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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 key parameters (reproduction number serial interval, proportion of presymptomatic transmission, case fatality risk and transmission route) and applied an unsupervised learning algorithm. This combined Monte Carlo sampling with ensemble clustering to classify pathogens into distinct epidemiological archetypes based on their shared characteristics.
Results: From 154 articles we extracted 302 epidemiological parameter estimates. The clustering algorithms categorise these pathogens into six archetypes (1) highly transmissible Coronaviruses, (2) moderately transmissible Coronaviruses, (3) high-severity contact and zoonotic pathogens, (4) Influenza viruses (5) MERS-CoV-like and (6) MPV-like.
Conclusion: Unsupervised learning on epidemiological data can be used to define 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 (Rietveld et al., 2024; Rt Hon the Baroness Hallett, 2024). 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 (Looi, 2023), but only a fraction of these viruses will possess the ability for widespread transmission in the community (Adalja et al., 2019). 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 (Adalja et al., 2019). A trait based

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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 (Adalja et al., 2019).

To address these gaps, we propose classifying pathogens into archetypes based on epidemiological traits. Using data collected from previous systematic reviews where possible, and individual papers and parameter estimation where necessary, we implement an unsupervised machine learning algorithm combining Monte Carlo sampling with ensemble clustering to identify relevant pathogen archetypes. By categorising pathogens by their key epidemiological parameters, we show how pathogens can be grouped by shared characteristics which may point to common approaches for their control.

2. Methods

2.1. Review of epidemiological parameters

We selected 19 pathogens for review based on their epidemic or pandemic potential. This list was primarily guided by the World Health Organisation's (WHO) R&D Blueprint (as of June 2024) (Prioritizing, 2024) and included: SARS-CoV-2 (Wild-Type, Alpha, Delta, Omicron), SARS-CoV-1, MERS-CoV, Crimean-Congo hemorrhagic fever orthonairovirus (CCHFV), Ebola virus (EBOV), Marburg virus (MARV), Lassa virus (LASV), Nipah virus (NiV), Rift Valley fever virus (RVFV), Zika virus (ZIKV), Mpox virus (MPV), and several influenza A viruses (H1N1, H2N2, H3N2, H1N1pdm09, and A/H5N1).

We sought to identify quantitative estimates for parameters related to each pathogen's transmission route(s), infection timeline, and severity. Key parameters included the reproduction number (R or R_0), overdispersion parameter for the reproduction number (k), incubation period, latent period, infectious period, serial interval, case fatality risk (CFR), and infection fatality risk (IFR).

Our search strategy involved systematic queries of PubMed for peer-reviewed articles and

preprints. Search terms were structured around three components: pathogen name, parameter type, and "systematic review" (Supplementary Table S1). Studies were required to report quantitative estimates derived from primary epidemiological data within systematic reviews or meta-analyses. For pathogens lacking comprehensive systematic reviews, we conducted targeted searches using pathogen-specific terminology, without a fixed strategy. We also included articles that 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 (Gressani, 2021; Gressani et al., 2025, 2022) 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} (Charniga et al., 2024; Abbott et al., 2025). For R_0, we used the package {epichains} (Abbott et al., 2025; Cases of Crimean, 2021), to provide an estimate for CCHFV on the basis of data collected by the European Centre for Disease Prevention and Control (Cases of Crimean, 2021). Full methodological details are provided in the Supplementary Information.

2.3. Clustering of epidemiological parameters

We compiled epidemiological estimates for each pathogen across a set of core parameters, including R, serial interval (SI), CFR, k, incubation period (IP), latent period, infectious period (Table 1), and transmission route. For each study, we reconstructed a full probability distribution from the reported summary statistics, applying Beta distributions for proportion outcomes (CFR) and Gamma distributions for non-negative continuous parameters (R and time to key events).

We performed a 5,000-iteration Monte Carlo simulation, using a non-parametric bootstrap-aggregation sampling method. In each of the Monte Carlo iterations, for a given pathogen and parameter, we resampled the available studies with replacement. A single random value was then drawn from each study's distribution. The final parameter value for that iteration was the average of these draws. Transmission routes were encoded as fixed binary indicators (presence/absence) and were not subject to sampling.

Pathogens were clustered in two stages. First, for each Monte Carlo iteration, we performed an independent K-means clustering on the resulting pathogen parameter profiles. This yielded 5000 plausible clustering solutions, each reflecting uncertainty in the underlying epidemiological estimates. Second, to obtain a single robust set of pathogen archetypes, we applied consensus clustering by constructing a co-assignment matrix representing the proportion of iterations in which each pair of pathogens clustered together. Hierarchical clustering of this matrix produced the final consensus dendrogram. The number of clusters was selected using silhouette width (how well a pathogen fits its assigned cluster) and epidemiological interpretability (Hamerly and Elkan, 2003).

When presymptomatic transmission was included within the algorithm, we defined it as the probability that the serial interval is shorter than the incubation period, P (SI < IP). To estimate this for each pathogen, we compiled SI and IP distributions. Within each Monte Carlo iteration, one SI distribution and one IP distribution were selected from the study selection. Using these distributions, we simulated 5000 paired SI–IP iterations. The final estimate for each iteration is the proportion of the 5000 pairs in which the sampled SI was less than the sampled IP. For influenza A subtypes data on SI and IP distributions were pooled.

2.3.1. Sensitivity analysis

We repeated the clustering using a restricted parameter set consisting R, SI, and CFR, with and without presymptomatic transmission. To determine how robust the pathogen classifications were to changes in the parameter space, and to evaluate the stability of pathogen groupings when the information content of the model was reduced.

To explore the flexibility and potential further application of our method, we performed an analysis on a widely available set of parameters: R, incubation period, and CFR. This enabled the incorporation of a more diverse range of pathogens, including those with different transmission dynamics, and to investigate how they fit within this classification. We extended this to include pathogens with had been excluded from the original analysis (RVFV), food and water borne pathogens (*Vibrio cholerae* and Norovirus), viruses common in paediatrics (Measles virus, Enterovirus A71 and Human metapneumovirus), bioterrorism related pathogens (*Yersinia pestis*, Variola virus and *Bacillus anthracis*), other vector borne pathogens (SFTS virus and Chikungunya), and a retrovirus (Human immunodeficiency virus) (Supplementary Table S3).

3. Results

3.1. Parameter review

A total of 154 articles were retrieved (Supplementary Figure S1). This included 43 articles obtained 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. We extracted 302 parameter estimates from the articles identified (Fig. 1).

28 articles were identified that provided sufficient data to estimate the incubation period with the {EpiLPS} package. Additionally, 14 articles contributed pre-existing datasets that were incorporated into the

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 (Biggerstaff et al., 2014)
		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: 3.82 (IQR: 2.68–4.84)	Biggerstaff et al. 2014 (Biggerstaff et al., 2014)
		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 (Biggerstaff et al., 2014)
		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 (Biggerstaff et al., 2014)
		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 (Biggerstaff et al., 2014)
	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 (Fraser et al., 2011)
	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 (Biggerstaff et al., 2014)
		Systematic review for serial interval estimates for influenza up to 2013.	6 studies with a range of 1.9–8.28 days	Vink et al. 2014 (Vink et al., 2014)
	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 (Nishiura, 2007)
	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 (Cori et al., 2012)
	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 (Cori et al., 2012)
	Case fatality risk (%)	Modelling, referenced range of CFR's for H1N1 pandemic.	1–4	Carrat et al. 2006 (Carrat et al., 2006)
		Pandemic Influenza Risk Management WHO Guidance. Estimated value (for 1918 pandemic)	2–3	WHO 2017 (WHO, 2017)
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 (Biggerstaff et al., 2014)
		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 (Biggerstaff et al., 2014)
		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 (Biggerstaff et al., 2014)
		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 (Biggerstaff et al., 2014)
	Dispersion parameter	Modelling seasonal influenza in Switzerland from 2003 to 2015	Mean: 7.38 (95 % CI: 5.30–10.64)	Brugger and Althaus 2020 (Brugger and Althaus, 2020)
	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 (Biggerstaff et al., 2014)
		Systematic review for serial interval estimates for influenza up to 2013.	36 studies ranging from 1.9 to 5 days	Vink et al. 2014 (Vink et al., 2014)
		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 (Vink et al., 2014)
		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 (Vink et al., 2014)
	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 (Tom et al., 2011)
		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 (Tom et al., 2011)
		EpiLPS - Dataset from Lessler et al. 2009 (Lessler et al., 2009a)	Semipar. Distribution with mean of 2.0 (95 % CrI: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 (Lessler et al., 2009b)
	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 (Tuite et al., 2010)

