Impact of public health responses during a measles outbreak in an Amish community in Ohio: modelling the dynamics of transmission

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Running head: Impact of control measures during a measles outbreak.

Abbreviations: R, effective reproduction number; MMR, measles-mumps-rubella; R_t, instantaneous reproduction number; R_c, case reproduction number; R_0, basic reproduction number; VC, vaccine coverage; VE, vaccine effectiveness; sU, proportion of unvaccinated individuals that are susceptible.

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ABSTRACT

We quantified measles transmissibility during a measles outbreak in Ohio in 2014 to evaluate the impact of public health responses. Case incidence and the serial interval (time between symptom onset in primary and secondary cases) were used to assess trends in the effective reproduction number *R* (average number of secondary cases generated per case). A mathematical model was parameterized by early *R* values to determine outbreak size and duration if containment measures had not been initiated, and the impact of vaccination. As containment started, we found a fourfold decline in *R* (~4 to 1) over 2 weeks, and maintenance of $R<1$ as control measures continued. Under a conservative scenario, the model estimated 8,472 cases (90% confidence interval [CI]: 8,447, 8,489) over 195 days (90% CI: 179, 223) without control efforts, and 715 cases (90% CI: 103, 1,338) over 128 days (90% CI: 117, 139) when including vaccination; 7,757 fewer cases (90% CI: 7,130, 8,365) and 67 fewer outbreak days (90% CI: 48, 98) were attributed to vaccination. Vaccination may not account entirely for transmission reductions, suggesting changes in community behavior (social distancing) and other control efforts (isolation, quarantining) are important. Our findings highlight the benefits of measles outbreak response and of understanding behavior change dynamics.

Keywords: Measles; outbreak response; transmissibility; reproduction number; United States

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Measles is a highly contagious viral disease that can lead to serious complications and death. Even with repeated importations of measles into the United States, most introductions do not result in additional transmission, outbreaks are generally small (1), and endemic measles transmission has been declared eliminated since 2000 (2). The success of the U.S. measles elimination program is credited to high measles-mumps-rubella (MMR) vaccine coverage, as well as the rapid implementation of control measures once cases are reported (2). Yet, the relative contributions of baseline coverage and of various simultaneous control measures (vaccination, isolation, quarantine) in preventing large outbreaks is not fully understood (3). Because, outbreak responses by health agencies are labor intensive and costly (4), efforts to measure the effectiveness of these interventions are important.

On March 2014, the return of two unvaccinated Amish men to Ohio from the Philippines, where they were unknowingly infected with measles, led to the largest outbreak of measles in the US in over two decades (5, 6). The outbreak provided an opportunity to measure the impact of public health responses in mitigating measles transmission in an under-immunized community. We aimed to quantify measles transmissibility during the outbreak, and to evaluate the effect of public health responses in limiting the size and duration of the outbreak.

METHODS

Transmissibility was measured by estimating the effective reproduction number, *R*, the average number of cases generated by a single infectious individual (7). The goal of outbreak response is to reduce *R* below the threshold value of 1; transmission wanes when *R* is maintained at <1, bringing an outbreak under control. Using a ready-to-use tool (8), *R* was estimated from case incidence time series data and the distribution of the serial interval (the time between the onset of symptoms in primary and secondary cases) (9). We tracked *R* over time during the outbreak and correlated changes in transmissibility to control efforts. Two distinct time-varying estimates of *R* were measured: the instantaneous reproduction number (R_t), and the case reproduction number (R_c) (8). R_t measures the expected transmissibility at

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calendar time, t, based on the ratio of the number of new infections in that time step, to the total infectiousness of previous cases. Thus, R_t can be estimated in real-time, as new cases are identified.(8) R_c measures the actual transmissibility of cases with symptom onset at calendar time, t, and is calculated once all secondary cases are detected and thus it is retrospective (8, 10). To maintain precision, R_t and R_c were calculated for each day of the outbreak over a 14-day time window ending on that day.(8) Details of these methods are available elsewhere (8, 10). The estimation procedures were applied to outbreak notification data (incidence by the date of rash onset) using a serial interval for measles derived from household studies (gamma distribution with mean of 11.1 days and a standard deviation of 2.47 days) (9).

