EE494

Health economic modelling approaches for assessing the value of a *Clostridioides difficile* vaccination programme: a literature review

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INTRODUCTION

- Clostridioides difficile (*C. diff*) outbreaks pose a substantial threat to public health globally[1], prompting the investigation of a *C. diff* vaccine in recent years[2]
- This targeted literature review (TLR) explored the mathematical modelling approaches used for assessing the potential socioeconomic value of implementing a *C. diff* vaccine programme to help inform future modelling activities

OBJECTIVE

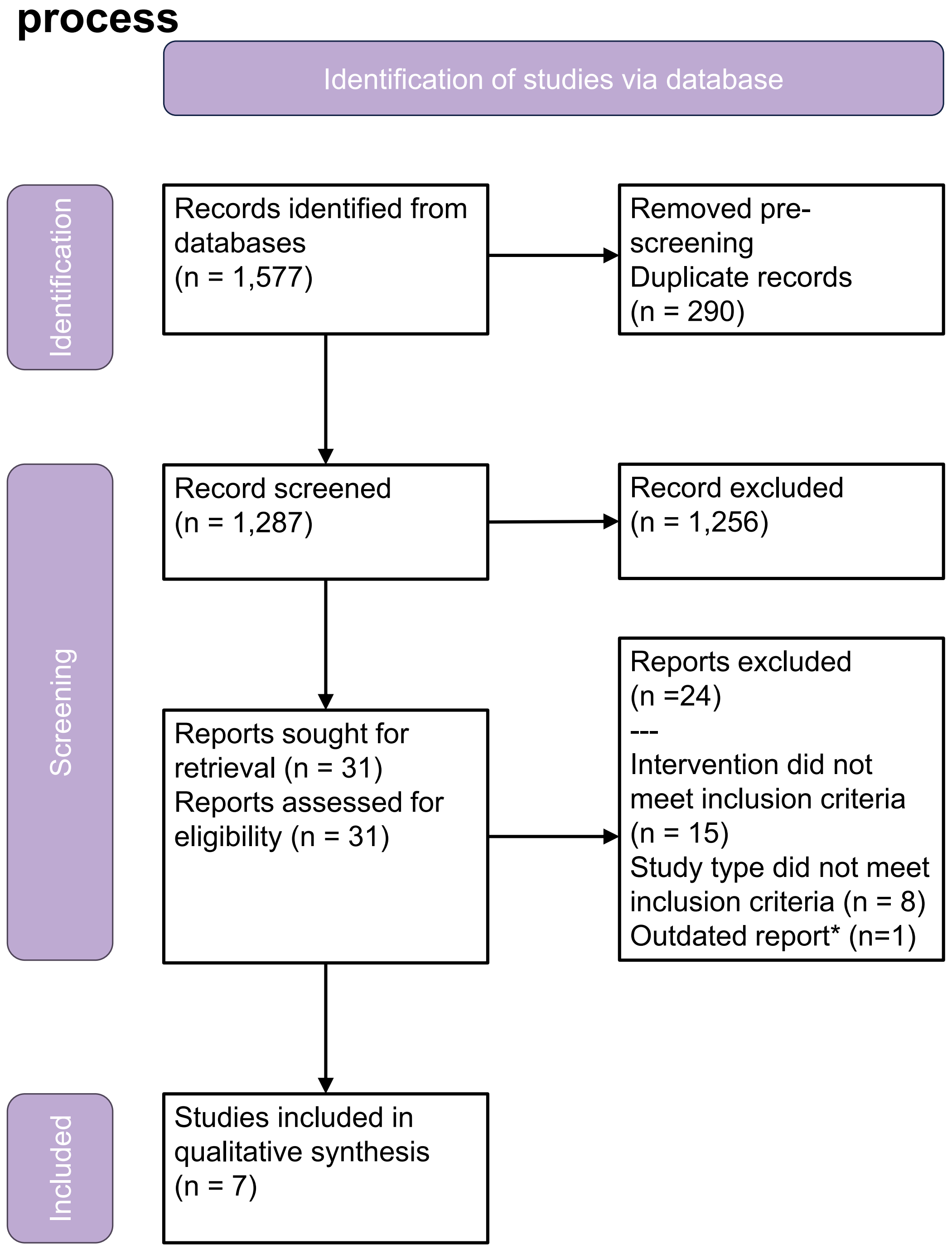
- The TLR aimed to answer the following questions:

1) What are the various mathematical modelling approaches previously employed to assess the impact of introducing a *C. diff* vaccine programme?
2) What are the key compartments that should be included within a mathematical model for a *C. diff* vaccine programme assessment?