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Table 1 (*continued*)

Pathogen	Parameter	Description	Value	Reference
	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 (Tuite et al., 2010)
	Case fatality risk (%)	Pandemic Influenza Risk Management WHO Guidance. Estimated value. 2009 pandemic	0.02	WHO 2017 (WHO, 2017)
		Sero-epidemiological study. Prevalence of cross-reactive antibodies to H1N1pdm virus and rates of H1N1pdm infection	0.02	Van Kerkhove et al. 2013 (Van Kerkhove et al., 2013)
	Infection fatality risk	Systematic review of published estimates of the case fatality risk of H1N1pdm09 up to 2013. Laboratory-confirmed cases	Point estimates 0–13,500 deaths per 100,000 cases	Wong et al. 2013 (Wong et al., 2013)
		Symptomatic cases	Point estimates 0–1200 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 1000 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 (Biggerstaff et al., 2014)
	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 (Biggerstaff et al., 2014)
	Incubation period (d)	Systematic review of volunteer challenge studies	Median: 2 (IQR: 2.00–2.50)	Carrat et al. 2008 (Carrat et al., 2008)
	Latent period (d)	Modelling study, assumed value	Mean: 1.9	Elveback et al. 1976 (Elveback et al., 1976)
	Infectious period (d)	Modelling study, assumed value	Mean: 4.1	Elveback et al. 1976 (Elveback et al., 1976)
	Case fatality risk (%)	Pandemic Influenza Risk Management WHO Guidance. Estimated value. (1957 pandemic)	0.2	WHO 2017 (WHO, 2017)
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 (Biggerstaff et al., 2014)
		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 (Biggerstaff et al., 2014)
		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 (Biggerstaff et al., 2014)
		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 (Biggerstaff et al., 2014)
	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 (Biggerstaff et al., 2014)
		Systematic review for serial interval estimates for influenza up to 2013.	Mean values of 3.1 and 3.4	Vink et al. 2014 (Vink et al., 2014)
		Estimates from household datasets with information on symptom onset dates.	Normal distribution with mean of 2.2	Vink et al. 2014 (Vink et al., 2014)
	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 (Ferguson et al., 2005)
	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 (Ferguson et al., 2005)
	Infectious period (d)	Modelling. Transmission model to estimate the main characteristics of influenza transmission in households	Gamma distribution with mean of 3.80 (95 % CI: 3.10–4.60)	Cauchemez et al. 2004 (Cauchemez et al., 2004)
		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 (Cauchemez et al., 2004)
		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 (Cauchemez et al., 2004)
	Case fatality risk (%)	Pandemic Influenza Risk Management WHO Guidance. Estimated value. (1964 pandemic)	0.2	WHO 2017 (WHO, 2017)
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 (Bettencourt and Ribeiro, 2008)
		Modelling study, estimated Re in Indonesia 2004–2006.	0.0 (95 % CI: 0.0–0.0)	Bettencourt and Ribeiro 2008 (Bettencourt and Ribeiro, 2008)
		Modelling study, estimated Re in Indonesia 2005–2009.	0.1–0.25 (95 % CI: 0.0–0.40)	Aditama et al. 2012 (Aditama et al., 2012)
		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 (Yang et al., 2007)
		Modelling. Estimated from previous human to human cases.	0.06 (95 % CI: 0.01–0.2)	Ferguson et al. 2004 (Ferguson et al., 2004)

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Table 1 (*continued*)

Pathogen	Parameter	Description	Value	Reference
	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 (Biggerstaff et al., 2014)
		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 (Ward et al., 2024a)
	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 (Beigel et al., 2005)
		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 (Huai et al., 2008)
		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 (Cowling et al., 2013)
		Estimated value, 8 human cases in Eastern Turkey in 2006	Mean: 5 (Range: 4.0–7.0)	Oner et al. 2006 (Oner et al., 2006)
	Infectious period (d)	Modelling. Assumed value. Family Cluster, Indonesia 2006	Uniform distribution with mean of 9 (range 5–13)	Yang et al. 2007 (Yang et al., 2007)
	Case fatality risk (%)	Systematic Review. Crude CFR 1997-2009	Median: 56.3 % (IQR: 32.5–77.8)	Van Kerkhove et al. 2011 (Van Kerkhove et al., 2011)
		Systematic review of individual case data. 1997–2015 (Overall)	53.5	Lai et al. 2016 (Lai et al., 2016)
		Systematic review of individual case data. 1997–2015 (Clade 0)	31.6	Lai et al. 2016 (Lai et al., 2016)
		Systematic review of individual case data. 1997–2015 (Clade 1)	58.6	Lai et al. 2016 (Lai et al., 2016)
		Systematic review of individual case data. 1997–2015 (Clade 2.1)	84.6	Lai et al. 2016 (Lai et al., 2016)
		Systematic review of individual case data. 1997–2015 (Clade 2.2)	33.2	Lai et al. 2016 (Lai et al., 2016)
		Systematic review of individual case data. 1997–2015 (Clade 2.3)	61.8	Lai et al. 2016 (Lai et al., 2016)
		Systematic review of individual case data. 1997–2015 (Clade 7)	100	Lai et al. 2016 (Lai et al., 2016)
	Infection fatality risk (%)	Adjusted CFR based on surveillance and seroprevalence studies	14–33	Li et al. 2008 (Li et al., 2008)
CCHFV	Basic reproduction number	Estimated using epichains. Using data from cases of CCHFV infected in the European union/European Economic Area from 2013 to 2024.	Median: 0.03 (95 % CrI: 0.004–0.09)	Estimated
	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 % CrI: 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 (Bente et al., 2013)
		Systematic review, CFR worldwide of confirmed cases 1948–2018	Mean: 19.9 (IQR: 8–32)	Belhadi et al. 2022 (Belhadi et al., 2022)
		Systematic review, Overall CFR (%) with ongoing CCHF infection up to 2020	11.7 % (95 % CI: 9.1–14.5)	Belobo et al. 2021 (Belobo et al., 2021)
		Systematic review, fatality rate in the Arab world 1978–2021	Mean: 29 (range: 0–61)	Perveen and Gulfaraz Khan 2022 (Perveen and Khan, 2022)
		Systematic review, CFR calculated from annual cases from 1944 to 2017	Mean: 32.2	Nasirian 2020 (Nasirian, 2020)
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 (Nash et al., 2024)
		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 (Muzembo et al., 2024)
		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 (Muzembo et al., 2024)
		Systematic review, Zaire ebolavirus,2013–2016 epidemic in Nigeria (pooled mean).	Mean: 9.38 (95 % CI: 4.16–14.59)	Muzembo et al. 2024 (Muzembo et al., 2024)
		Systematic review, Zaire ebolavirus,2013–2016 epidemic in DRC (pooled mean)	Mean: 3.31 (95 % CI: 2.3–4.32)	Muzembo et al. 2024 (Muzembo et al., 2024)
		Systematic review, Sudan ebolavirus, 2000 outbreak in Uganda (pooled mean Ebola).	Mean: 2.0 (95 % CI: 1.25–2.76)	Muzembo et al. 2024 (Muzembo et al., 2024)
		Systematic review, Zaire ebolavirus, 2013–2016 epidemic in Liberia (pooled mean)	Mean: 1.83 (95 % CI: 1.61–2.05)	Muzembo et al. 2024 (Muzembo et al., 2024)
		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 (Muzembo et al., 2024)
		Systematic review, Zaire ebolavirus,2013–2016 epidemic in Guinea (pooled mean	Mean: 1.44 (95 % CI: 1.29–1.6)	Muzembo et al. 2024 (Muzembo et al., 2024)
		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 (Wong et al., 2017)
	Dispersion parameter	Systematic review. K reported as a range of central estimates, up to July 2023	0.02–2.20	Nash et al. 2024 (Nash et al., 2024)
	Serial interval (d)	Systematic review, up to July 2023 (Pooled value).	Mean: 15.4 (95 % CI: 13.20–17.50)	Nash et al. 2024 (Nash et al., 2024)
		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 (Wong et al., 2017)
	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 (Nash et al., 2024)