To evaluate the probable size and duration of the outbreak if control measures had not been introduced, we simulated potential outbreak trajectories using a continuous time stochastic susceptible-exposed-infectious-recovered compartmental model; stochastic variability was incorporated using the adaptive tau-leaping algorithm (11). The model tracks 4 classes of persons: 1) susceptible to infection and disease (S), 2) exposed but not yet infectious and asymptomatic (E), 3) infectious with symptoms (I), and 4) recovered and immune (R) (Figure 1). All persons in the S class can be infected at a rate $\lambda(t)$, the force of infection, and move into the E class. Exposed individuals then become infectious, and progress from the E class into the I class at a rate σ. Finally, persons recover (i.e., become immune) and move from the I class into the R class at a rate γ.

Static model inputs are detailed in Table 1. $\lambda(t)$ is proportional to β, the per capita rate at which two individuals come into sufficient contact to lead to infection per unit time, and to the number of infectious individuals at time t (I_t). The rate β itself can be written as a combination of three parameters: the basic reproduction number R_0 (the average number of cases generated by a single infectious individual if the entire population is susceptible), the duration of infectiousness, and the population size. R_0 may vary considerably for the same disease in different populations (7). However, R_0 in a particular population can

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be estimated from R and the ≥1-dose MMR vaccine coverage (V_C), as follows: $R=sR_0$, where s is the proportion of the population that is susceptible,

$$s=V_C(1-V_E)+s_U(1-V_C),$$

where V_E is the median vaccine effectiveness of 1 dose of MMR (93%) (12), and s_U is the proportion of unvaccinated individuals that are susceptible (i.e., not immune through previous exposure), so that

$$R_0=R/[V_C(1-V_E)+s_U(1-V_C)].$$

Immunization levels in the Amish community were unknown. Thus, we modeled two distinct scenarios, using a lower and upper bound in V_C. A lower bound in V_C of 14% was derived from a coverage assessment in a subset of affected Amish families (62 households with measles cases selected by convenience sampling, totaling 451 individuals) (5); these data were obtained through review of vaccination cards and of the Ohio immunization registry (ImpactSIIS) (5). An upper bound in V_C of 68% was obtained from a recent study showing that this was proportion of Amish children in Holmes County, Ohio that were reported to have received ≥1 doses of any vaccine (13). The estimate of s_U was based on a measles attack rate of 67.5% among 160 exposed unvaccinated family members, part of a household transmission study conducted during the outbreak. Lower and upper bounds in V_C were then used to calculate the corresponding R_0 and β parameters to model a range of possible scenarios. Reassuringly, our R_0 estimates ranged between 7-16 (Table 1), consistent with prior estimates for measles in various settings (ranging between 5-18) (7). Of note, in any given population with a particular contact pattern, the transmissibility potential of measles would be described by a single R_0 value; the true R_0 for this community is likely somewhere in between the range estimated.

The σ and γ parameters are inversely proportional, respectively, to the pre-infectious period (the time period between infection and onset of infectiousness), and to the duration of infectiousness.

We assumed random mixing and a finite population size of 32,630 persons – the estimated Amish population in the affected settlement during 2014 (14). Due to natural (and maternal) immunity, as well

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as vaccine coverage prior to the outbreak, a proportion of the population was assumed to be recovered at the outset, bypassing the S class, although they were allowed make contacts and thus were accounted for in the calculation of the incidence.

To assess the impact of the vaccination campaign, we queried ImpactSIIS for the number of doses of MMR given at local health departments in affected counties during the time vaccine clinics were offered (April 22-July 24, 2014). Unvaccinated individuals who received MMR were removed from the S class and added to the R class based on day of vaccine receipt; during broad vaccination campaigns, the vaccine may reach unvaccinated individuals before or around the time of exposure (5, 15), and when administered within 72 hours after exposure, MMR vaccine can protect or modify the clinical course of measles (12, 16).

