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Measles transmission-related epidemiological parameter estimates: a systematic review and meta-analysis

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Review

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Abstract

With the recent resurgence of global measles outbreaks, it is crucial to understand measles transmission dynamics to guide timely and effective public health responses and parameterize infectious disease models for accurate outbreak projections. This systematic review aims to provide a comprehensive resource of measles transmission-related epidemiological parameters. A search was conducted from inception to 14 May 2024. English and French primary studies of transmission-related epidemiological parameters were included, and standard systematic review methodology was followed. Evidence was synthesized using random-effects meta-analyses and descriptive plots. Subgroup analyses by World Health Organization (WHO) region, population, decade, and quality of reporting were conducted to explore heterogeneity. Between 1910 and 2024, 1 209 estimates across 32 transmission-related epidemiological parameters from 612 studies were reported. Measles was characterized by a pooled incubation period (13.5 days, 95%CI 12.6–14.4; $I^2 = 95.9\%$), serial interval (12.4 days, 95%CI 11.5–13.4; $I^2 = 97.6\%$), symptom onset to hospitalization (4.8 days, 95%CI 3.7–5.8, $I^2 = 99.7\%$), and basic reproduction number median 11.5 (range of 0–57). This work is part of a global epidemic preparedness and response project to establish an accessible living Global Repository of Epidemiological Parameters aimed at reducing duplicative efforts in identifying and summarizing epidemiological parameters.

Background

Measles is a highly contagious virus that is transmitted between humans through direct contact with respiratory droplets or aerosol particles [1, 2]. Measles can cause serious health complications including pneumonia, encephalitis, subacute panencephalitis, blindness, and neurological complications, which can lead to death, particularly among children and malnourished populations [1, 2]. Following the introduction of the measles vaccine in 1963, public health efforts to globally eradicate measles through vaccination have contributed to reduced disease incidence and measles-related deaths, and elimination status in some regions [2–4]. Despite the commitment by the World Health Organization (WHO) to eliminate measles by 2020, a global rise in the number of measles cases was reported in recent years, with 254 384 cases reported in 2025 and 68 502 cases reported in the first 4 months of 2026, resulting in some countries in the Americas and Europe losing elimination status [4–8]. This highlights the global concern of measles resurgence and spread owing largely to declining immunization rates [1].

Recent public health emergencies have demonstrated how infectious disease models, which encompass mathematical and statistical outputs, have played a central role in forecasting infectious disease outbreaks to support and manage public health responses [9, 10]. These models simulate scenarios to understand the transmission dynamics of infectious disease pathogens and predict the impacts of interventions on outbreaks [9, 10]. Epidemiological parameter estimates gathered from the literature feed directly into these models, which support risk assessment, guideline development, and other public health response activities. This highlights the importance of the input parameters being underpinned by the most robust estimates for reliable and transparent evidence-based projections [9, 10]. Concerns about the duplicative effort to identify and synthesize parameter estimates led to the development of the Global Repository of Epidemiological Parameters (grEPI) project coordinated by the WHO Collaboratory. The project aims to create a publicly accessible living repository of extracted epidemiological parameters from the literature for a suite of priority infectious disease pathogens [11].

Previous systematic reviews (SR) on measles have focused on a handful of transmission parameters such as basic reproduction number, vaccine efficacy/effectiveness, case-fatality, and risk of certain clinical outcomes [2, 12–15]. To the best of our knowledge, this is the first comprehensive synthesis of global measles transmission parameters and knowledge gap analysis. This SR aims to provide a comprehensive resource of measles transmission-related epidemiological parameters gathered from observational and transmission model studies. These estimates

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will feed into grEPI as a resource to support measles epidemic preparedness and response activities globally [16].

Methods

This SR was conducted in accordance with established methodological standards and adhered to the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines (Supplementary 1) [17, 18]. The protocol for this SR was registered in PROSPERO (CRD42025648371) and developed *a priori*. It was built on the framework developed by the Pathogen Epidemiology Review Group for their recent infectious disease evidence syntheses [19–21], informed by consultations with the WHO Epidemiological Parameter Community, and adjustments were made to meet the needs for pandemic preparedness by the Public Health Agency of Canada. Full details of the methods and any deviations are documented in the protocol and Supplementary 2. The full dataset of transmission and severity measles parameters is available in the Open Science Framework https://doi.org/10.17605/OSF.IO/7K4GU, and a less detailed dataset can be found on grEPI until it is fully deployed [22].

Research question

The initial SR was designed to identify key epidemiological parameter estimates of the measles virus in humans to feed into the grEPI database. Given the substantial volume of available literature, the research question was split into two separate SRs prior to analysis to improve the clarity and the interpretation of the findings. This SR was designed to answer the question 'What are the transmission-related epidemiological parameters of measles virus in humans?' while the synthesis of severity-related parameters is reported in a separate companion SR [23].

Eligibility criteria

Studies were included if they met the following criteria: original peer-reviewed research published in English or French, studies involving human populations, and those reporting transmission-related epidemiological parameters of measles. These include reproductive number (R_0), effective reproductive number (R_e), doubling time, growth rate, halving time, attack rate (AR), secondary attack rate (SAR), overdispersion, incubation period, infectious period, latent period, generation time, serial interval, case identification delay, and human delays (Supplementary 2). Theoretical modelling studies and experimental interventions not generalizable to broader populations were excluded (e.g., clinical trials). Case reports and case series with fewer than ten observations were also excluded from this SR; however, parameters represented by fewer than ten observations were retained if the study included more than ten observations. Evidence syntheses that included transmission parameters can be found in the full dataset and were used in search verification but were excluded from the analyses in this SR to prevent double counting of data.

Search strategy

A comprehensive search strategy was developed and tested through an iterative process by an experienced research librarian in collaboration with the review team. The search was conducted in MEDLINE, Scopus, and Global Health, from the date of database inception to 14 May 2024 (see protocol for the full search strategy). Reference lists of 26 relevant reviews were hand-searched to capture studies not identified by the electronic database search. Search results were imported into EndNote 20 (Clarivate, Philadelphia, PA) for de-duplication. Unique references were imported into DistillerSR [24] for SR management.

Study selection and data extraction

All screening and data extraction forms were developed *a priori*, piloted by all reviewers, and refined until questions were interpreted consistently across all reviewers (Kappa ≥ 0.8). Relevance screening of the first 3 948 titles and abstracts, and all full texts were completed by two independent reviewers and disagreements were resolved by consensus. DistillerSR's Artificial Intelligence SYstem (DAISY) was used to assist as a second reviewer during title and abstract screening for 8 777 citations [25, 26]. Discrepancies between DAISY and human reviewers were resolved by a third reviewer.