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Table 1 (*continued*)

Pathogen	Parameter	Description	Value	Reference
	Latent period (d)	Systematic review- 1976–2000. Data from individuals with single-day exposures	Mean: 12.27	Velásquez et al. 2015 (Velásquez et al., 2015)
		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 (Wong et al., 2017)
		Systematic review up to July 2023. Pooled random effect	0.10–31.20	Nash et al. 2024 (Nash et al., 2024)
	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 (Nash et al., 2024)
		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 (Wong et al., 2017)
		Systematic review- 1976–2000. data from individuals with single-day exposures (Survivors)	Mean:9.4	Velásquez et al. 2015 (Velásquez et al., 2015)
		Systematic review- 1976–2000. data from individuals with single-day exposures (fatal infections)	Mean: 5.33	Velásquez et al. 2015 (Velásquez et al., 2015)
	Case fatality risk (%)	Systematic review up to July 2023. Mean CFR across all estimates	Mean: 57.8	Nash et al. 2024 (Nash et al., 2024)
		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 (Khan et al., 2022)
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 (Lo Iacono et al., 2015)
	Serial interval (d)	Estimated using Lo Iacono et al. 2015 (Lo Iacono et al., 2015) 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 (Lo Iacono et al., 2015))	Gamma distribution with mean of 7.8	Zhao et al. 2020 (Zhao et al., 2020)
	Incubation period (d)	Systematic review, range of central estimates reported	Range: 7.0–12.80	Doohan et al. 2024 (Doohan et al., 2024)
		EpiLPS – Dataset from Akhmetzhanov et al. 2019 (Akhmetzhanov et al., 2019)	Lognormal distribution with mean of 12.6 (95 % CrI: 11.8–13.8)	Estimated
	Latent period (d)	Modelling study, Referenced value	Lognormal distribution with mean of 10.0 (Range: 5–21)	Tuite et al. 2019 (Tuite et al., 2019)
	Infectious period (d)	Modelling study, Referenced value	Lognormal distribution with mean of 10.0 (Range: 6–17)	Tuite et al. 2019 (Tuite et al., 2019)
	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 (Wolf et al., 2020)
		Systematic review, overall fatality rate in sub-Saharan Africa 1972-2020	29.7 (95 % CI: 22.3–37.5)	Kenmoe et al. 2020 (Kenmoe et al., 2020)
		Systematic review, pooled estimate up to 2023	33.1 (95 % CI: 25.7–41.5)	Doohan et al. 2024 (Doohan et al., 2024)
	Infection fatality risk (%)	Crude estimate of the overall case-fatality rate	1 %	Dwalu et al. 2024 (Dwalu et al., 2024)
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 (Qian et al., 2023)
		Modelling study, R0 estimated for the 2005 epidemic in Angola	1.59 (95 % CI: 1.53–1.66)	Ajelli and Merle 2012 (Ajelli and Merler, 2012)
	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 (Qian et al., 2023)
	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 (Qian et al., 2023)
	Incubation period (d)	Modelling study, estimated range of cental values	5.0–10.0	Qian et al. 2023 (Qian et al., 2023)
		EpiLPS - Dataset from Pavlin 2014 (Pavlin, 2014)	Weibull distribution with mean of 6.90 (95 % CrI: 6.20–7.60)	Estimated
		Modelling study, estimated from pooled data from all Marburg cases between 1967 and 2008	Median: 7 (range: 2.0–13.0)	Pavlin 2014 (Pavlin, 2014)
	Latent period (d)	Modelling study, latent period estimated using the average viral load in non-human primates	Mean: 3	Ajelli and Merle 2012 (Ajelli and Merler, 2012)
		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 (Bettencourt, 2009)
	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 (Bettencourt, 2009)
	Case fatality risk (%)	Systematic review, from database inception to March 2023 (estimated pooled total random)	61.9 (95 % CI: 38.8–80.6)	Cuomo-Dannenburg et al. 2024 (Cuomo-Dannenburg et al., 2024)
MERS-CoV	Basic reproduction number	Systematic review, Saudi Arabia or Middle East area data	Range: 0.45–0.98	Park et al. 2018 (Park et al., 2018)
		Systematic review, South Korea data (Early stage)	Range: 2.5–8.09	Park et al. 2018 (Park et al., 2018)
		Modelling. Referenced value derived from Cauchemez et al. 2014	Median: 0.95 (95 % CI: 0.6–1.3)	Peak et al. 2017 (Peak et al., 2017)
	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 (Wang et al., 2021)

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Pathogen	Parameter	Description	Value	Reference
	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 (Assiri et al., 2013)
		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 (Park et al., 2016)
		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 (Cowling et al., 2015)
	Incubation period (d)	EpiLPS – Dataset from Cauchemez et al. 2014 (Cauchemez et al., 2014)	Lognormal distribution with mean of 5.40 (95 % CrI: 4.50–6.50)	Estimated
		Systematic review up to 2017	Range: 4.50–7.80	Park et al. 2018 (Park et al., 2018)
	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 (Lessler et al., 2014)
	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 (Peak et al., 2017)
	Case fatality risk (%)	Systematic review, up to 2017. Mortality rate in South Korea	Range: 14.5–47.8	Park et al. 2018 (Park et al., 2018)
		Systematic review, up to 2017. Mortality rate in Saudi Arabia	Range: 22–69.2	Park et al. 2018 (Park et al., 2018)
		Systematic review, up to 2017. Mortality rate from multiple areas.	Range: 26.6–59.4	Park et al. 2018 (Park et al., 2018)
MPV	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 (Okoli et al., 2024)
		Systematic review. Analysis of active surveillance data collected in the DRC between 1980 and 1984.	0.8	Beer et al. 2019 (Beer and Rao, 2019)
	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 (Blumberg and Lloyd-Smith, 2013)
		Modelling study 2022 Mpox outbreak. Estimated using genomic and epidemiological metadata.	0.3 (95 % CI: 0.18–0.54)	Paredes et al. 2024 (Paredes et al., 2024)
	Serial interval (d)	Systematic review of the 2022 Mpox outbreaks. Pooled mean.	Mean of 8.5 (95 % CI: 7.3–9.9)	Okoli et al. 2024 (Okoli et al., 2024)
		Estimate from 17 case-contact pairs in the United Kingdom 2022	Mean of 9.8 (95 % CI: 5.9–21.4)	WHO 2022 (Second meeting of the International Health Regulations, 20052025)
		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 (Ward et al., 2022)
	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 (Chenchula et al., 2023)
		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. 2024 (Okoli et al., 2024)
		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 (Okoli et al., 2023)
		Systematic review of previous Mpox outbreaks. Pooled mean	Mean: 12.9 (95 % CI: 10.4–15.5)	Okoli et al. 2023 (Okoli et al., 2023)
		Systematic Review, analysis of outbreaks pre and post 2022	Mean: 7.9 (Range: 1–21)	Hatami et al. 2023 (Hatami et al., 2023)
		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 (Madewell et al., 2023)
		EpiLPS – dataset from Miura et al. 2022 (Miura et al., 2022)	Weibull distribution with mean of 7.6 (95 % CrI: 6.5–9.9)	Estimated
		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 (Ward et al., 2022)
	Latent period (d)	Modelling study, assumed value from viral shedding data (Preprint)	3.0	Asakura et al. 2024 (Asakura et al., 2024)
	Infectious period (d)	Modelling study, assumed value from documented duration of illness	21	Endo et al. 2022 (Endo et al., 2022)
		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 (Xiridou et al., 2024)
		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 (Xiridou et al., 2024)
		Modelling study, assumed value based on viral shedding data (Preprint)	10.0	Asakura et al. 2024 (Asakura et al., 2024)
	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 (Bunge et al., 2022)
		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 (Bunge et al., 2022)
		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 (Bunge et al., 2022)
		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 (Bunge et al., 2022)
		Systematic review 1950–2022. CFR when hospital care is available	0.03 (95 % CI: 0.0–0.44)	DeWitt et al. 2022 (DeWitt et al., 2022)
		Systematic review 1980–2022, CFR in hospitalised patients	4 (95 % CI:1–9 %)	Benites-Zapata et al. 2022 (Benites-Zapata et al., 2022)
NiV	Basic reproduction number	Review of hospital-based surveillance and outbreak investigations in Bangladesh from 2001 to 2014. Hospital-based surveillance implemented in 2007	0.33 (95 % CI: 0.19–0.59)	Nikolay et al. 2019 (Nikolay et al., 2019)