Five hundred iterations of the model were run for each of the two scenarios, in the absence and presence of the vaccination campaign. The median size and duration of predicted outbreak trajectories, and the corresponding daily changes in R_c, are presented and compared to what was observed. We modeled transmission in the affected Amish community only, without potential spill over to the general (non-Amish) population, where immunity levels are high and almost no measles spread was seen (5).

To evaluate the appropriateness of using early estimates of R to inform the susceptible-exposed-infectious-recovered model, we compared the expected (as predicted by the model) and the observed number of cases during the first 29 days of the outbreak, prior to initiation of the control measures.

Sensitivity analyses were conducted to examine (1) the choice of time window width used to estimate R_t, (2) the use of symptom onset instead of rash onset to estimate R, (3) the impact of advancing or delaying the vaccination campaign by 1 week (to evaluate delays in vaccine protection [immunologic response] and outbreak response), (4) a range of measles vaccine effectiveness (84.8% to 97.0%) at baseline (17), (5) a measles vaccine effectiveness of 90.5% for campaign doses (18), and (6) a shorter infectious period of 5 days (19).

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Analyses were performed in R 3.2.3.

Since the investigation was part of a public health response, it was not considered by the Centers for Disease and Control to be research, and was designated as exempt from human subject policy.

RESULTS

The outbreak affected one of the largest Amish communities in North America, located in the Holmes County, Ohio area (14). A total of 383 confirmed measles cases were reported over 121 days. Vigorous containment efforts were instituted by local health departments to limit measles spread, including the delivery of MMR doses to 8,726 unvaccinated individuals (5).

The epidemic curve and the estimated R_t and R_c are shown in Figure 2. R_t increased from an initial value of 1.2 (90% confidence interval (CI): 0.4-2.8) at the end of the third week to a maximum value of 9.6 (90% CI: 6.6-13.4) in the mid-fifth week, then varied between 3.1 and 4.6 from the mid-sixth week to the mid-seventh week. Thereafter, as the vaccination campaign started to get under way, estimates declined over two weeks, with R_t falling below 1 by the mid-ninth week. As the campaign continued, R_t remained below 1 during the next 2 months, except at the very end of the epidemic, when it increased from a minimum value of 0.16 (90% CI: 0.07-0.3) to 1.4 (90% CI: 0.7-2.5). This late increase in R_t occurred after introduction of measles into a single, unimmunized family consisting of six individuals, four of which developed measles. Similar patterns in transmissibility were observed with R_c, i.e., high initial values with variability, a steady decrease as control measures started, and maintenance below 1 thereafter.

The distribution of the expected number of cases (as determined by the model) during the first 29 days of the outbreak, prior to initiation of control measures, captured well the number of observed cases; the observed and projected daily case incidence tracked each other well in the early stages of the outbreak (Figure 3B), and the number of observed cases consistently fell between the 25th and 50th percentiles of the predicted data, for the range of scenarios that were evaluated.

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The range of possible outbreak sizes and durations projected by the model are shown in Table 2. Under the first scenario, assuming an initial V_C of 14%, the model estimated approximately 19,000 measles cases presenting over 215 days if no control efforts had been introduced, and approximately 9,500 measles cases presenting over 260 days when including the vaccination campaign; the model attributes ~9,500 fewer cases to vaccination efforts. Under the second scenario, assuming an initial V_C of 68%, the model estimated approximately 8,500 measles cases presenting over 200 days if no control efforts had been introduced, and approximately 700 measles cases presenting over 130 days when including the vaccination campaign; ~7,700 fewer cases and 65 fewer outbreak days were attributed to vaccination efforts.

Results based on anecdotal immunization levels in the community of 40-50% reported by local health departments, are presented in Figure 3. Assuming an initial V_C of 45%, in the absence of containment measures, the model predicts an outbreak with a median of approximately 13,000 cases. When the vaccination campaign is included, the model predicts a smaller outbreak, with a median of approximately 3,400 cases (Figure 3A); 9,600 fewer cases are attributed to vaccination efforts. When comparing model predictions that include the vaccination campaign with what was observed (Figure 3B), an excess ~3,000 cases were projected by the model, which may be accounted by other factors (e.g., changes in community behavior including social distancing, and other control efforts such as isolation and quarantining).