Briefly, study characteristics and parameter information (e.g., value, context, affected population) were extracted. A quality of reporting (QR) tool was developed by the review team, which included a minimal set of quality indicators to flag concerns with the study from which the parameters were extracted: (i) well-reported studies with reproducible parameters (no concerns), (ii) studies with some reporting concerns around study conduct and/or unclear reporting (some concerns), and (iii) poorly reported studies with insufficient information to understand how the study was conducted (major concerns). Data extraction and QR were performed by one reviewer and verified by a senior reviewer. Disagreements were resolved through consensus or adjudication by a third reviewer when necessary.

Data analysis

Random-effects meta-analyses of transmission-related parameters with >2 eligible estimates (i.e., estimates from observational studies with a sample size along with a central estimate and paired variability) were conducted using the meta R package (version 4.4.2), following similar methods as previously published reviews [19–21, 27]. A list of parameters eligible for meta-analysis and additional data analysis details are provided in Supplementary 2. All parameter estimates reported as means with standard errors, or as medians with ranges or interquartile ranges, were converted to means and standard deviations (SDs) using the method of Cai et al. [28].

Subgroup analyses were performed to identify trends and explore heterogeneity by WHO region, population, decade, outbreak timing, and QR. Populations identified through contact tracing from an outbreak investigation were grouped as persons/children under investigation. Estimates derived from transmission models were excluded from the meta-analysis but were compared narratively with meta-analysis results from the observational studies.

Continuous transmission-related parameters (e.g., incubation period and infectious period), were synthesized using the *metamean* function from the meta R package. Between-study variance was estimated using the restricted maximum likelihood method (REML) to estimate weights for individual studies when pooling the means [29]. Results from meta-analyses with substantial heterogeneity (i.e., $I^2 > 75\%$) should be interpreted with caution, as the findings may not apply to specific scenarios (e.g., regions, population groups, sex or gender, ethnicity) [30]. A synthesis for the effective reproduction number was not conducted as the parameter estimates are highly dependent on the context and scenarios; however, they are provided in the full dataset of this SR (Supplementary 3).

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Proportion estimates for AR and SAR were synthesized using the *metaprop* function from the meta R package. A REML method was used to estimate the between-study variance, estimates were transformed using the logit transformation, and pooled using a random-effects model [18].

Descriptive plots were generated to visualize the range of the estimates for parameters that were not eligible for meta-analysis and described narratively (Supplementary 2). Within the plots, different types of central estimates (e.g., mean, median, or unspecified) are distinguished by distinct symbols and colours to differentiate subgroups. All estimates, regardless of QR rating, were included in the descriptive plots. Subgroup plots were generated for parameters with a sufficient number of estimates. Parameters with insufficient estimates to descriptively plot are reported in tables and described narratively.

Results

Results of the search and study selection

The database search identified 15 667 citations and an additional 82 citations were identified from the verification process (Figure 1). A total of 4 095 citations were screened at full-text, of which 612 citations were included in this SR. A list of included and excluded studies with reasons for exclusion is available in Supplementary 3 and 4, Page 2, respectively.

Characteristics of included studies

There were 1 208 parameter estimates identified across 612 studies published between 1910 and 2024, of which 32 parameters were only reported in figures and excluded from the analysis, resulting in 1 176 parameters across 605 studies (Supplementary 5, Table 1). The most frequently reported parameters were SAR (17%; 201/1 176) and R_e (16%; 187/1 176) (Figure 2). Among 524 observational studies and 83 transmission models, 968 and 207 parameters were extracted, respectively. One experiment, a generalizable human challenge trial, reported incubation period in children [31]. Most parameter estimates were identified from studies conducted in Europe (29%; 177/605) and the Americas (24%; 142/605) (Figure 2a). Apart from the basic reproduction number, AR and SAR, most parameter estimates are from studies conducted from 2000 onward (Figure 2b).

Reproduction number

R_0 was reported in 68 studies between 1837 and 2021 and included 115 analyzable estimates, which ranged from 0 to 57 with a median

