondary data analysis. Pan Afr Med J 2024;47:22.
[78] Qian GY, Edmunds WJ, Bausch DG, Jombart T. A mathematical model of Marburg virus disease outbreaks and the potential role of vaccination in control. BMC Med 2023;21:439.
[79] Ajelli M, Merler S. Transmission potential and design of adequate control measures for Marburg hemorrhagic fever. PLoS One 2012;7:e50948.
[80] Pavlin BI. Calculation of incubation period and serial interval from multiple outbreaks of Marburg virus disease. BMC Res Notes 2014;7:906.
[81] Bettencourt LMA. An Ensemble Trajectory Method for Real-Time Modeling and Prediction of Unfolding Epidemics: Analysis of the 2005 Marburg Fever Outbreak in Angola. Mathematical and Statistical Estimation Approaches in Epidemiology 2009:143.
[82] Cuomo-Dannenburg G, McCain K, McCabe R, Unwin HJT, Doohan P, Nash RK, et al. Marburg virus disease outbreaks, mathematical models, and disease parameters: a systematic review. Lancet Infect Dis 2024;24:e307–17.
[83] Park J-E, Jung S, Kim A, Park J-E. MERS transmission and risk factors: a systematic review. BMC Public Health 2018;18:574.
[84] Peak CM, Childs LM, Grad YH, Buckee CO. Comparing nonpharmaceutical interventions for containing emerging epidemics. Proc Natl Acad Sci U S A 2017;114:4023–8.
[85] Wang J, Chen X, Guo Z, Zhao S, Huang Z, Zhuang Z, et al. Superspreading and heterogeneity in transmission of SARS, MERS, and COVID-19: A systematic review. Comput Struct Biotechnol J 2021;19:5039–46.
[86] Assiri A, McGeer A, Perl TM, Price CS, Al Rabeeah AA, Cummings DAT, et al. Hospital outbreak of Middle East respiratory syndrome coronavirus. N Engl J Med 2013;369:407–16.
[87] Park SH, Kim Y-S, Jung Y, Choi SY, Cho N-H, Jeong HW, et al. Outbreaks of Middle East Respiratory Syndrome in Two Hospitals Initiated by a Single Patient in Daejeon, South Korea. Infect Chemother 2016;48:99–107.
[88] Cowling BJ, Park M, Fang VJ, Wu P, Leung GM, Wu JT. Preliminary epidemiological assessment of MERS-CoV outbreak in South Korea, May to June 2015. Euro Surveill 2015;20:7–13.
[89] Cauchemez S, Fraser C, Van Kerkhove MD, Donnelly CA, Riley S, Rambaut A, et al. Middle East respiratory syndrome coronavirus: quantification of the extent of the epidemic, surveillance biases, and transmissibility. Lancet Infect Dis 2014;14:50–6.
[90] Virlogeux V, Fang VJ, Park M, Wu JT, Cowling BJ. Comparison of incubation period distribution of human infections with MERS-CoV in South Korea and Saudi Arabia. Sci Rep 2016;6:35839.
[91] Lessler J, Rodriguez-Barraquer I, Cummings DAT, Garske T, Van Kerkhove M, Mills H, et al. Estimating Potential Incidence of MERS-CoV Associated with Hajj Pilgrims to Saudi Arabia, 2014. PLoS Curr 2014;6.

https://doi.org/10.1371/currents.outbreaks.c5c9c9abd636164a9b6fd4dbda974369.
[92] Matsuyama R, Nishiura H, Kutsuna S, Hayakawa K, Ohmagari N. Clinical determinants of the severity of Middle East respiratory syndrome (MERS): a systematic review and meta-analysis. BMC Public Health 2016;16:1203.
[93] Okoli GN, Van Caeseele P, Askin N, Abou-Setta AM. A global systematic evidence review with meta-analysis of the epidemiological characteristics of the 2022 Mpox outbreaks. Infection 2024;52:901–21.
[94] Blumberg S, Lloyd-Smith JO. Inference of R(0) and transmission heterogeneity from the size distribution of stuttering chains. PLoS Comput Biol 2013;9:e1002993.
[95] Paredes MI, Ahmed N, Figgins M, Colizza V, Lemey P, McCrone JT, et al. Underdetected dispersal and extensive local transmission drove the 2022 mpox epidemic. Cell 2024;187:1374–86.e13.
[96] Okoli GN, Van Caeseele P, Askin N, Abou-Setta AM. Comparative evaluation of the clinical presentation and epidemiology of the 2022 and previous Mpox outbreaks: a rapid review and meta-analysis. Infect Dis 2023;55:490–508.