METHODS

- A TLR was conducted focussing on *C. diff* vaccination and corresponding mathematical modelling approaches per **Table 1**
- MEDLINE and Embase were searched from their inception date up to 10th July 2024, using a pre-defined search strategy, followed by two-stage screening and data extraction, as per **Figure 1**
- Backwards citation searching of the reference lists of relevant SLRs and meta-analyses captured in the database search was carried out to identify additional relevant papers. Duplicate records were removed using EndNote prior to the initiation of record screening
- Key information extracted included modelling approach, time horizon, transmission pathways, natural history, and vaccine assumptions

Figure 1. PRISMA diagram showing selection process



Identification of studies via database

Identification

Records identified from databases
(n = 1,577)

Removed pre-screening
Duplicate records
(n = 290)

Screening

Record screened
(n = 1,287)

Record excluded
(n = 1,256)

Reports sought for retrieval (n = 31)
Reports assessed for eligibility (n = 31)

Reports excluded
(n =24)

Intervention did not meet inclusion criteria
(n = 15)
Study type did not meet inclusion criteria (n = 8)
Outdated report* (n=1)

Included

Studies included in qualitative synthesis
(n = 7)

METHODS (continued)

Table 1. Eligibility criteria established using the PICOS framework

PICOS criteria	Inclusion	Exclusion
Population	Adults (≥18 years old) with confirmed *C.diff* infection	• Non-adult (<18 years old) • Non-*C.diff* patients
Intervention	Vaccination	No vaccination
Comparator	Not restricted	Not applicable
Outcomes	Not restricted	Not applicable
Study type	• Mathematical model • Economic analysis • Human studies	Animal studies
Language	English	Non-English
Date of publication	Up to 10th of July 2024	After 10th of July 2024
Geography	All countries	Not applicable
Full text	Available	Unavailable

RESULTS

- 1,577 studies were screened, of which seven studies were ultimately included within the review, these are shown in **Table 2**
- Three different modelling approaches were identified, agent-based model (ABM, n = 3), decision tree (n = 2), and dynamic transmission modelling (DTM, n = 2), as per Figure 2
- *C. diff* natural history was represented in each of the modelling approaches, with all studies including health states for at least susceptible, infected and recovered individuals
- A key difference in modelled natural history was the depiction of *C. diff* colonisation. Colonised patients (patients with consistent *C. diff* over time) were captured in most studies (n = 6), although usually with limited modelling impact. Likewise *C. diff* transmission was represented in most of the studies (n = 5), characterised through three key contact pathways; healthcare workers, patients and the environment