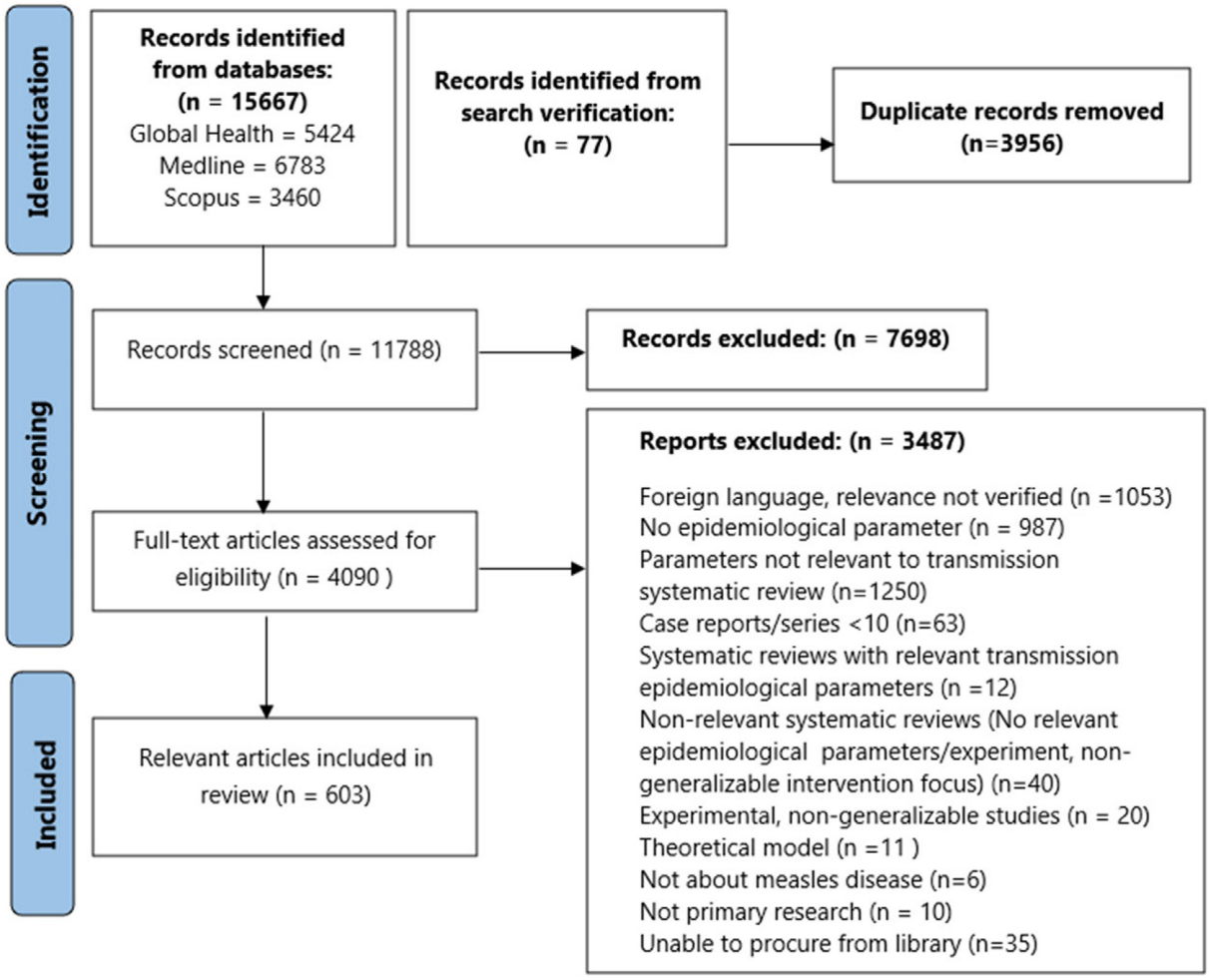


Figure 1. PRISMA flow diagram.

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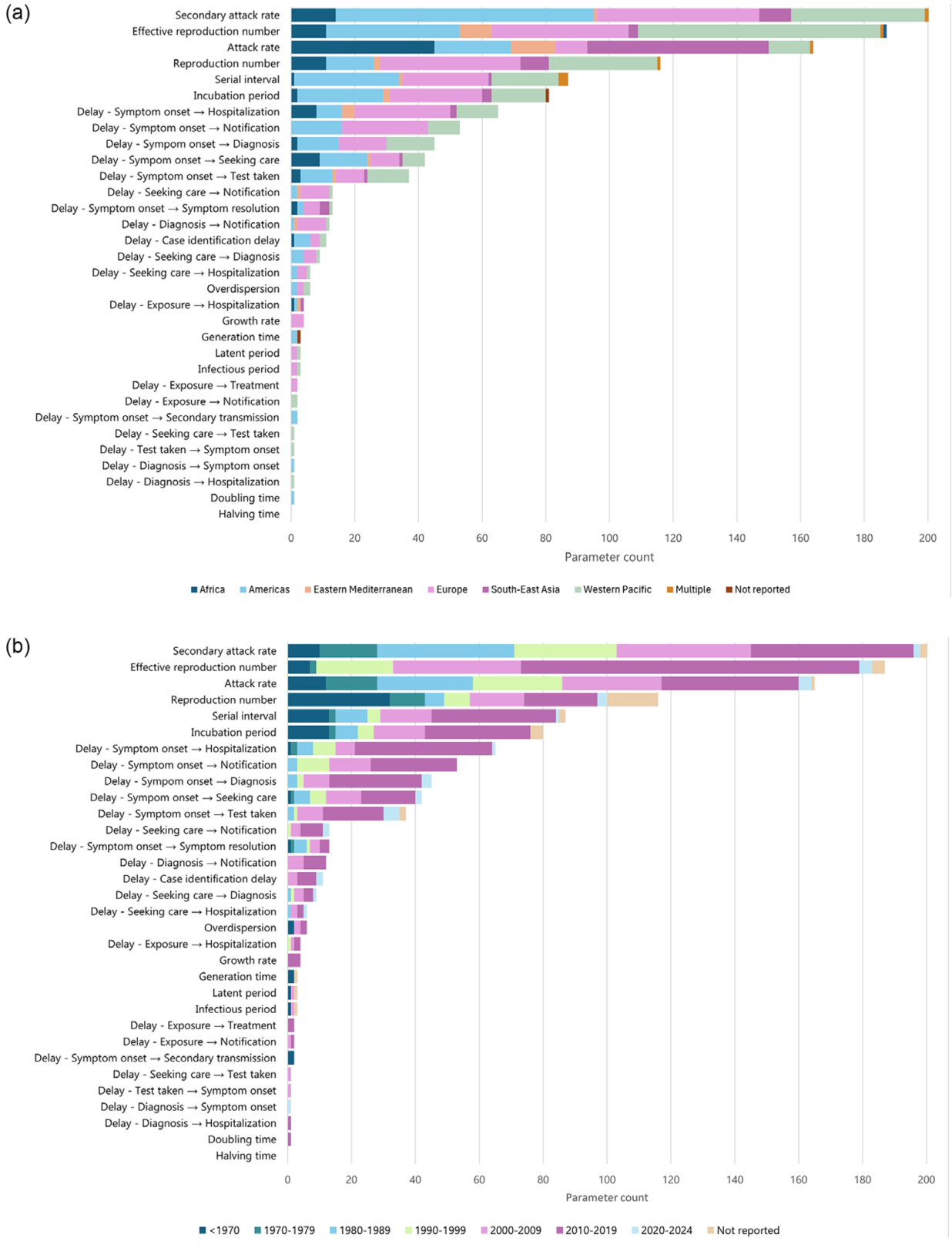


Figure 2. Number of parameter estimates across 32 different transmission parameters by (a) WHO region (b) Time of outbreak.

value of 11.5 (Supplementary 6). The high outliers were reanalyses of older outbreaks; one was a transmission model of a 1904 school outbreak that reported R_0 40 (8–93) [32]. A second model used data from 20 United Kingdom (UK) communities in 1950 reporting unspecified central estimates of R_0 between 21 and 57 across communities [33]. Subgroup analyses did not identify study-level

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variables (populations, WHO regions, or QR) that explained significant portions of the between-study variability.

Doubling time and growth rate

Doubling time was reported in one transmission model from the United States (US) in 2014 as an unspecified central estimate of 5.2 days [34] (Supplementary 5, Table 2). Five growth rate parameter estimates were reported in two transmission models in Italy between 2010 and 2017 and ranged from 0.25 to 1.22 [35, 36] (Supplementary 5, Table 2).

Overdispersion

Six estimates were reported for the overdispersion parameter transmission (k), from transmission models (n = 5) and an observational study. The parameter k quantifies heterogeneity in transmission by measuring how variable the number of secondary cases is across infected individuals. Lower k values indicate greater variability, meaning that a small proportion of cases account for a large share of transmission, whereas higher k values indicate more homogeneous transmission (Supplementary 5, Table 2). In the general population, between 2000 and 2018 the central estimate of overdispersion ranged from 0.15 to 0.4. Two transmission models from the pre-vaccine era reported a wider range of estimates ranging from 0.12 to 2.87 using data from 1950 [33] and 1.3 in children from a 1904 school outbreak of measles [32].