[97] Madewell ZJ, Charniga K, Masters NB, Asher J, Fahrenwald L, Still W, et al. Serial Interval and Incubation Period Estimates of Monkeypox Virus Infection in 12 Jurisdictions, United States, May-August 2022. Emerg Infect Dis 2023;29:818–21.
[98] Chenchula S, Ghanta MK, Amerneni KC, Rajakarunakaran P, Chandra MB, Chavan M, et al. A systematic review to identify novel clinical characteristics of monkeypox virus infection and therapeutic and preventive strategies to combat the virus. Arch Virol 2023;168:195.
[99] Hatami H, Jamshidi P, Arbabi M, Safavi-Naini SAA, Farokh P, Izadi-Jorshari G, et al. Demographic, Epidemiologic, and Clinical Characteristics of Human Monkeypox Disease Pre- and Post-2022 Outbreaks: A Systematic Review and Meta-Analysis. Biomedicines 2023;11. https://doi.org/10.3390/biomedicines11030957.
[100] Miura F, van Ewijk CE, Backer JA, Xiridou M, Franz E, Op de Coul E, et al. Estimated incubation period for monkeypox cases confirmed in the Netherlands, May 2022. Euro Surveill 2022;27:2200448.
[101] Asakura TR, Jung S-M, Murayama H, Ghaznavi C, Sakamoto H, Teshima A, et al. Projecting international mpox spread in Asia: ongoing global health risk. medRxiv 2024. https://doi.org/10.1101/2024.04.17.24305832.
[102] Endo A, Murayama H, Abbott S, Ratnayake R, Pearson CAB, Edmunds WJ, et al. Heavy-tailed sexual contact networks and monkeypox epidemiology in the global outbreak, 2022. Science 2022;378:90–4.
[103] Xiridou M, Miura F, Adam P, Op de Coul E, de Wit J, Wallinga J. The Fading of the Mpox Outbreak Among Men Who Have Sex With Men: A Mathematical Modelling Study. The Journal of Infectious Diseases 2024;230:e121–30.
[104] Benites-Zapata VA, Ulloque-Badaracco JR, Alarcon-Braga EA, Hernandez-Bustamante EA, Mosquera-Rojas MD, Bonilla-Aldana DK, et al. Clinical features, hospitalisation and deaths associated with monkeypox: a systematic review and meta-analysis. Ann Clin Microbiol Antimicrob 2022;21:36.
[105] Nikolay B, Salje H, Hossain MJ, Khan AKMD, Sazzad HMS, Rahman M, et al. Transmission of Nipah Virus - 14 Years of Investigations in Bangladesh. N Engl J Med 2019;380:1804–14.
[106] Bradbury NV, Hart WS, Lovell-Read FA, Polonsky JA, Thompson RN. Exact calculation of end-of-outbreak probabilities using contact tracing data. J R Soc Interface 2023;20:20230374.
[107] Kenmoe S, Demanou M, Bigna JJ, Nde Kengne C, Fatawou Modiyinji A, Simo FBN, et al. Case fatality rate and risk factors for Nipah virus encephalitis: A systematic review and meta-analysis. J Clin Virol 2019;117:19–26.
[108] Suman N, Khandelwal E, Chiluvuri P, Rami DS, Chansoria S, Jerry A, et al. NIPAH virus encephalitis: Unveiling the epidemiology, risk factors, and clinical outcomes - A systematic review and meta-analysis. J Pharm Bioallied Sci 2024;16:S102–5.
[109] Rudolph KE, Lessler J, Moloney RM, Kmush B, Cummings DAT. Incubation periods

of mosquito-borne viral infections: a systematic review. Am J Trop Med Hyg 2014;90:882–91.
[110] Ebogo-Belobo JT, Kenmoe S, Abanda NN, Bowo-Ngandji A, Mbaga DS, Magoudjou-Pekam JN, et al. Contemporary epidemiological data of Rift Valley fever virus in humans, mosquitoes and other animal species in Africa: A systematic review and meta-analysis. Vet Med Sci 2023;9:2309–28.
[111] Lipsitch M, Cohen T, Cooper B, Robins JM, Ma S, James L, et al. Transmission dynamics and control of severe acute respiratory syndrome. Science 2003;300:1966–70.
[112] Riley S, Fraser C, Donnelly CA, Ghani AC, Abu-Raddad LJ, Hedley AJ, et al. Transmission dynamics of the etiological agent of SARS in Hong Kong: impact of public health interventions. Science 2003;300:1961–6.