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Pathogen	Parameter	Description	Value	Reference
		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 (Nikolay et al., 2019)
		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 (Nikolay et al., 2019)
		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 (Nikolay et al., 2019)
	Dispersion parameter	Modelling study, referenced value	0.06	Bradbury et al. 2023 (Bradbury et al., 2023)
	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 (Nikolay et al., 2019)
	Incubation period (d)	EpiLPS – Dataset from Nikolay et al. 2019 (Nikolay et al., 2019)	Gamma distribution with mean of 9.4 (95 % CrI: 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 (Hegde et al., 2024)
		Systematic review up to 30 May 2019. Incubation period in Bangladesh	Median: 9.0 (Range: 6–14)	Hegde et al. 2023 (Hegde et al., 2024)
		Systematic review up to 30 May 2019. Incubation period in India	Median: 10.0 (Range: 6–18)	Hegde et al. 2023 (Hegde et al., 2024)
	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 (Nikolay et al., 2019)
	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 (Kenmoe et al., 2019)
		Systematic review, Bangladesh random effect meta-analysis from Bangladesh 2001–2014	67.9 (95 % CI: 47.7–85.4 %)	Kenmoe et al. 2019 (Kenmoe et al., 2019)
		Systematic review, random effect meta-analysis from India 2001	71.3 (95 % CI: 63.2–78.8)	Kenmoe et al. 2019 (Kenmoe et al., 2019)
		Systematic review, random effect meta-analysis from Malaysia 1998–1999	32.6 % (95 % CI: 25.8–39.8)	Kenmoe et al. 2019 (Kenmoe et al., 2019)
		Systematic review, random effect meta-analysis from the Philippines 2014	81.8 (95 % CI: 52.7–99.5)	Kenmoe et al. 2019 (Kenmoe et al., 2019)
		Systematic review, random effect meta-analysis from Singapore 1999	2.9 (0.0–11.9)	Kenmoe et al. 2019 (Kenmoe et al., 2019)
		Systematic review, CFR in Singapore 1999. Pig imports from Malaysia banned; abattoirs closed; preventive control measures in hospitals	8.3	Hegde et al. 2024 (Hegde et al., 2024)
		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 (Hegde et al., 2024)
		Systematic review, CFR in the Philippines 2014. Contact tracing implemented	53	Hegde et al. 2024 (Hegde et al., 2024)
		Systematic review, CFR in Bangladesh 2001–2014	78	Hegde et al. 2024 (Hegde et al., 2024)
		Systematic review, CFR in India 2001–2018	93	Hegde et al. 2024 (Hegde et al., 2024)
		Systematic review, CFR in Bangladesh and Malaysia 1999-2016	61 (95 % CI: 45.7–75.4)	Suman et al. 2024 (Suman et al., 2024)
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 (Rudolph et al., 2014)
		EpiLPS – Dataset collected from outbreak reports with reported exposure and symptom onset times	Semipar. with mean of 4.0 (95 % CrI: 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 (Ebogo-Belobo et al., 2023)
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 (Lipsitch et al., 2003)	Mean: 2.9 (95 % CI: 2.2–3.6)	Peak et al. 2017 (Peak et al., 2017)
		Modelling, R0 estimate at the start of the epidemic in Hong Kong (excluding superspreading events)	2.7 (95 % C): 2.2–3.7)	Riley et al. 2003 (Riley et al., 2003)
		Modelling. Estimated R0 from outbreak at the National Taiwan University Hospital	Lognormal distribution with mean of 2.65	Chen et al. 2006 (Chen et al., 2006)
		Modelling, estimated R0 distribution for SARS	Median 1.1 (IQR: 0.43–2.41)	Chowell et al. 2004 (Chowell et al., 2004)
		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 (Chowell et al., 2004)

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Pathogen	Parameter	Description	Value	Reference
		Modelling study, estimated R0 distribution Hong Kong 2003	Median: 1.1 (IQR: 0.44–2.29)	Chowell et al. 2004 (Chowell et al., 2004)
		Modelling study, estimated R0 distribution Singapore 2003	Median: 1.17 (IQR: 0.47–2.47)	Chowell et al. 2004 (Chowell et al., 2004)
	Dispersion parameter	Systematic review, range of k estimates	Range: 0.12 (90 % CI: 0.08–0.42) to 0.20 (95 % CI: 0.13–0.27)	Wang et al. 2021 (Wang et al., 2021)
	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 (Lipsitch et al., 2003)
		Modelling study, estimated by analysing 205 probable cases reported in Singapore (before full-scale interventions)	Mean 10.0	Lipsitch et al. 2003 (Lipsitch et al., 2003)
	Incubation period (d)	Systematic review, pooled analysis	Lognormal distribution with median of 4.0 (95 % CI: 3.6–4.4)	Lessler et al. 2009 (Lessler et al., 2009a)
		EpiLPS – Dataset from Tsang et al. 2003 (Tsang et al., 2003)	Semipar with mean of 4.70 (95 % CrI: 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 (Becker et al., 2005)
		Modelling study. Assumed to be a fixed value.	6.81	Klinkenberg et al. 2006 (Klinkenberg et al., 2006)
		Modelling study assumed value. Average time of progression from latent infection to infectious	5.0	Lipsitch et al. 2003 (Lipsitch et al., 2003)
	Infectious period (d)	Modelling study. Assumed value. Average duration of infectiousness	Mean: 5.0 (Range: 1–5)	Lipsitch et al. 2003 (Lipsitch et al., 2003)
		Modelling study referenced value. Symptomatic period assumed to be infectious period	Gamma distribution with mean of 16.3	Lloyd-Smith et al. 2003 (Lloyd-Smith et al., 2003)
		Modelling study, estimated value	Gamma distribution with mean of 9.25	Fraser et al. 2004 (Fraser et al., 2004)
		Modelling study referenced value. Effective infectious period	9.0	Becker et al. 2005 (Becker et al., 2005)
		Modelling study referenced value. Effective infectious period	3.87	Klinkenberg et al. 2006 (Klinkenberg et al., 2006)
	Case fatality risk (%)	Epidemiology review article	9.55 (95 % CI: 8.94–10.2)	Hui et al. 2004 (Hui et al., 2004)
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 (Ahammed et al., 2021)
		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 (Ahammed et al., 2021)
		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 (Ahammed et al., 2021)
		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 (Ahammed et al., 2021)
		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 (Lin et al., 2020)
		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 (Lin et al., 2020)
		Systematic review and meta-analysis of Epidemiologic, clinical, and laboratory findings. 1st December 2019–16 th July 2020.	Mean: 3.32 (95 % CI: 3.24–3.39)	Xie et al. 2020 (Xie et al., 2020)
		Systematic Review and Meta-Analysis December 2019 up to March 2020	Mean: 2.99 (95 % CI: 2.71–3.27)	Izadi et al. 2022 (Izadi et al., 2022)
	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 (Du et al., 2022)
	Serial interval (d)	Systematic review of serial intervals 2020–2023	Mean: 4.82 (95 % CI: 4.50–5.14)	Xu et al. 2023 (Xu et al., 2023)
	Incubation period (d)	Systematic review of Incubation periods 2020–2023	Mean: 6.50 (95 % CI: 5.88–7.12)	Xu et al. 2023 (Xu et al., 2023)
		EpiLPS - Using dataset from Backer et al. 2020 (Backer et al., 2020)	Lognormal distribution with mean of 4.40 (95 % CrI: 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 (Xin et al., 2022)
		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 (Lin et al., 2020)
	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 (Xie et al., 2020)
		Modelling, estimated based on exposure information on COVID-19 cases in China	Lognormal distribution with mean of 5.51	Xin et al. 2022 (Xie et al., 2020)
		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 (Xie et al., 2020)
		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 (Xie et al., 2020)
	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 (He et al., 2020)
		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 (Zhu et al., 2021)