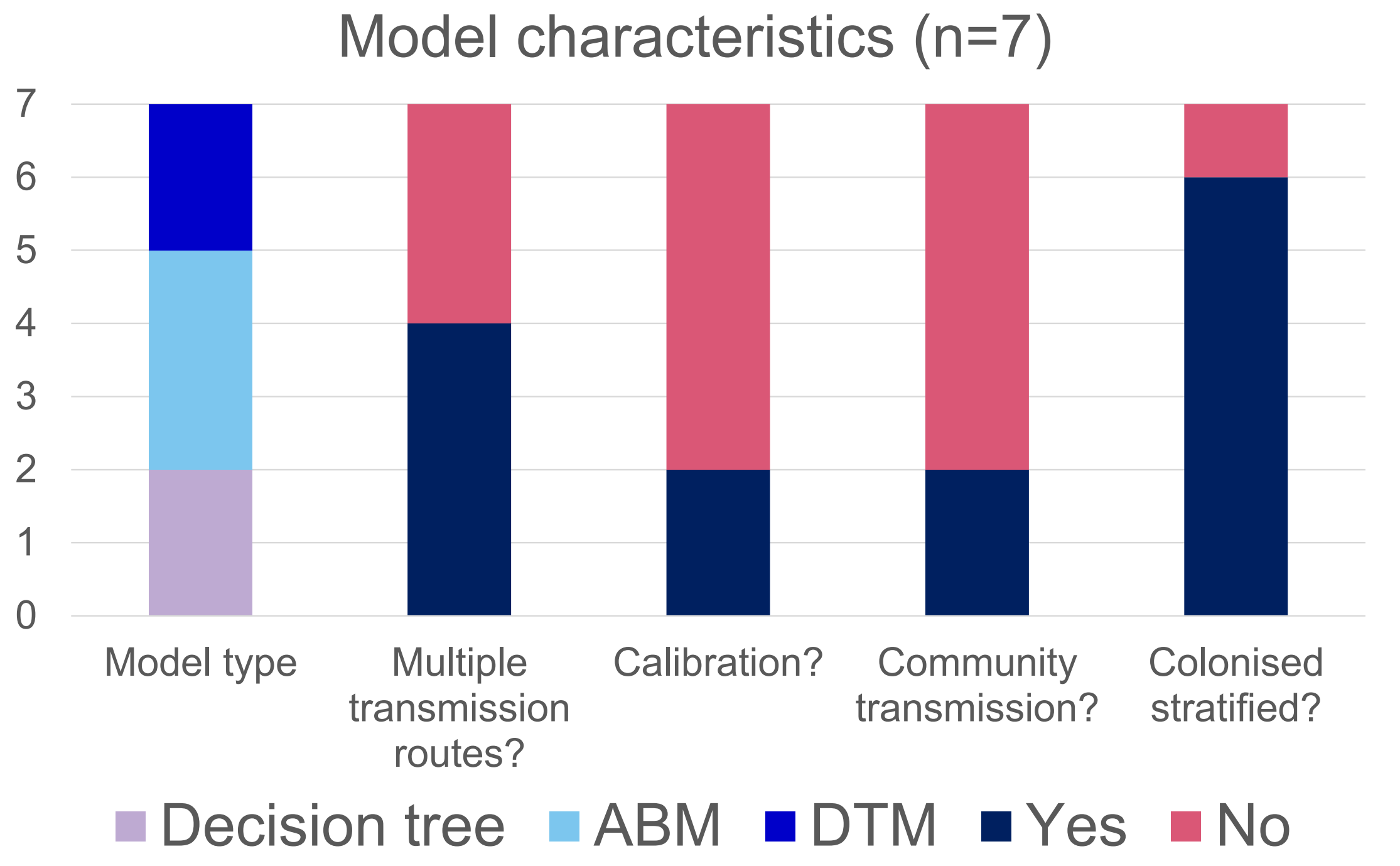
Table 2. Overview of included studies

Author	Country	Time horizon	Model type	Transm.	Calib-ration	Community transm.
Champredon et al.[3]	Canada	2 years	ABM	Patients, HCW, Enviro.	Yes	No
Lee et al.[4]	USA	N/A	Decision tree	N/A	No	No
Neri et al.[5]	UK	1 year	Decision tree	N/A	No	No
Stephenson et al.[6]	USA	30 days	DTM	Patients	No	No
Stephenson et al.[7]	USA	1 year	ABM	Patients, HCW, Enviro.	No	No
Toth et al.[8]	USA	5 years	ABM	Patients	Yes	Yes
Van Kleef et al.[9]	UK	5 years	DTM	Patients, HCW, Enviro.	No	Yes

RESULTS (continued)

- Vaccine assumptions were heterogeneous- mostly focussed on reduced probability or symptoms of infection. Several papers mentioned this was due to assuming a toxoid platform for vaccination
- Modelling studies all described a consistent natural history for *C. diff* irrespective to the intervention being assessed. Furthermore, transmission dynamics were modelled utilising the same three vectors in the studies captured in the TLR: patients, environment, and healthcare workers (HCWs)

Figure 2. Modelling approach in included papers



CONCLUSIONS

- **In the current literature, there exists multiple modelling approaches for *C. diff* transmission as well as diverse key modelling assumptions around potential vaccination impact, disease reservoirs and health states**
- **This highlights the complexity of *C. diff* vaccinology and the careful considerations needed to produce fit for purpose future models**

References

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