A comparison of the changes in the observed and projected daily estimates of R_c are shown in Figure 4. The observed R_c trajectory (which represents the effect of the vaccination campaign, other control efforts, and changes in community behavior) indicated a rapid decline in measles transmissibility over time. By contrast, declines in transmissibility were slower from a depletion of susceptible individuals from infection plus the vaccination campaign (model with the vaccination campaign), and from a depletion of susceptible individuals from infection alone (model without the vaccination campaign).

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Sensitivity analyses found that varying several of the assumptions in this evaluation resulted in little change on the overall patterns of measles transmissibility; these include the choice of time window used to estimate *R* (Web Figure 1), the use of daily counts of onset of symptoms (instead of onset of rash) to estimate *R* (Web Figure 2), an evaluation of a range of measles vaccine effectiveness at baseline (Web Table 1), an evaluation of the effect of vaccination assuming an effectiveness of 90.5% for campaign doses (Web Table 2), and an evaluation of delays in vaccine protection (immunologic response) and outbreak response (Web Table 3).

DISCUSSION

Through monitoring of measles communicability during this outbreak, we show that containment efforts likely contributed to reducing measles spread, and demonstrate that launching comprehensive and timely public health responses can help avert large outbreaks from occurring in under-immunized populations. These findings corroborate previous results of an individual-based model, also showing the potential of measles spread to other North American Amish communities in the absence of outbreak responses (6). As containment measures started to get underway, we found a ~4-fold reduction in transmissibility (R_t declined from 4.6 to 1) over 2 weeks, and subsequent maintenance of R_t below unity as control measures continued. Based on the observed epidemic curve, in the absence of vaccination or behavioral changes, cases could have continued to double approximately every 5 days in the early stages of the outbreak (Web Appendix), and assuming a conservative scenario (initial vaccination coverage of 68%), the number of affected individuals might have increased to ~8,400, i.e., >20 times the number of cases observed (383 cases). Outbreaks of this magnitude have not been seen in the US since elimination was declared.(1) Based on hospitalization rates for measles in this community (5), and post-elimination measles case-fatality ratios (20), such an outbreak could have resulted in ~275 hospitalizations and ~9 deaths (12 hospitalizations and no deaths were reported during the outbreak).

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Evidence supporting measles outbreak response immunization is increasing. A review of vaccination during outbreaks in middle- and low-income countries noted an impact in 16 (42%) of 38 papers (3), and updated WHO guidelines recommend this strategy in countries with measles mortality reduction goals (21). Fewer studies have evaluated the benefits of vaccination during outbreaks in elimination settings (5, 22-27), where background immunization coverage is high and outbreaks occur in under-vaccinated subpopulations. In such evaluations, it is often challenging to account for a depletion of susceptible persons from infection, or for other aspects related to outbreak control and community behavior – isolation of cases, quarantining of susceptible contacts, and self-imposed social distancing, e.g., limited attendance to church gatherings or social events because of measles awareness. Our results suggest that the vaccination campaign could not have accounted entirely for the observed decrease in transmissibility (Figure 4). By immediately reducing the number of susceptible contacts each ill individual makes, these other factors seem to play an important role. Based on an initial coverage of ~45%, we show that ~3,000 fewer cases might be attributed to community engagement and behavioral changes. Yet, any factor that affects the force of infection during an outbreak, including spatial and social heterogeneity in mixing, unevenness in MMR coverage, or varying effects of control interventions in different areas (e.g., targeting primarily those exposed), could also have curbed transmission. Data on each of the components of outbreak response (particularly isolation and quarantining) are needed to disentangle their relative effectiveness (28), and quantifying and modeling the dynamics of behavior change in response to epidemics is a particular challenge and priority.