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Pathogen	Parameter	Description	Value	Reference
		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 (Lin et al., 2020)
	Case fatality risk (%)	Systematic review of CFR's worldwide from January 1 to August 31, 2020	Mean: 2.67 (95 % CI: 2.25–3.13)	Ahammed et al. 2021 (Ahammed et al., 2021)
		Systematic Review and Meta-Analysis December 2019 up to March 2020	Mean: 3.29	Izadi et al. 2020 (Izadi et al., 2022)
		Systematic review and meta-analysis of Epidemiologic, clinical, and laboratory findings. 1st December 2019–16 th July 2020	4.4	Xie et al. 2020 (Xie et al., 2020)
		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 (Lin et al., 2020)
	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 (Nishiura et al., 2020b)
		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 (Mizumoto et al., 2020)
		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 (Brazeau et al., 2022)
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 43–90 % higher reproduction number	Davies et al. 2021 (Davies et al., 2021)
	Serial interval (d)	Systematic review of serial intervals 2020–2023	Mean: 3.47 (95 % CI: 2.52–4.41)	Xu et al. 2023 (Xu et al., 2023)
		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 (An der Heiden and Buchholz, 2022)
	Incubation period (d)	Systematic review of Incubation periods 2020–2023	Mean: 4.92 (95 % CI: 4.53–5.30)	Xu et al. 2023 (Xu et al., 2023)
	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 (Hart et al., 2022)
	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 (Hart et al., 2022)
	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 (Xie et al., 2020)
	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 (Zhang and Nishiura, 2023)
		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 (Zhang and Nishiura, 2023)
		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 (Zhang and Nishiura, 2023)
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 (Liu and Rocklöv, 2021)
	Dispersion parameter	Modelling study. Calculated using 1344 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 (Ryu et al., 2022)
		Modelling study. Calculated using 2384 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 (Ryu et al., 2022)
		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 (Zhao et al., 2022)
	Serial interval (d)	Systematic review of serial intervals 2020–2023	Mean: 3.59 (95 % CI: 3.26–3.92)	Xu et al. 2023 (Xu et al., 2023)
		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 (An der Heiden and Buchholz, 2022)
	Incubation period (d)	Systematic review of Incubation periods 2020–2023	Mean: 4.63 (95 % CI: 4.11–5.15)	Xu et al. 2023 (Xu et al., 2023)
		EpiLPS- Data set from Backer et al. 2022 (Backer et al., 2022)	Lognormal distribution with mean of 4.30 (95 % CrI: 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 (Li et al., 2024)
	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 (Li et al., 2024)
	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 (Garcia-Knight et al., 2022)
	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 (Xia et al., 2024)
		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 (Yuan et al., 2023)

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Table 1 (*continued*)

Pathogen	Parameter	Description	Value	Reference
	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 before the end of July 2021. Ages 20–39 years	0.01 (95 % CI: 0.01–0.01)	Zhang and Nishiura 2023 (Zhang and Nishiura, 2023)
		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 (Zhang and Nishiura, 2023)
		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 (Zhang and Nishiura, 2023)
		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 (Ward et al., 2024b)
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 (Liu and Rocklöv, 2022)
	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 (Liu and Rocklöv, 2022)
	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 (Guo et al., 2022)
		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 (Guo et al., 2022)
	Serial interval (d)	Systematic review of serial intervals 2020–2023	Mean: 3.21 (95 % CI: 2.94–3.48)	Xu et al. 2023 (Xu et al., 2023)
	Incubation period (d)	Systematic review of Incubation periods. (BA.1)	Mean: 3.49 (95 % CI: 3.13–4.86)	Xu et al. 2023 (Xu et al., 2023)
		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 (Li et al., 2024)
		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 (Li et al., 2024)
		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 (Li et al., 2024)
		EpiLPS - Dataset from Backer et al. 2022 (Backer et al., 2022)	Lognormal distribution with mean of 3.30 (95 % CrI: 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 (Xin et al., 2022)
		Modelling, estimated 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 (Li et al., 2024)
		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 (Li et al., 2024)
		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 (Li et al., 2024)
	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 (Del Águila-Mejía et al., 2022)
		Time to first negative viral culture (USA). (BA.2, 5, XBB)	Median: 4.0 (IQR: 3.0–4.0)	Edelstein et al. 2023 (Edelstein et al., 2023)
	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 (Xia et al., 2024)
		Systematic review confirmed case-fatality risk. 18 January 2021 to December 2021	0.04 (95 % CI: 0–0.61)	Yuan et al. 2023 (Yuan et al., 2023)
		Systematic review, patient deaths/omicron patients. From 14/11/2021–07/03/2022	0.21	Ahmad et al. 2024 (Ahmad et al., 2024)
	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 (Zhang and Nishiura, 2023)
		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 (Zhang and Nishiura, 2023)
		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 (Zhang and Nishiura, 2023)
		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 (Ward et al., 2024b)
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 (Liu et al., 2020)
		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 (Liu et al., 2020)

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Table 1 (*continued*)

Pathogen	Parameter	Description	Value	Reference
		Reproduction number for ZIKV sexual transmission	Median: 0.136 (95 % CI: 0.009–0.521)	Gao et al. 2016 (Gao et al., 2016)
	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 (Counotte et al., 2018)
	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 (Lessler et al., 2016)
		EpiLPS - Dataset from lessler et al. 2016 (Lessler et al., 2016)	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 the intrinsic incubation period and is a constant value	6.8	Agudelo et al. 2022 (Agudelo and Ventresca, 2022)
		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 (Kucharski et al., 2016)
	Infectious period (d)	Systematic review up to 2016. Time period that Zika virus is detectable in blood	Mean: 9.9	Lessler et al. 2016 (Lessler et al., 2016)
		Modelling study. Referenced value	Gamma distribution with mean of 5.0	Kucharski et al. 2016 (Kucharski et al., 2016)
		Systematic review, range of zika virus shedding in male genital tract	Range: 3–69	Moreira et al. 2017 (Moreira et al., 2017)
	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 (Cardona-Ospina et al., 2019)

* 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.