[113] Chen S-C, Chang C-F, Liao C-M. Predictive models of control strategies involved in containing indoor airborne infections. Indoor Air 2006;16:469–81.
[114] Chowell G, Castillo-Chavez C, Fenimore PW, Kribs-Zaleta CM, Arriola L, Hyman JM. Model parameters and outbreak control for SARS. Emerg Infect Dis 2004;10:1258–63.
[115] Tsang KW, Ho PL, Ooi GC, Yee WK, Wang T, Chan-Yeung M, et al. A cluster of cases of severe acute respiratory syndrome in Hong Kong. N Engl J Med 2003;348:1977–85.
[116] Becker NG, Glass K, Li Z, Aldis GK. Controlling emerging infectious diseases like SARS. Math Biosci 2005;193:205–21.
[117] Klinkenberg D, Fraser C, Heesterbeek H. The effectiveness of contact tracing in emerging epidemics. PLoS One 2006;1:e12.
[118] Lloyd-Smith JO, Galvani AP, Getz WM. Curtailing transmission of severe acute respiratory syndrome within a community and its hospital. Proc Biol Sci 2003;270:1979–89.
[119] Hui DSC, Chan MCH, Wu AK, Ng PC. Severe acute respiratory syndrome (SARS): epidemiology and clinical features. Postgrad Med J 2004;80:373–81.
[120] Ahammed T, Anjum A, Rahman MM, Haider N, Kock R, Uddin MJ. Estimation of novel coronavirus (COVID-19) reproduction number and case fatality rate: A systematic review and meta-analysis. Health Sci Rep 2021;4:e274.
[121] Lin Y-F, Duan Q, Zhou Y, Yuan T, Li P, Fitzpatrick T, et al. Spread and Impact of COVID-19 in China: A Systematic Review and Synthesis of Predictions From Transmission-Dynamic Models. Front Med 2020;7:321.
[122] Xie Y, Wang Z, Liao H, Marley G, Wu D, Tang W. Epidemiologic, clinical, and laboratory findings of the COVID-19 in the current pandemic: systematic review and meta-analysis. BMC Infect Dis 2020;20:640.
[123] Izadi N, Taherpour N, Mokhayeri Y, Sotoodeh Ghorbani S, Rahmani K, Hashemi Nazari SS. Epidemiologic Parameters for COVID-19: A Systematic Review and Meta-Analysis. Med J Islam Repub Iran 2022;36:155.
[124] Du Z, Wang C, Liu C, Bai Y, Pei S, Adam DC, et al. Systematic review and meta-analyses of superspreading of SARS-CoV-2 infections. Transbound Emerg Dis 2022;69:e3007–14.
[125] Xu X, Wu Y, Kummer AG, Zhao Y, Hu Z, Wang Y, et al. Assessing changes in incubation period, serial interval, and generation time of SARS-CoV-2 variants of concern: a systematic review and meta-analysis. BMC Med 2023;21:374.
[126] Yang L, Dai J, Zhao J, Wang Y, Deng P, Wang J. Estimation of incubation period and serial interval of COVID-19: analysis of 178 cases and 131 transmission chains in Hubei province, China. Epidemiol Infect 2020;148:e117.
[127] Alene M, Yismaw L, Assemie MA, Ketema DB, Gietaneh W, Birhan TY. Serial interval and incubation period of COVID-19: a systematic review and meta-analysis. BMC Infect Dis 2021;21:257.
[128] Rai B, Shukla A, Dwivedi LK. Estimates of serial interval for COVID-19: A systematic review and meta-analysis. Clin Epidemiol Glob Health 2021;9:157–61.
[129] Backer JA, Klinkenberg D, Wallinga J. Incubation period of 2019 novel coronavirus

(2019-nCoV) infections among travellers from Wuhan, China, 20-28 January 2020. Euro Surveill 2020;25. https://doi.org/10.2807/1560-7917.ES.2020.25.5.2000062.
[130] Xin H, Li Y, Wu P, Li Z, Lau EHY, Qin Y, et al. Estimating the Latent Period of Coronavirus Disease 2019 (COVID-19). Clin Infect Dis 2022;74:1678–81.
[131] He X, Lau EHY, Wu P, Deng X, Wang J, Hao X, et al. Temporal dynamics in viral shedding and transmissibility of COVID-19. Nat Med 2020;26:672–5.