Our evaluation highlighted a few interesting aspects of measles transmissibility and outbreak control. First, considerable variability in transmission was evident early during the outbreak; estimates of R_c varied between 3.1 and 10.2 before interventions began. This variability may be an artifact of the estimation method resulting from an initial low number of incident cases (8), or a reflection of differences in the contact rates of the first several case-patients. The latter could be an observation bias –

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if the first few cases generate many other cases, the outbreak gets past the chance of initial extinction and can spread beyond the initial cluster. Second, cases continued to occur for ~2 months after *R* fell below 1, indicating that sustained transmission can occur when *R* is near unity, and that both elimination efforts and outbreak control measures should aim to reduce *R* as close to 0 as possible. A similar effect has been observed in a previous outbreak of influenza (29) and could be the effect of the interaction with the behavioral or public health response, where cases cause small clusters of secondary cases that are largely contained but might seed other sub-outbreaks elsewhere (30). Third, measures to control an exceedingly contagious disease like measles are likely more successful when the susceptible population is embedded in a general population with high MMR vaccine uptake.

The measles containment strategies (16) implemented during this outbreak could serve as a guide on how to halt propagation of the disease in non-immunized subpopulations in elimination settings. In the Region of the Americas, for example, despite 1-dose measles vaccine coverage being maintained at ≥90% since 1998 (31), and a declaration of measles elimination in 2016 (32), recent outbreaks reported in Ecuador, Canada (33), the US (1, 34), and Brazil (35), indicate that coverage is not homogenous. These outbreaks ranged considerably in size and duration (147 to 1,065 confirmed measles cases, 9 weeks to 1.5 years long), and were characterized by varying containment efforts. In the US, reports of measles cases are expected within 24 hours of confirmation (16), triggering the implementation of enhanced surveillance, and of measures to limit spread. Key elements to curtail transmission include isolation of cases until no longer infectious, vaccination of susceptible contacts, and quarantining of susceptible contacts who cannot be vaccinated (16).

Our analysis has several limitations. First, often all causes of heterogeneity cannot be accounted for in models. Measles was reported in nine Ohio counties (5), and homogenous mixing does not account for more complex spatial patterns of spread in this community, or for preferential mixing by age. However, at least part of the heterogeneity in contact rates is captured by the initial *R* values, which we then use to

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get the projected model estimates. Similarly, any underlying heterogeneity in immunity was unknown, yet, a broad range of coverage scenarios were modeled, and an impact of controls measures was evident under a conservative scenario. Of note, the model also assumes a homogenous effect of vaccination efforts, which may underestimate their impact. In addition, final outbreak sizes and the impact of the interventions depend on the estimated population at risk, and we did not measure the impact of the response in limiting spread to other Amish communities, including outside Ohio (6). Because of these caveats, the trajectories we present should not be viewed as exact projections, but characterize probable trends in transmissibility and in the potential for control. Second, case under-ascertainment might have occurred, however, enhanced surveillance, widespread knowledge of the outbreak, and established relationships with the community likely improved case identification (5). Importantly, estimates of *R* would not be affected as long as surveillance does not change considerably during the outbreak (8, 10), and sudden decreases or increases in case reporting were unlikely. Third, we chose an infectious period of 9 days based on outbreak control guidelines (16, 36, 37), which may be closer to maximum duration of infectiousness, and long for models assuming this period is the mean of an exponential distribution. However, the number of cases prevented by vaccination using a shorter infectious period (19) was still significant, and our base model tracked the initial outbreak trajectory better (Web Table 4). Fourth, we did not account for imperfect or delayed vaccine protection from campaign doses. However, sensitivity analyses using a lower effectiveness (18), and delaying vaccine protection by 1 week, did not have a substantial impact on our findings. Finally, this is an evaluation of a single outbreak and our findings may not be generalizable to all communities where importations occur, and the assumption of homogenous mixing may not be applicable to other measles outbreaks in post-elimination settings.

The findings in this report demonstrate the substantial public health impact of rapid measles containment efforts in an unvaccinated community in an elimination setting. Our results reinforce WHO's measles elimination strategy, that includes outbreak preparedness as one of the core components to achieve

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elimination targets in 5 of the 6 WHO regions by 2020 (21). Measles elimination is a fragile state (38) and the data provided here may serve as an impetus for local and international health organizations to allocate resources to build and maintain capacity for measles outbreak readiness, including in countries where measles incidence is sufficiently low or elimination has been achieved. The single best means of measles containment, however, is maintaining high initial levels of vaccination coverage across the population.