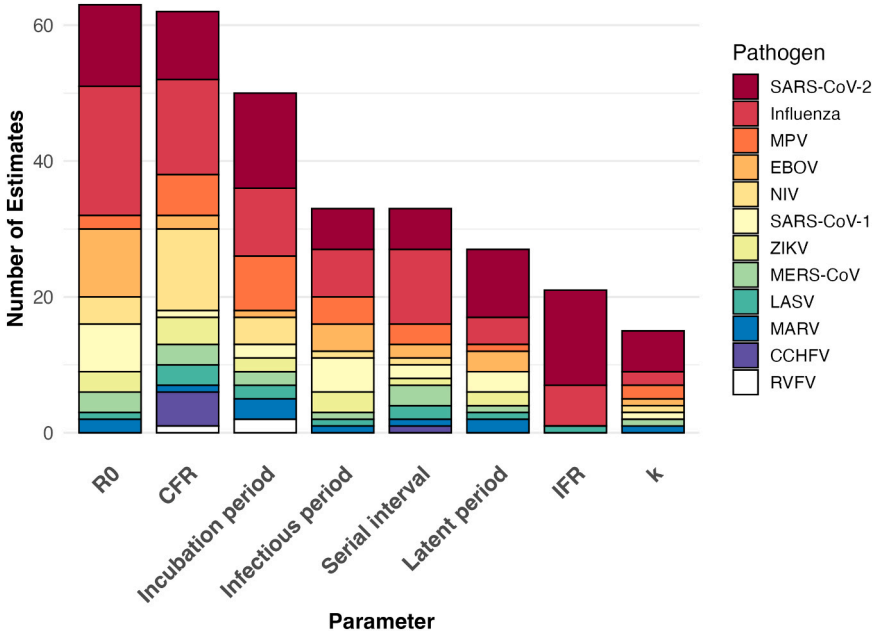

Fig. 1. Distribution of parameter estimates from the literature search. From 154 articles we extracted 302 parameter estimates. 63 for the reproduction number, 15 for the dispersion parameter, 51 for the incubation period, 33 for the serial interval, 27 for the latent period, 33 for the infectious period, 59 for the CFR, and 21 for the IFR.

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 (Supplementary figure S4).

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).

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) (Supplementary Figure S2) and 12.0 days (95 % CrI: 3.0–27.2) (Supplementary Figure S3), 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 21 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)

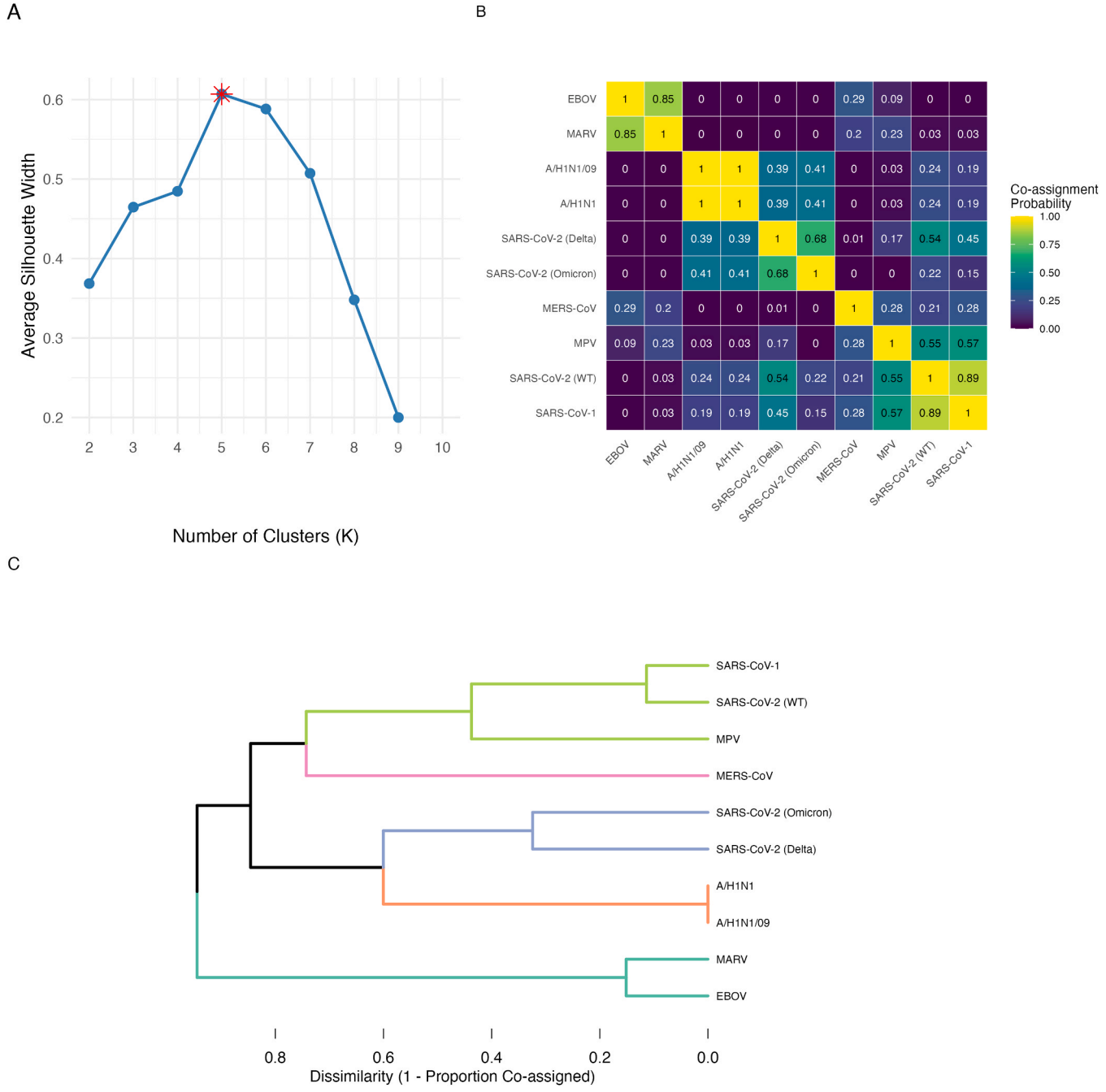

Fig. 2. Hierarchical clustering with R_0, serial interval, *k*, incubation period, latent and infectious period, case fatality risk and transmission route. A) The optimal number of consensus clusters determined by maximizing the average silhouette width. The optimal number of clusters is identified as K= 5 indicated by the red asterisk. B) The co-assignment matrix, visualised as a heatmap, displays the proportion of the 5000 Monte Carlo iterations in which each pair of pathogens was assigned to the same cluster. C) The final, stable classification of 18 pathogens based on their epidemiological and transmission characteristics. The horizontal branch lengths represent the dissimilarity between clusters, with shorter branches indicating a higher frequency of co-assignment in the underlying Monte Carlo simulations.

3.3. Ensemble clustering

We evaluated consensus clustering under the full parameter set, including and excluding the proportion of presymptomatic transmission (Fig. 2 & Supplementary Figure S9). Although presymptomatic transmission estimates were generated for all pathogens, these values were highly uncertain, in some cases extending beyond realistic bounds (Supplementary Table S2). For this reason, and because their inclusion did not materially improve cluster stability, the clustering solution excluding presymptomatic transmission (Fig. 2) was retained as the primary group.

The silhouette analysis (Fig. 2**A**) suggested that five clusters maximised average silhouette width; however, one of the resulting groups combined SARS-CoV-1, SARS-CoV-2 (WT) and MPV, which is potentially epidemiologically conflicting. The co-assignment heatmap (Fig. 2**B**) shows instability within this cluster: while SARS-CoV-1 and SARS-CoV-2 (WT) co-assign in 89 % of Monte Carlo iterations, MPV co-assigns with both, slightly more than half of the time.

When the dendrogram was instead cut at K= 6 (Fig. 3), it resolved into more epidemiologically coherent clusters, with all major pathogen groups forming stable, internally consistent archetypes across the ensemble of Monte Carlo simulations. Given this, the six-cluster solution was selected as the final consensus classification. The characteristics of each archetype are detailed in Table 2.

