Systematic review of transmission and modelling parameters of nine WHO blue-print priority pathogens

Citation

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Review question

What are the transmission and modelling parameters for the nine WHO blue-print priority pathogens (Nairo virus (Crimean-Congo haemorrhagic fever), Ebola virus, Henipa virus, Lassa mammarenavirus, Marburg virus, Middle East respiratory syndrome coronavirus (MERS-CoV), Rift Valley fever virus, Severe Acute Respiratory Syndrome coronavirus (SARS-CoV), Zika virus)?

Searches

pathogen AND ((transmissi* OR epidemiolog*) OR (model* NOT imag*) OR (“severity” OR “case fatality ratio*” OR “CFR” OR “case fatality rate*” OR “mortality rate$” OR “attack rate$”) OR (“infectious period” OR “serial interval*” OR “incubation period*” OR “generation time*” OR “generation interval*” OR “latent period” OR “latency”) OR (“heterogeneit*” OR “superspread*” OR “super spread*” OR “super-spread*” OR “overdispers*”) OR (“infectivity” OR “infectiousness” OR “growth rate*” OR “reproduction number$” OR "reproductive number$" OR "R0" OR “reproduction ratio” OR “reproductive rate”) OR (“pre-existing immunity” OR “serological” OR “serology” OR “serosurvey*”) OR ("evolution*" OR "mutation$" OR “substitution$”) OR (outbreak$ OR cluster$ OR epidemic$) OR (“risk factor*”))

Types of study to be included

INCLUSION:

Original peer reviewed research

EXCLUSION as listed under section 19.

Non-English, conference proceedings, abstracts, posters,

- Case (clinical) reports/series (for diseases with limited data, these might be worth considering. These are also often travel related

- in-vitro studies

- animal studies that do not report R, Rt etc -- see inclusion criteria.

- Accidental outbreaks

Condition or domain being studied

WHO blue-print priority pathogens including: Nairo virus (Crimean-Congo haemorrhagic fever), Ebola virus, Henipa virus, Lassa mammarenavirus, Marburg virus, Middle East respiratory syndrome coronavirus (MERS-CoV), Rift Valley

fever virus, Severe Acute Respiratory Syndrome coronavirus (SARS-CoV), Zika virus

Participants/population

INCLUSION CRITERIA

- Measures/estimates of human: R, R0, Rt, r, Re, growth rate, generation time, serial interval, incubation/latent period, CFR, attack rate, mutation rate, overdispersion, risk factors (risk and the measure), other?

- Mention of historical or any outbreak in humans -- size, year, location, duration, spatial scale (local, regional, national, international)

- Measures/estimates of animal: R, R0, Rt, r, Re, growth rate, mutation rate,

- Mathematical or statistical model of transmission

- Measures of seroprevalence

EXCLUSION CRITERIA

- Non-English, conference proceedings, abstracts, posters,

- Case (clinical) reports/series (for diseases with limited data, these might be worth considering. These are also often travel related

- in-vitro studies

- animal studies that do not report R, Rt etc -- see inclusion criteria.

- Accidental outbreaks

Intervention(s), exposure(s)

All parameters to be extracted are specified in the inclusion / exclusion criteria (listed under section 19). Any mention of intervention explored with statistical or mathematical modelling will be noted.

Comparator(s)/control

All parameters to be extracted are specified in the inclusion / exclusion criteria (listed under section 19). Comparator(s)/control are extracted for risk-factors and seroprevalence.

Main outcome(s)

The most important outcome is an overview of parameters for each of the nine WHO blue-print priority pathogens (Nairo virus (Crimean-Congo haemorrhagic fever), Ebola virus, Henipa virus, Lassa mammarenavirus, Marburg virus, Middle East respiratory syndrome coronavirus (MERS-CoV), Rift Valley fever virus, Severe Acute Respiratory Syndrome coronavirus (SARS-CoV), Zika virus). Specified in inclusion criteria listed under section 19.

Measures/estimates of human: R, R0, Rt, r, Re, growth rate, generation time, serial interval, incubation/latent period, CFR, attack rate, mutation rate, overdispersion, risk factors (risk and the measure); mathematical or statistical model of transmission; measures of seroprevalence; outbreak details including cases and deaths.

Additional outcome(s)

Not Applicable

Data extraction (selection and coding)

Studies will be selected for inclusion based on the inclusion / exclusion criteria described in section 19. This is done using Covidence.org with two reviewers screening all selection stages and conflicts resolved by consensus.