Attack rate parameters

Attack rates were highly variable (0%–99%) across the 165 estimates extracted from 138 studies between 1861 and 2023, and the study-level variables did not significantly explain the heterogeneity (Supplementary 7). Examination of the 155 estimates (119 218 070 observations) in 133 studies included in the meta-analysis shows an overall trend of decreasing AR over time, with rates prior to 1970 (pre-vaccination era) reporting the highest ARs and 2020 onwards reporting the lowest ARs (Figure 3). To help the reader understand the context behind the estimates, a description of the population, country, region, and year is reported in Supplementary 7. Significant differences were observed across population subgroups; outbreak investigations of children had the highest ARs, and when the sample represented all age groups combined, the ARs were lower, suggesting susceptible children account for a significant proportion of onward transmission of measles (Supplementary 8, Figure 1). This trend was retained when evaluating estimates that were only reported in the post-vaccine era. Across WHO regions, Europe had the highest AR while Eastern Mediterranean had the lowest. When evaluating

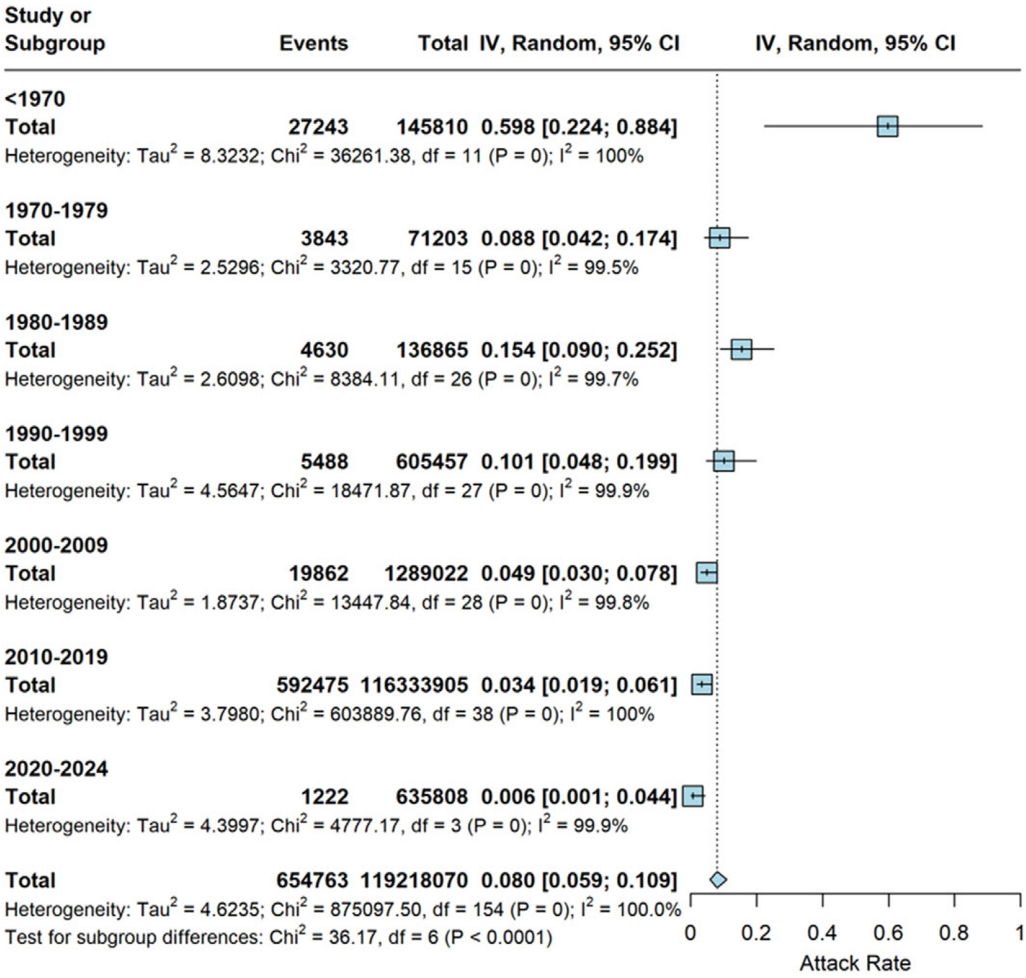


Figure 3. A random-effects meta-analysis (REML) of pooled attack rates by decade for 155 parameter estimates across 133 studies.

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parameters reported only in the post-vaccine era, South-East Asia had the highest AR and the Americas had the lowest. AR for estimates of no QR concerns were lower than those rated as some or major QR concerns; however, there was no significant difference by QR rating across estimates reported in the post-vaccine era.

Similarly, SAR was highly variable (0%–100%) across the 201 estimates that were extracted from 167 studies between 1884 and 2025 and the study-level variables did not significantly explain the heterogeneity (Supplementary 9). Meta-analysis was conducted on 191 estimates (267 493 observations) from 160 studies and shows a decreasing trend in SAR over time (Figure 4). The substantial heterogeneity is likely due to the highly contextual nature of the parameter; specific estimates can be found in Supplementary 9. One estimate derived from a transmission model suggested the SAR among susceptible exposed individuals was 88.2% [37]. Across populations, SAR was lower for outbreak investigations of all age groups combined compared to all the other populations, and across WHO regions the South-East Asia SAR were higher than other regions (Supplementary 8, Figure 2). Estimates with major QR concerns were similar to estimates with no and some concern. These trends were retained when evaluating estimates reported only in the post-vaccine era.

Incubation period

Eighty estimates across 74 studies between 1887 and 2019 reported incubation period, of which 73 estimates from 70 studies were descriptively plotted, showing the range of central estimates was 9 to 21 days and the range of observations was 2 to 25 days (Supplementary 8, Figure 3). One outlier estimate from the UK (1974–1984) that had major QR concerns reported a range of 3 to 61 days among children in remission from leukaemia; the upper estimate was reported by the authors as 'possibly two months' [38].