The dendrogram from Fig. 2 is cut at K = 4, 5, and 6 clusters to show how pathogen groupings change as the tree is partitioned at different resolutions. Stable groupings appear where pathogens remain together across multiple values of K, whereas splits or reassignments indicate less well-defined relationships within the consensus structure.

3.4. Archetype characterisation

3.4.1. Highly transmissible Coronaviruses

Archetype 1 contains the SARS-CoV-2 Delta and Omicron variants, which form a distinct high-transmission respiratory group. These pathogens have the highest reproductive number among all clusters (mean R

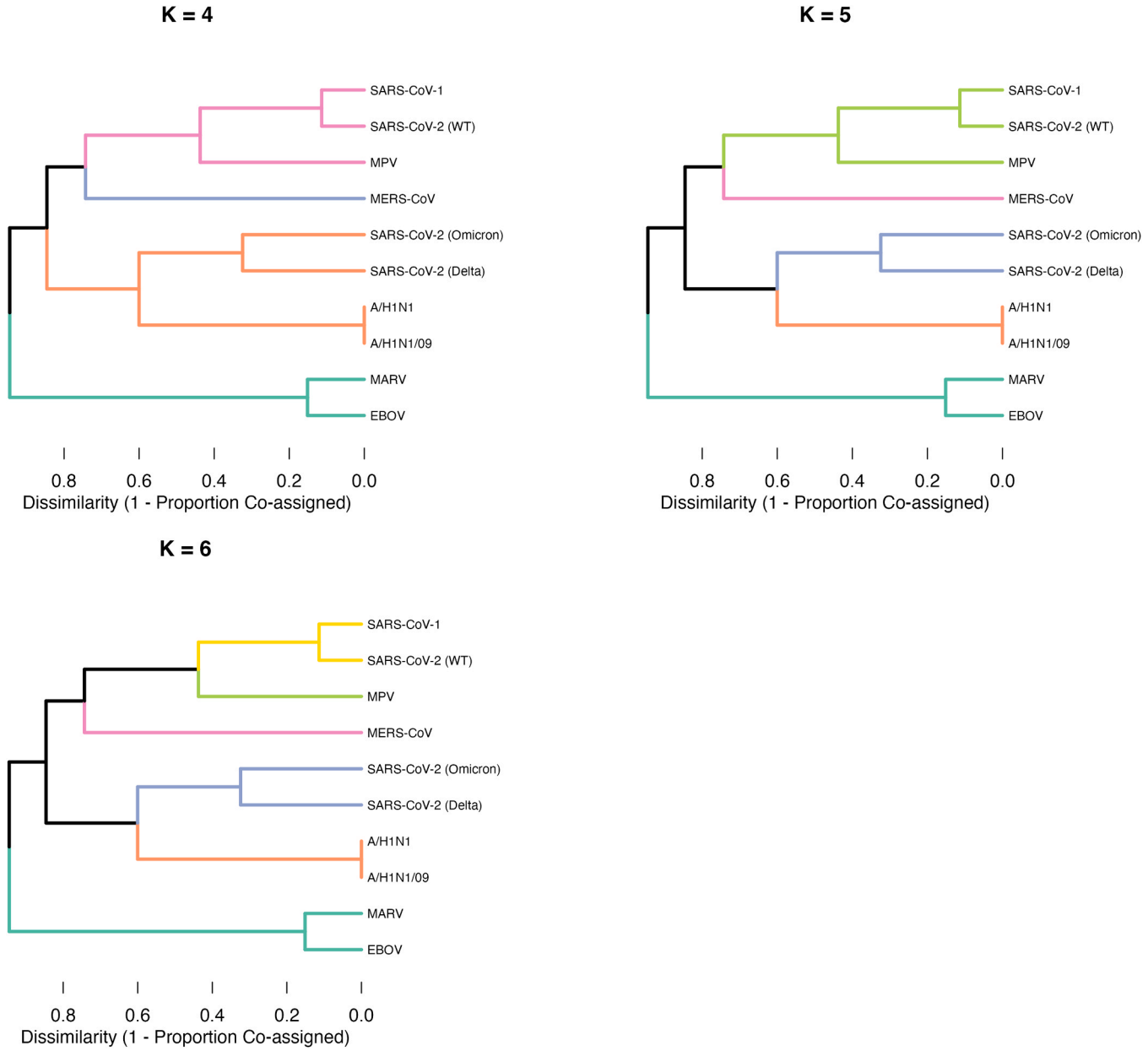

Fig. 3. Hierarchical clustering with R_0, serial interval, *k*, incubation period, latent and infectious period, case fatality risk and transmission route. K= 4, 5, 6.

Table 2
Archetype characterisation of Fig. 3 when K= 6.

Cluster	Pathogens	Archetype parameters (mean (95 % CI))							Transmission route
		R	*k*	Serial interval (d)	Incubation period (d)	Latent period (d)	Infectious period (d)	CFR (%)	
1	COVID-19 (Delta and Omicron)	7.38 (3.50–11.40)	0.41 (0.10–0.82)	3.55 (2.99–4.20)	4.09 (3.33–5.03)	3.57 (2.51–4.60)	4.94 (3.06–7.74)	0.1 (0.0–0.2)	Respiratory (n = 2)
2	COVID-19 (WT), SARS-CoV-1	1.36 (1.22–3.37)	0.36 (0.14–0.74)	6.36 (2.17–16.38)	5.08 (3.85–6.64)	5.77 (5.01–6.71)	8.33 (4.63–12.07)	0.6 (0.2–10)	Respiratory (n = 2)
3	EBOV, MARV	1.88 (0.38–4.11)	0.57 (0.18–1.06)	11.92 (3.47–17.18)	7.52 (4.37–9.34)	8.71 (6.06–12.27)	5.03 (3.07–8.38)	60 (43–78)	Animal to human (n = 2) Direct contact (n = 2)
4	A/H1N1, A/H1N1pdm09	1.88 (1.44–2.85)	4.43 (0.65–10.15)	2.73 (2.12–3.38)	1.50 (1.34–1.85)	2.14 (1.51–3.04)	2.13 (0.56–4.42)	0.1 (0.0–0.3)	Respiratory (n = 2)
5	MERS-CoV	1.40 (0.42–3.08)	4.41 (0.0–49.01)	12.41 (7.67–16.50)	6.71 (5.73–8.03)	7.00 (7.00–7.00)	16.01 (9.45–24.27)	39 (26–53)	Animal to human (n = 1) Respiratory (n = 1)
6	MPV	1.30 (0.80–1.85)	0.48 (0.23–1.01)	9.69 (7.38–13.97)	8.58 (6.62–11.13)	3.00 (3.00–3.00)	6.36 (3.19–10.00)	5.4 (2.4–8.3)	Animal to human (n = 1) Direct contact (n = 1)

of 7.38 (95 % CI: 3.50–11.40) short serial intervals (3.55 (95 % CI:2.99–4.20), and relatively short latent and infectious periods. The CFR is low (0.1 (95 % CI: 0.0–0.2)).

3.4.2. *Moderately transmissible Coronaviruses*

Archetype 2 comprises SARS-CoV-1 and the wild-type strain of SARS-CoV-2. These pathogens exhibit lower transmissivity (1.36 (95 % CI: 1.22–3.37)), longer serial intervals (6.36 (95 % CI: 2.17–16.38)), and longer infectious periods compared with Archetype 1. CFR displays a wider interval from 0.2 % to 10 %

3.4.3. *High-severity contact and zoonotic pathogens*

Archetype 3 groups EBOV and MARV. These pathogens have very high CFRs (60 (95 % CI: 43–78)), with the interval for human-to-human transmissibility ranging from 0.38 to 4.11. They display long serial, incubation and latent periods.