Risk of bias (quality) assessment [1 change]

The risk of bias will be assessed using a questionnaire from Hoy et al, 2012 which has been validated to show high concordance between reviewer assessments of study quality and high values of the Kappa statistic. This assessment will measure both the internal and external validity of studies based on how study participants are selective, the representativeness of the sample, how the data was collected and tested and the validity of analysis methodologies. Two reviewers will independently perform the quality assessment for the same sample of studies (~10% for each pathogen) which are double extracted to enable assessment of consistency in quality assessment in our review. The bias assessment will be used to repeat analyses with only high-quality studies to see how this may affect conclusions and estimates.

Strategy for data synthesis [1 change]

The purpose of our review is to fill a need for an existing database of information to assist in guiding infectious disease response efforts for the World Health Organization's nine priority pathogens as outlined in the 2019 blueprint. Our review will provide information on the size of previous outbreaks of the pathogen, estimates of important infectious disease metrics such as the reproduction number, case fatality ratio and mathematical modelling structures which reflect the mechanisms of disease transmission and potential interventions. Through the use of a meta-analysis, we are able to assess the body of evidence and certainty of parameter estimates, alongside collating significant risk factors for infection, severe disease, infection-associated deaths and seropositivity. This information has two important utilities in terms of the public health response to an outbreak of one of these nine pathogens. Firstly, to facilitate knowledge and understanding of disease transmission mechanisms, background levels of immunity based on previous disease exposures, previously used interventions and demographics at elevated risk of infection in order to target resources effectively to reduce transmission. Secondly, this systematic review intends to collate all necessary information for effective nowcasting and forecasting of outbreaks using mathematical modelling. Infectious disease modelling is a highly useful tool to estimate potential epidemic size, required hospital capacity and the effect of interventions and has been utilised across a huge array of infectious disease pathogens.

All data will be collated including uncertainty estimates of parameters (including but not limited to reproduction number, mutation rate, doubling time, incubation period, transmission rate, duration of infectiousness, case fatality ratio), risk factors and parameter context (i.e. population age, gender, occupation etc), survey method, mathematical or statistical model type, stochasticity, structure, intervention and transmission routes, fitting to disease

data or outbreak data, outbreak data including duration, location, size, estimates of cases and deaths.

Analysis of subgroups or subsets

People infected with the disease, whole population surveys where the outbreak has occurred.

Contact details for further information

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Organisational affiliation of the review

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Type and method of review

Epidemiologic, Meta-analysis, Methodology, Systematic review

Anticipated or actual start date

08 March 2019

Anticipated completion date

08 March 2024

Funding sources/sponsors

The team acknowledges funding from the MRC Centre for Global Infectious Disease Analysis (reference MR/R015600/1), jointly funded by the UK Medical Research Council (MRC) and the UK Foreign, Commonwealth & Development Office (FCDO), under the MRC/FCDO Concordat agreement and is also part of the EDCTP2 programme supported by the European Union.

Grant number(s)

State the funder, grant or award number and the date of award

Reference MR/R015600/1

Conflicts of interest

Language

English

Country

England

Stage of review

Review Ongoing

Subject index terms status

Subject indexing assigned by CRD

Subject index terms

Animals; Ebolavirus; Hemorrhagic Fever Virus, Crimean-Congo; Hemorrhagic Fever, Ebola; Humans; Lassa virus; Marburgvirus; Middle East Respiratory Syndrome Coronavirus; Rift Valley fever virus; Severe acute respiratory syndrome-related coronavirus; World Health Organization; Zika Virus; Zika Virus Infection

Date of registration in PROSPERO

17 February 2023

Date of first submission

20 January 2023

Details of any existing review of the same topic by the same authors [1 change]

This review is being undertaken under our body of work as the WHO Collaborating Centre for Infectious Disease Modelling with the intention of facilitating preparation for possible future outbreaks of one of the nine priority pathogens and support faster response times and provision of evidence and effective targeting of public health interventions.

Stage of review at time of this submission

Stage	Started	Completed
Preliminary searches	Yes	Yes
Piloting of the study selection process	Yes	Yes
Formal screening of search results against eligibility criteria	Yes	No
Data extraction	No	No
Risk of bias (quality) assessment	No	No
Data analysis	No	No

The record owner confirms that the information they have supplied for this submission is accurate and complete and they understand that deliberate provision of inaccurate information or omission of data may be construed as scientific

misconduct.

The record owner confirms that they will update the status of the review when it is completed and will add publication details in due course.

Versions

17 February 2023