Ten estimates were eligible for meta-analysis, of which seven had no concerns with QR, one had some concerns, and two had major concerns. Among estimates with no concerns, the pooled mean incubation period was 14.0 days (95%CI 13.3–14.8, sample size = 169) with moderate heterogeneity (I^2 = 67.5%) (Figure 5). The mean incubation period was significantly shorter for the estimates with major concerns compared to estimates with no concerns and some

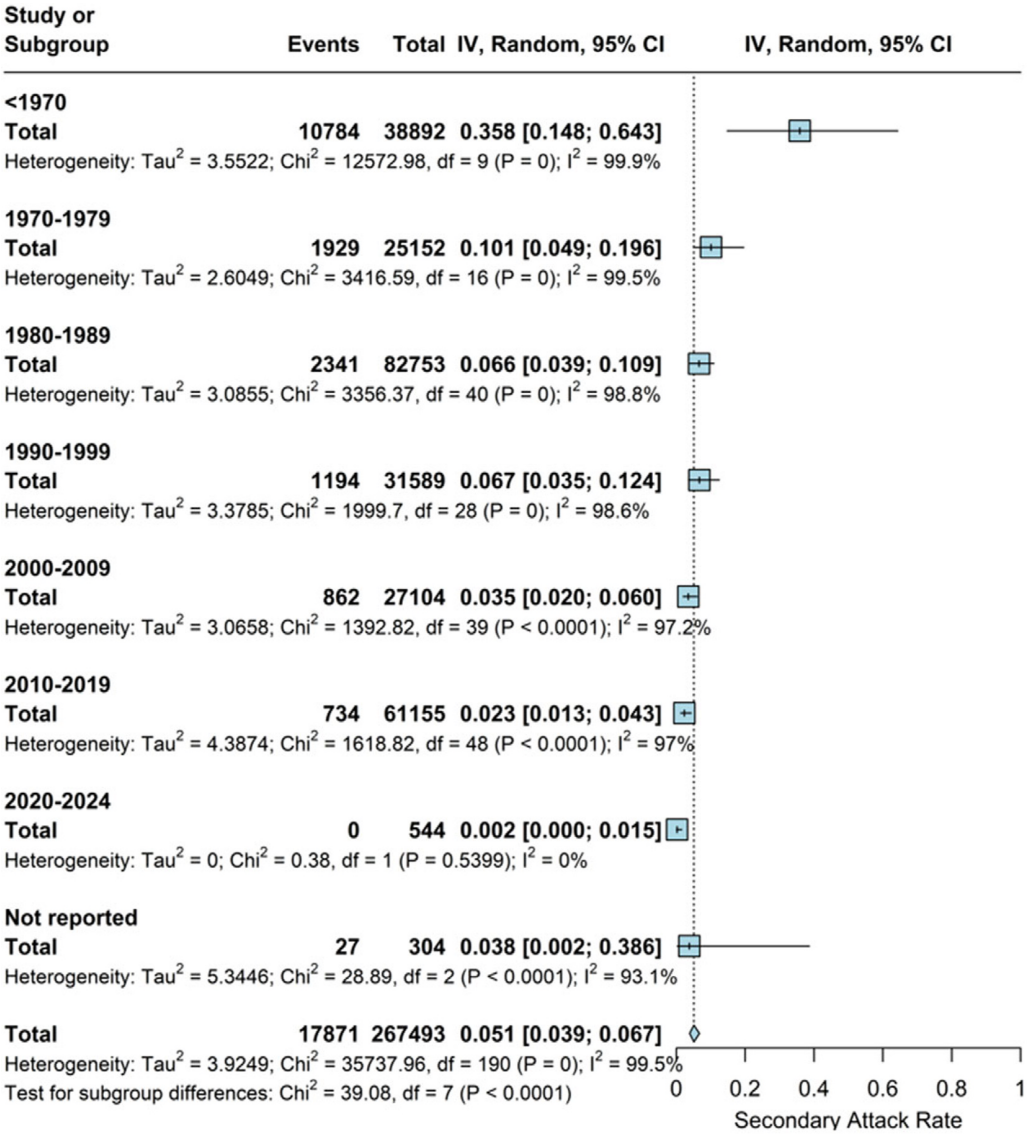


Figure 4. A random-effects meta-analysis (REML) of pooled secondary attack rates by decade for 191 parameter estimates across 160 studies.

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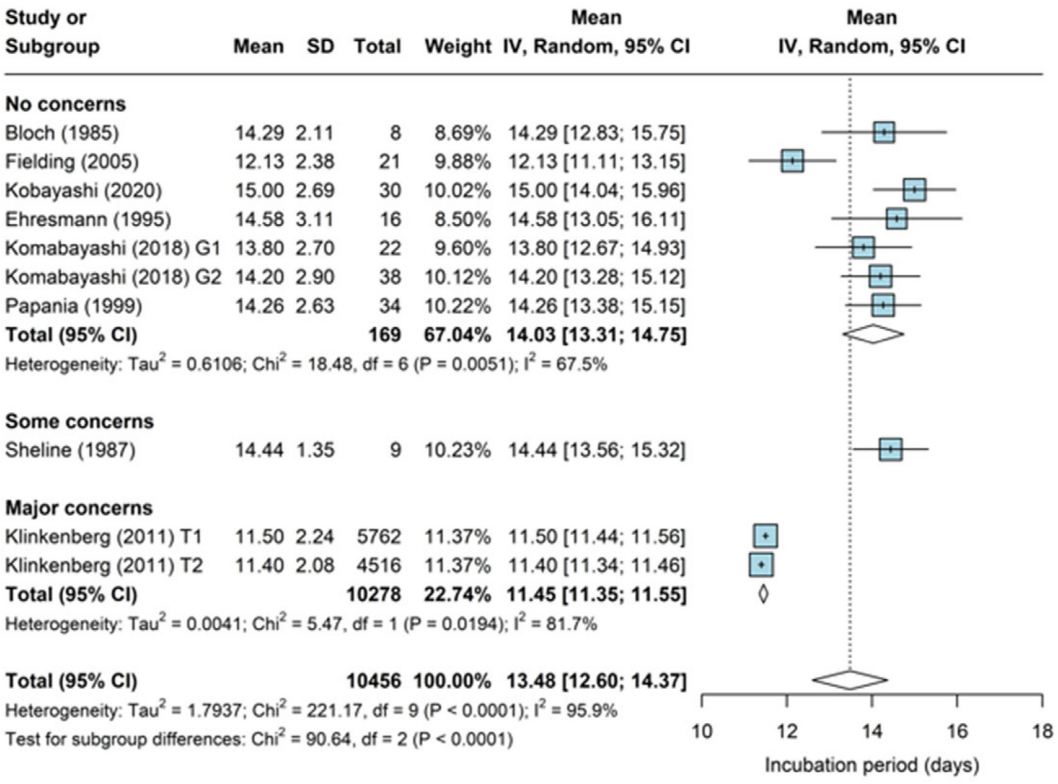


Figure 5. Random-effects meta-analysis (REML) of ten incubation periods across eight studies subgrouped by QR. Only disaggregated data available for Komabayashi et al. [42] and Klinkenberg and Nishiura [40].

concerns (11.5 versus 14.0 versus 14.4 days, $p < 0.0001$). Compared to the other estimates with no concerns from Japan and the US, one outlier estimate with no concerns from Australia in 2003 showed a shorter mean incubation period of 12.1 days in a relatively young, moderately unvaccinated sample (median age 23; 60% unvaccinated) [39]. Subgroup analyses by WHO region and population did not show any trends or provide an explanation for the heterogeneity observed (Supplementary 8, Figure 4). However, the study with major concerns was the only large general population study, and the incubation period was significantly shorter than in the smaller studies in other populations [40]. One study that did not report sample size and could not be included in the meta-analysis reported a mean incubation period of 13.4 days (SD 1.3) [41], which aligned with the meta-analysis [42].