3.4.4. *Influenza viruses*

Archetype 4 contains A/H1N1 and A/H1N1pdm09. These pathogens show moderately high transmissibility (1.88 (95 % CI:1.44–2.85)), short incubation periods (1.50 (95 % CI:1.34–1.85)) and short infectious periods (2.13 (95 % CI: 0.56–4.42)). CFRs are low (0.1 % (95 % CI: 0.0–0.3)).

3.4.5. *MERS-CoV-like*

Archetype 5 consists solely of MERS-CoV. The pathogen is characterised by a long serial interval (12.41 (95 % CI:7.67–16.50)), long infectious period (16.01 (95 % CI: 9.45–24.27)), and very high CFR (39 % (CI:26–53)). Transmissibility is varied with the confidence interval ranging from 0.42 to 3.0.

3.4.6. *MPV-like*

Archetype 6 consists of MPV. MPV exhibits moderate incubation (8.58 (95 % CI:6.62–11.13)) and infectious periods (6.36 (95 % CI: 3.19–10.00)). Moderate contact driven transmissibility (1.30 (95 % CI: 0.80–1.85)), and a CFR of 5.4 % (95 % CI: 2.4–8.3).

3.4.7. *Sensitivity analysis*

To assess the robustness of the consensus clustering, we repeated the analysis using a reduced parameter set consisting of R, SI, and CFR, with (Supplementary Figures S5 and S6) and without presymptomatic transmission (Supplementary Figures S7 and S8). In both scenarios, pathogens grouped into larger and less clearly defined clusters, reflecting the limited discriminatory power of these parameters when used in isolation. When presymptomatic transmission was introduced SARS-CoV-2 viruses formed their own cluster separate to the Influenza A viruses (Supplementary Figures S5 **& S7).** Additionally, LASV also changed clusters when this parameter was added.

We assessed the flexibility of the framework by applying it to a more diverse range of pathogens using a core set of widely applicable parameters: R, IP, CFR, and transmission route. The framework incorporated and classified a wide variety of additional pathogens (Supplementary Figure S11).

4. Discussion

We reviewed key epidemiological parameters for 19 pathogens with pandemic potential and applied clustering algorithms to identify pathogen archetypes that share similar characteristics. Our findings suggest that grouping pathogens based on transmission traits 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 (Nash et al., 2024). Notably, R, serial interval, and CFR estimates were highly context dependent. For example, MERS-CoV R 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 (Biggerstaff et al., 2014). Likewise, EBOV estimates varied by country during the 2013–2016 epidemic (Muzembo et al., 2024). 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 (Lai et al., 2016). MPV varies when hospital care is available (DeWitt et al., 2022) 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) (Hegde et al., 2024). 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 modelling efforts.

Our clustering analysis identified six pathogen archetypes, each with shared characteristics that could inform the development of group-based, rather than pathogen-specific, control strategies (Fig. 3). Given that key interventions like contact tracing and case isolation are directly influenced by parameters such as R, the serial interval, and the proportion of presymptomatic transmission (Nishiura et al., 2020a; Fraser et al., 2004). Pathogen-specific planning however, is and will remain useful. Clustering pathogens with shared epidemiology would allow for specific plans to be adapted for pathogens that share similar characteristics. A dual approach would ideally allow for both in depth preparation for known risks and breadth in preparedness for a wider range of pathogens.

The archetypes proposed are a result of the quality, context, and variability of the underlying input parameters. Without classifying pathogens by setting and context, the archetypes must try and capture the range of plausible epidemiological behaviours that a pathogen can exhibit across different settings. However, this may bias the central tendency for parameters like R upwards, potentially misrepresenting a pathogen's behaviour in more common scenarios. Therefore, the use of this framework is to outline a plausible parameter range for each archetype. Archetype 3 (EBOV and MARV) for example spans 0.38–4.11 with a mean of 1.88. When planning for an EBOV/MARV-like pathogen there may be settings where transmission is limited (Nash et al., 2024) or uncontrolled (Muzembo et al., 2024). Likewise for a MERS-CoV-like pathogen in community settings transmission potential may be small, however in hospital settings there is a greater risk of secondary transmission (Park et al., 2018). Therefore, capturing the heterogeneity of these estimates is important to effectively plan for these pathogens.

Presymptomatic transmission was excluded from the main analysis as the estimates proved too uncertain to be meaningfully interpreted (Supplementary Table S2**)**. The values for SARS-CoV-2 variants and MPV were broadly consistent with published ranges (Tindale et al., 2020; Casey-Bryars et al., 2021; Ward et al., 2022). Others showed biologically implausible estimates, such as MERS-CoV. This estimation is highly influenced by uncertainty in serial interval and incubation period estimates (Slifka and Gao, 2020). Because of the sensitivity to the underlying distributions, even small uncertainties or inconsistencies in the source data can produce large fluctuations in the presymptomatic estimates. Although including presymptomatic transmission in the clustering process (Supplementary Figures S5 & S9) produced some shifts in cluster membership, the consensus structure remained broadly robust. Given these issues, the presymptomatic transmission parameter was omitted from the primary clustering analysis to avoid overinterpreting estimates stemming from data uncertainty.

The estimates generated for the serial interval and R_0 for LASV and CCHFV respectively are subject to considerable uncertainty. Human-to-human transmission for these pathogens is best studied in hospital settings, where nosocomial outbreaks have been documented. Identifying transmission for these pathogens in community or household settings is particularly difficult as it is hard to distinguish between vector/animal-to-human from human-to-human transmission. As a result, estimation of transmission parameters will largely rely on hospital-based outbreaks, as used in this study. Whilst these estimates are subject to significant uncertainty, they provide a feasible basis for inference. As such utilising these parameters within our framework (Supplementary figure S5 & S7) introduces additional uncertainty, which is a limitation for this method.

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. We extended the number of pathogens in the sensitivity analysis (Supplementary Figure S11) to include pathogens with different characteristics to the original selection. Highlighting that the framework could be used to classify water-borne pathogens, bioterrorism-related pathogens and pathogens with extended delay periods such as HIV. Additional work should address the impact of key interventions across each archetype. Moreover, the framework should be continuously updated as new epidemiological data emerge, refining the clustering methods and integrating additional pathogens, including both novel and emerging threats. To that end, the development of a global, standardised repository for epidemiological parameters would enable the rapid integration of data on novel and emerging threats.

Further research should be directed to explore the use of machine learning techniques to group pathogens. Our analysis reflects a set of decisions and assumptions that could reasonably be handled differently. Exploring how cluster membership changes under different approaches would help identify which aspects of the clustering are robust and which are most dependent on methodological choices. Such comparative work would support the development of more generalisable frameworks for future pandemic preparedness.

5. Conclusion

Documenting epidemiological parameters is crucial for effective outbreak risk analysis. We provide 302 parameter estimates for 19 pathogens, offering a valuable foundation for modelling 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 plausible parameter ranges 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.

CRediT authorship contribution statement

Edmunds William John: Writing – review & editing, Writing – original draft, Methodology, Funding acquisition, Conceptualization. **Niel Hens:** Writing – review & editing, Writing – original draft, Methodology, Funding acquisition, Conceptualization. **Sol Kim:** Writing – review & editing, Writing – original draft, Methodology, Data curation. **Oswaldo Gressani:** Writing – review & editing, Writing – original draft, Methodology, Formal analysis, Data curation. **Jack Ward:** Writing – review & editing, Writing – original draft, Visualization, Methodology, Formal analysis, Data curation.

Declaration of generative AI and AI-assisted technologies in the writing process

During the preparation of this work the author(s) used Gemini 2.5 pro, within the Cursor editor in order to generate code used in this analysis. After using this tool/service, the author(s) reviewed and edited the content as needed and take(s) full responsibility for the content of the publication.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at doi:10.1016/j.epidem.2025.100882.

Data availability

Link to all code/data is available within the paper

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