[132] Zhu H, Li Y, Jin X, Huang J, Liu X, Qian Y, et al. Transmission dynamics and control methodology of COVID-19: A modeling study. Appl Math Model 2021;89:1983–98.
[133] Nishiura H, Kobayashi T, Yang Y, Hayashi K, Miyama T, Kinoshita R, et al. The rate of underascertainment of novel Coronavirus (2019-nCoV) infection: Estimation using Japanese passengers data on evacuation flights. J Clin Med 2020;9:419.
[134] Mizumoto K, Kagaya K, Chowell G. Early epidemiological assessment of the transmission potential and virulence of coronavirus disease 2019 (COVID-19) in Wuhan City, China, January-February, 2020. BMC Med 2020;18:217.
[135] Brazeau NF, Verity R, Jenks S, Fu H, Whittaker C, Winskill P, et al. Estimating the COVID-19 infection fatality ratio accounting for seroreversion using statistical modelling. Commun Med (Lond) 2022;2:54.
[136] Davies NG, Abbott S, Barnard RC, Jarvis CI, Kucharski AJ, Munday JD, et al. Estimated transmissibility and impact of SARS-CoV-2 lineage B.1.1.7 in England. Science 2021;372. https://doi.org/10.1126/science.abg3055.
[137] An der Heiden M, Buchholz U. Serial interval in households infected with SARS-CoV-2 variant B.1.1.529 (Omicron) is even shorter compared to Delta. Epidemiol Infect 2022;150:e165.
[138] Galmiche S, Cortier T, Charmet T, Schaeffer L, Chény O, von Platen C, et al. SARS-CoV-2 incubation period across variants of concern, individual factors, and circumstances of infection in France: a case series analysis from the ComCor study. Lancet Microbe 2023;4:e409–17.
[139] Wu Y, Kang L, Guo Z, Liu J, Liu M, Liang W. Incubation Period of COVID-19 Caused by Unique SARS-CoV-2 Strains: A Systematic Review and Meta-analysis. JAMA Netw Open 2022;5:e2228008.
[140] Hart WS, Miller E, Andrews NJ, Waight P, Maini PK, Funk S, et al. Generation time of the alpha and delta SARS-CoV-2 variants: an epidemiological analysis. Lancet Infect Dis 2022;22:603–10.
[141] Zhang T, Nishiura H. Estimating infection fatality risk and ascertainment bias of COVID-19 in Osaka, Japan from February 2020 to January 2022. Sci Rep 2023;13:5540.
[142] Liu Y, Rocklöv J. The reproductive number of the Delta variant of SARS-CoV-2 is far higher compared to the ancestral SARS-CoV-2 virus. J Travel Med 2021;28. https://doi.org/10.1093/jtm/taab124.
[143] Ryu S, Kim D, Lim J-S, Ali ST, Cowling BJ. Serial Interval and Transmission Dynamics during SARS-CoV-2 Delta Variant Predominance, South Korea. Emerg Infect Dis 2022;28:407–10.
[144] Zhao S, Guo Z, Chong MKC, He D, Wang MH. Superspreading potential of SARS-CoV-2 Delta variants under intensive disease control measures in China. J Travel Med 2022;29. https://doi.org/10.1093/jtm/taac025.
[145] Du Z, Liu C, Wang L, Bai Y, Lau EHY, Wu P, et al. Shorter serial intervals and incubation periods in SARS-CoV-2 variants than the SARS-CoV-2 ancestral strain. J Travel Med 2022;29. https://doi.org/10.1093/jtm/taac052.
[146] Backer JA, Eggink D, Andeweg SP, Veldhuijzen IK, van Maarseveen N, Vermaas K, et al. Shorter serial intervals in SARS-CoV-2 cases with Omicron BA.1 variant compared with Delta variant, the Netherlands, 13 to 26 December 2021. Euro Surveill 2022;27:2200042.
[147] Li Y, Jiang X, Qiu Y, Gao F, Xin H, Li D, et al. Latent and incubation periods of Delta, BA.1, and BA.2 variant cases and associated factors: a cross-sectional study in China. BMC Infect Dis 2024;24:294.

[148] Garcia-Knight M, Anglin K, Tassetto M, Lu S, Zhang A, Goldberg SA, et al. Infectious viral shedding of SARS-CoV-2 Delta following vaccination: A longitudinal cohort study. PLoS Pathog 2022;18:e1010802.
[149] Xia Q, Yang Y, Wang F, Huang Z, Qiu W, Mao A. Case fatality rates of COVID-19 during epidemic periods of variants of concern: A meta-analysis by continents. Int J Infect Dis 2024;141:106950.