Latent period

Three estimates across three studies reported latent period in the general population (Supplementary 5, Table 2). One model used data from 1950 across several countries in Europe to estimate a range of 5.5 to 13 days [33]; the other model from China in 2005 reported an unspecified central estimate of 8.1 days (95%CrI 7.3–9.0) [43], and an observational study in the UK published in 1954 reported a mean of 9.5 (SD 1.32) [41].

Infectious period

The same three studies that reported latent period also estimated infectious period (Supplementary 5, Table 2). The models provided a range of 1.8 to 12.5 days in the UK using data from 1950 [33], an unspecified central estimate that fell within this range (5 days, 95%CrI 4.2–5.8) in China using data from 2005 [43], and an observational study in the UK published in 1954 with major QR concerns reported a mean 3.84 days, SD 0.43 [41].

Generation time

Generation time central estimates ranged from 10.5 to 11.9 days in two studies. One estimate was from a transmission model published in the UK at an unknown time period [44] and two estimates were from an observational study in the US between 1917 and 1929 with major QR concerns [40] (Supplementary 5, Table 2).

Serial interval

There were 87 estimates across 79 studies between 1837 and 2021 that reported a serial interval central estimate range of 5 to 18 days and an unspecified range of 6 to 29 days (Supplementary 8, Figure 5). Twelve estimates across eight studies were eligible for meta-analysis and yielded a pooled mean serial interval of 12.4 days (95%CI 11.5–13.4; I^2 = 97.6%, sample size = 13 312) (Figure 6). An estimate reported from a study with major QR concerns in the US with data from 1917 to 1934 was not significantly different than the estimates with no and some concerns [40] (Supplementary 8, Figure 6). Across WHO regions, Europe was observed to have shorter serial intervals compared to other regions (Figure 6). Other subgroup analyses did not explain the substantial amount of heterogeneity observed across groups.

Case identification delay

Across 11 unspecified estimates from ten studies between 2003 and 2023, case identification delay (i.e., the time between soliciting a test

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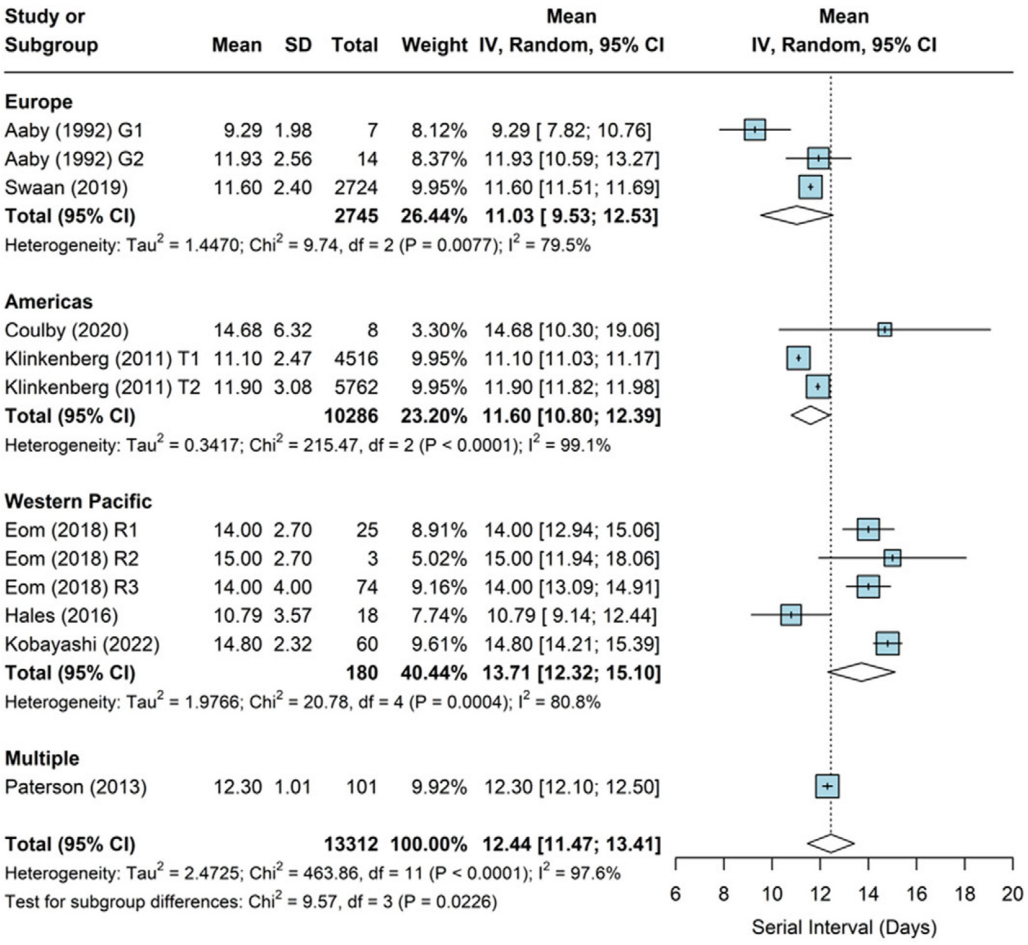


Figure 6. Random-effects meta-analysis (REML) of serial interval by WHO region for 12 parameter estimates across eight studies. Multiple = Multiple WHO Regions. Only disaggregated data is available for Aaby [45], Eom [46], and Klinkenberg and Nishiura [40].

or getting tested and the results being returned) ranged from 1 to 25 days (Supplementary 8, Figure 7).

Symptom onset to outcome delays

Forty-one studies reported 42 estimates between 1951 and 2023 for the delay from symptom onset to seeking care. Five studies reported central estimates that ranged from 1 to 7 days and variability from 0 to 51 days (Supplementary 8, Figure 8). Eight estimates were eligible for meta-analysis, which identified a pooled estimate of 4.4 days (95% CI 3.1–5.8, I^2 = 98.9%, sample size = 2 485) (Supplementary 8, Figure 9). The majority of estimates were reported in the general population and from Africa and Western Pacific, with the Western Pacific region reporting the shortest interval (Supplementary 8, Figure 9). Limited studies across remaining subgroups did not allow for trends to be identified.

Thirty-four studies reported 37 estimates between 1987 and 2023 of the interval between symptom onset and test taken. The range of central estimates was 1 to 36 days, with the range of observations from 0 to 57 days (Supplementary 8, Figure 10).

Thirty-nine studies reported 45 estimates between 1994 and 2023 of the interval between symptom onset and diagnosis. Central estimates ranged from 2 to 45 days, and variability ranged from 0 to 28 days (Supplementary 8, Figure 11). Ten estimates eligible for inclusion in the meta-analysis had a pooled estimate of 6.6 days (95%CI 3.9–9.2, I^2 = 97.7%, sample size = 10) (Supplementary 8, Figure 12). One transmission model estimating the delay from symptom onset to diagnosis reported a maximum likelihood delay of 4.5 days (95%CI 4.0–5.0), which is consistent with ranges reported in observational studies [47] (Supplementary 8, Figures 11–12). One outlier had a mean symptom onset to diagnosis of 19.2 days (95%CI 15.1–23.3) among six pregnant women [48].

Fifty-three estimates across 46 studies between 1983 and 2019 reported the time between symptom onset and notification to public health, with central estimates ranging from 1 to 43 days and variability ranging from 0 to 213 days (Supplementary 8, Figure 13). Eleven estimates across 11 studies eligible for inclusion in the meta-analysis reported an overall estimate of 6.7 days (95%CI 3.5–10.0, I^2 = 98.4%, sample size = 8 514) (Supplementary 8, Figure 14). Subgroup analyses by WHO region indicated the Western Pacific region had the longest delay compared to other regions. Other subgroup analyses did not explain the variability.

Sixty-two studies reported 65 estimates between 1930 and 2023 for time from symptom onset to hospitalization. The range of central estimates was 1 to 14 days, with the range of observations of 0 to 147 days (Supplementary 8, Figure 15). One outlier was a case-control study conducted in Romania from 2016 to 2017 in hospitalized children that reported a mean of 2 days (range 0–147) [49]. Twenty-two estimates included in the meta-analysis reported an overall pooled estimate of 4.8 days (95%CI 3.7–5.8, I^2 = 99.7%,

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sample size = 4 201) (Supplementary 8, Figure 16). One outlier study showed a mean delay of 14 days (95%CI 13.8–14.2) among 368 hospitalized infants (fatal and non-fatal cases) during an outbreak in Mongolia from 2015 to 2016, likely indicative of barriers to timely healthcare access [50]. Substantial heterogeneity was observed across all subgroups; only pooled estimates by WHO region suggested Europe had a shorter delay compared to Africa, South-East Asia and the Western Pacific (Supplementary 8, Figure 16). Across overall outbreak phases (including endemic, mid-outbreak, and post-outbreak periods), the delay from symptom onset to hospitalization was generally similar; however, a slightly longer delay was observed during mid-outbreak situations (mean 6.83 days, 95%CI 3.89–9.76; I^2 = 99.9%, sample size = 830) (Supplementary 8, Figure 16).

Eleven studies reported 13 estimates between 1966 and 2017 for time from symptom onset to resolution, with central estimates ranging from 3 to 16 days and variability ranging from 1 to 37 days (Supplementary 8, Figure 17). Six estimates were eligible for a meta-analysis and had a pooled estimate of 7.9 days (95%CI 4.7–11.3, I^2 = 99.2%, sample size = 376) (Supplementary 8, Figure 18). Subgroup analyses by WHO region and population did not explain the variability (Supplementary 8, Figure 18).

Diagnosis to outcome delays

Twelve estimates reported time from diagnosis to notification of measles to a health authority across 10 studies between 2003 and 2018. Most estimates were between 0 and 11 days, and nine estimates were from Europe, one from the Western Pacific and one from the Americas (Supplementary 8, Figure 19). One outlier from Qatar in 2008 reported a median notification delay of 4 days (range 1–67) [51]. One study identified time from diagnosis to hospitalization (Western Pacific countries 2018; 1 day) [52], diagnosis to symptom onset (US 2023; 7 days) [53], and test taken to symptom onset (China 2007; mean 6.2 days) [54] by testing epidemiologically linked cases during outbreak investigations.

Exposure to outcome delays

Four estimates across four studies between 1999 and 2019 reported time from exposure to hospital admission with an unspecified range of 6 to 26 days (Supplementary 8, Figure 20). Time from exposure to notification was reported by one study as a mean of 6.5 days in airplane passengers from Australia in 2007 [55], while another study noted 10 days in a child from New Zealand in 2011 [56]. Two estimates in one study from Israel in 2018 reported a median range of 3 to 4 days (range: 1–6 days) from time of exposure to treatment.

Seeking care to outcome delays

Twenty-five studies reported 29 estimates between 1985 and 2023 for the delay from seeking care to outcome: notification (n = 1 study, median range: 1–6 days, unspecified range: 1–20 days), diagnosis/test result (n = 9, range: 0–27 days), hospital admission (n = 6, range: 1–8 days), and test taken (n = 1, 13 days) (Supplementary 8, Figure 21).

Discussion

This SR provides a comprehensive synthesis of the epidemiological parameters that characterize measles transmission. The epidemiological parameter dataset was incorporated into grEPI and serves as an accessible and collaborative centralized resource for modellers, epidemiologists, and decision makers [11]. Within this review, we examine the characteristics of each epidemiological parameter to strengthen our understanding, explore the challenges with synthesizing these parameters, and describe how the data can be used to support evidence-based decision-making for public health response and epidemic preparedness, thereby reducing research waste [16, 57].

Five previous evidence syntheses summarized incubation period, serial interval, and reproduction number and are in alignment with the findings of this SR [12, 58–61]. Seven evidence syntheses reporting ARs were also in line with our findings [62–68], however, our SR was the only one that looked at trends over time and noted a distinct decrease in the ARs over time. Despite literature on measles being reported since the 1900s, certain transmission parameters were poorly characterized. These include AR, basic reproduction number, and serial interval parameters, which have been captured by outbreak investigations for over 100 years. Some parameters have become regularly reported in recent literature (e.g., the many different types of delays) but not previously synthesized, while others were either not identified in the literature (i.e., halving time and asymptomatic transmission) or underpinned by less than five estimates, including infectious period, latent period, generation time, doubling time, growth rate, and overdispersion. Infectious period, for example, was only estimated in three transmission models, which suggested the range may be as wide as 2 to 12.5 days [33, 41, 43]. These did not speak to the pre-symptomatic infectious period, which could be 6 to 7 days based on two delays from diagnosis or test taken to symptom onset [53, 54]. Furthermore, modelled estimates can be statistical artefacts from oversimplified transmission models in large populations, which can occur when several small outbreaks are combined. The resulting overall epidemic appears slower and more continuous, leading to longer estimates for infectious periods instead of recognizing the variable spread across communities [33]. Additional research to establish better estimates of the infectious period before and after symptom onset is warranted to validate whether the commonly used estimate of 4 days prior to 4 days after symptom onset is robust [1]. Estimates underpinned by few observations (e.g., infectious period and latent period) should be prioritized as they are essential parameters needed to improve the knowledge base to inform infectious disease models and outbreak management.