[150] Yuan Z, Shao Z, Ma L, Guo R. Clinical Severity of SARS-CoV-2 Variants during COVID-19 Vaccination: A Systematic Review and Meta-Analysis. Viruses 2023;15. https://doi.org/10.3390/v15101994.
[151] Ward T, Fyles M, Glaser A, Paton RS, Ferguson W, Overton CE. The real-time infection hospitalisation and fatality risk across the COVID-19 pandemic in England. Nat Commun 2024;15:4633.
[152] Liu Y, Rocklöv J. The effective reproductive number of the Omicron variant of SARS-CoV-2 is several times relative to Delta. J Travel Med 2022;29. https://doi.org/10.1093/jtm/taac037.
[153] Guo Z, Zhao S, Ryu S, Mok CKP, Hung CT, Chong KC, et al. Superspreading potential of infection seeded by the SARS-CoV-2 Omicron BA.1 variant in South Korea. J Infect 2022;85:e77–9.
[154] Zeng K, Santhya S, Soong A, Malhotra N, Pushparajah D, Thoon KC, et al. Serial Intervals and Incubation Periods of SARS-CoV-2 Omicron and Delta Variants, Singapore. Emerg Infect Dis 2023;29:814–7.
[155] Kremer C, Braeye T, Proesmans K, André E, Torneri A, Hens N. Serial Intervals for SARS-CoV-2 Omicron and Delta Variants, Belgium, November 19-December 31, 2021. Emerg Infect Dis 2022;28:1699–702.
[156] Del Águila-Mejía J, Wallmann R, Calvo-Montes J, Rodríguez-Lozano J, Valle-Madrazo T, Aginagalde-Llorente A. Secondary Attack Rate, Transmission and Incubation Periods, and Serial Interval of SARS-CoV-2 Omicron Variant, Spain. Emerg Infect Dis 2022;28:1224–8.
[157] Edelstein GE, Boucau J, Uddin R, Marino C, Liew MY, Barry M, et al. SARS-CoV-2 virologic rebound with nirmatrelvir-ritonavir therapy : An observational study: An observational study. Ann Intern Med 2023;176:1577–85.
[158] Ahmad SJ, Degiannis JR, Borucki J, Pouwels S, Rawaf DL, Lala A, et al. Fatality Rates After Infection With the Omicron Variant (B.1.1.529): How Deadly has it been? A Systematic Review and Meta-Analysis. J Acute Med 2024;14:51–60.
[159] Liu Y, Lillepold K, Semenza JC, Tozan Y, Quam MBM, Rocklöv J. Reviewing estimates of the basic reproduction number for dengue, Zika and chikungunya across global climate zones. Environ Res 2020;182:109114.
[160] Gao D, Lou Y, He D, Porco TC, Kuang Y, Chowell G, et al. Prevention and Control of Zika as a Mosquito-Borne and Sexually Transmitted Disease: A Mathematical Modeling Analysis. Sci Rep 2016;6:28070.
[161] Counotte MJ, Kim CR, Wang J, Bernstein K, Deal CD, Broutet NJN, et al. Sexual transmission of Zika virus and other flaviviruses: A living systematic review. PLoS Med 2018;15:e1002611.
[162] Lessler J, Ott CT, Carcelen AC, Konikoff JM, Williamson J, Bi Q, et al. Times to key events in Zika virus infection and implications for blood donation: a systematic review. Bull World Health Organ 2016;94:841–9.
[163] Agudelo S, Ventresca M. Modeling the spread of the Zika virus by sexual and mosquito transmission. PLoS One 2022;17:e0270127.
[164] Kucharski AJ, Funk S, Eggo RM, Mallet H-P, Edmunds WJ, Nilles EJ. Transmission Dynamics of Zika Virus in Island Populations: A Modelling Analysis of the 2013-14 French Polynesia Outbreak. PLoS Negl Trop Dis 2016;10:e0004726.
[165] Moreira J, Peixoto TM, Siqueira AM, Lamas CC. Sexually acquired Zika virus: a systematic review. Clin Microbiol Infect 2017;23:296–305.
[166] Cardona-Ospina JA, Henao-SanMartin V, Acevedo-Mendoza WF, Nasner-Posso KM, Martínez-Pulgarín DF, Restrepo-López A, et al. Fatal Zika virus infection in the

Americas: A systematic review. Int J Infect Dis 2019;88:49–59.

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