The majority of the parameters in this SR are crude estimates that are highly sensitive to the context in which they are measured; thus, we reported significant heterogeneity that was not explained by the study-level variables: decade, population, WHO region, outbreak timing, or QR. Differences in timing of outcome measurements, populations, population immunity, geography, settings, and the public health system/infrastructure, outbreak and/or disease management protocols will all contribute to the variability [69]. Bias inherent to different types of observational studies (87%) and the transmission models (13%) will also contribute to the heterogeneity within parameter estimates [70]. End users of the grEPI database will need to keep the specific context (e.g., regions and socioeconomic status) in mind when selecting the best parameter estimates for their context, as there is likely no single best estimate. This SR prioritized showing the parameter estimates in forest plots and describing overall trends and ranges for each parameter. These estimates and ranges should be interpreted with caution, as the study type, specific context each estimate was derived from, and QR indicators should be considered in further

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syntheses to inform sensitivity analyses and context-specific policy-relevant metrics.

Many different delay parameters were identified in this SR, some with limited observations. The methods for collecting delay data can impact different biases that can skew the parameter estimate, leading to an underestimation or overestimation, which notably was rarely adjusted for by studies [26]. For example, outbreak investigations are often better at identifying shorter delays (e.g., incubation period) more easily with better recall of exposure and symptoms and may not necessarily identify individuals with longer delays resulting in fewer data points for longer delays. A broad range of different delay types were reported in the literature (e.g., serial interval, symptom onset to hospitalization, diagnosis, and public health notification), and it is unclear whether the delays that were most frequently reported are also the most useful inputs for infectious disease models or for understanding measles disease management. Efforts by modellers or other users to define a set of critical delays that should be prioritized for future research and outbreak reports would lead to better collection and reporting, improved confidence in the estimates derived from these delays, and an improved knowledge base on the most critical delays.

Many estimates could not be used in the meta-analyses because they were poorly reported. In most cases, there were critical details missing, such as sample size, an appropriately defined central tendency or a measure of variability. As an example, approximately 40% of estimates from continuous parameters (e.g., incubation period and serial interval) were reported as a range or a single estimate without a measure of variability, and over 80% of estimates were not usable in a meta-analysis because they were missing one or more of these critical details. Across all extracted parameters, 8% and 39% of parameters had major and some QR concerns, respectively, and QR was identified as a source of heterogeneity for some parameters (e.g., incubation period). Clearly reported parameter estimates that include measures of variability with central tendency, sample size and the use of validated methods for confirming cases to avoid misclassification are essential for robust parameter estimates that can then be used to parameterize infectious disease models and guide response activities [59, 71]. Future research should focus on clear reporting of parameters to facilitate research use and identification, and accurate extraction of parameters by AI-assisted tools designed to maintain living SRs such as grEPI [72].

In this SR, we recorded where studies had results disaggregated by potential sex and gender-based risk factors and population immunity so readers could easily identify studies with disaggregated parameters of interest [73]. Differences in measles incidence and severity have been observed by age, gender, socioeconomic status, and vaccine status [73–75]. However, we found that only 35% of studies reported epidemiological parameters disaggregated by any of these important factors that influence measles transmission dynamics, and disaggregation by gender, ethnicity, and sexual orientation (3%, 1.5%, and 0% of studies, respectively) was rarely reported. This highlights knowledge gaps of the impact of sex and gender-based factors on measles epidemiological parameter estimates, which could be important for implementing equitable public health response strategies [76].

There were some limitations in this SR. For feasibility, a grey literature search was not conducted, and only English and French studies were assessed for relevance. We anticipate that more than 60% of foreign language articles would not contain any relevant transmission-related epidemiological parameters based on the observations from English and French language studies. Future research is recommended to explore estimates reported in additional languages. We also utilized an AI tool to assist as a second reviewer with title and abstract screening for a subset of studies once the classifiers were trained and validated to an acceptable threshold. To mitigate the risk of excluding potentially relevant studies, a human reviewer independently assessed all AI-reviewed citations and conflicts were resolved by a second human reviewer. Data were extracted by one reviewer and verified by another, which may increase the risk of dataset errors when using this shortcut compared to duplicate independent review. Some observations were omitted from analyses because numerical estimates were not extracted from figures, which was 3% of the total parameters; however, the characteristics for these parameters were included in the complete dataset. We developed QR questions to flag concerns of parameter estimates across all study types in a standardized and uniform manner for grEPI. This tool requires further validation, and end-users are cautioned that the overall QR scores should not be interpreted as risk of bias assessments. Finally, updated searches to continuously capture emerging evidence on measles will be conducted through grEPI using an AI-assisted pipeline, an essential component in maintaining the results of this SR [11, 72].

Conclusion

This SR provides a comprehensive synthesis of key measles transmission parameters from literature since the early 1900s and broadens our understanding of how measles transmission dynamics have changed over time (e.g., in the post-vaccine era). There was unexpectedly sparse data for some transmission parameters, which are highly sought after by infectious disease modellers, including latent period, infectious period, and some human delays. This underscores the need for further investigations into measles outbreaks to identify and clearly report the epidemiological parameters that address the knowledge gaps identified in this SR. Future research will focus on using grEPI to continuously collate infectious disease epidemiological parameters using a living systematic review process. GrEPI will provide a collaborative space for accessing the most up-to-date epidemiological parameter data, reducing duplicative efforts by researchers, and supporting timely evidence-based public health response activities during the ongoing global measles epidemics.

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Data availability statement. All relevant data are included in this manuscript or supplementary materials: https://doi.org/10.17605/OSF.IO/7K4GU.

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Validation: K.P., M.S., A.B., T.C.; Visualization: K.P., M.Q., M.S., A.B.; Writing - original draft: K.P., M.Q., M.S., A.B.; Writing - review & editing: K.P., M.Q., M.S., A.B., T.C., A.T., L.A.W.

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