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Figure 1. Schematic representation of disease states, flow between states, and parameters controlling flow in the measles model. The model represents a constant (closed) population in which individuals are either susceptible (S) or recovered (R) to measles infection and disease, and into which a measles introduction occurs (i.e., a number of infectious individuals (I) is introduced). Persons in the susceptible pool become exposed at the force of infection $\lambda(t)$, and then progress through the exposed pre-infectious (E) and the infectious (I) stages, before arriving in the removed compartment (R), where individuals are immune. The symbols σ and γ denote the rates at which individuals progress into the I and R compartments, respectively. The model tracks, each day, the number of individuals in each of the compartments, and incorporates stochasticity using the adaptive tau-leaping algorithm.(11) The effect of the vaccination campaign is represented by θ, the number of unvaccinated individuals who received a dose of MMR during containment efforts. Unvaccinated individuals are removed from the S compartment and added to R compartment (bypassing E and I) based on the day MMR was administered.

Figure 2. A) The daily epidemiologic curve; the daily total numbers of confirmed outbreak-associated measles case-patients in Ohio in 2014 according to day of rash onset are shown (N=383); for three case-patients, the rash onset date could not be determined, and the illness onset date +2 days (the median number of days between illness onset and rash for all other cases) is shown; one lab-confirmed case-patient did not develop rash and the date of illness onset is shown. B) Daily estimates of the instantaneous reproduction number R_t over sliding 14-day windows; the black line shows the median estimate, the gray areas the 90% confidence intervals, and the horizontal dashed line the threshold value R_t=1; C) Daily estimates of the case reproduction number (R_c) over sliding 14-day windows; the red circle shows the mean estimate, the bars the 90% confidence intervals, and the horizontal dashed line the threshold value R_c=1. As expected, estimates of R_c were ahead of the estimates of R_t, with the highest estimate of R_c occurring around the end of the third week, about one serial interval (11-12 days) before the peak in R_t; the peak in R_t in the mid-fifth week indicates increased transmissibility among cases with rash onset one generation before.(8) Superimposed in all figures is the cumulative number of daily doses of MMR vaccine given at local health department vaccination clinics during the outbreak.

Figure 3. Projected and observed daily measles case incidence assuming an initial vaccination coverage of 45%. One hundred iterations of the modeled epidemic curves are presented; dashed lines show the median daily measles case incidence of all iterations. Panel A compares model trajectories with and without the vaccination campaign. Panel B compares the model trajectories including the vaccination campaign to the observed epidemic curve (that included other control measures). Note that the scale of the axes differ. Cumulative case incidence was as follows: model without vaccination, 12,946 (90% confidence interval [CI] 12,919, 12,968) cases over 207 (90% CI: 187, 233) days; model with vaccination campaign, 3,353 (90% CI: 2,551, 4,003) cases over 247 (90% CI: 183, 370); observed with control interventions, 383 cases over 121 days.

Figure 4. Panel A shows the observed and projected daily estimates of the case reproduction number (R_c) over sliding 14-day windows; the black and blue circles show the median R_c of 100 model trajectories without and with the vaccination campaign, respectively, assuming an initial vaccination coverage of 45%. The red circles show the observed mean R_c estimate (that included other control measures, changes in community behavior), the red bars represent the 90% confidence intervals, and the horizontal dashed line indicates the threshold value R_c=1. Observed and projected R_c estimates were derived from the likelihood-based estimation procedure and directly from the models, respectively. Panel B shows the proportion of decline in R_c attributable to changes in community behavior (social distancing) and other control efforts (isolation, quarantining) during the outbreak; data presented are

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from the initiation of containment efforts, to the time when projected estimates of R_c fall below 1. The reduction in transmissibility that may be ascribed to these factors varied between ~30-90% during the outbreak.

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Table 1. Fixed input parameters for each model scenario

Parameter	Symbol	Formula	Value	References
Transmission probability	β	R_0/ND	Scenario 1[a]: $2.74*10^{-5}$ per day	NA
Transmission probability	β	R_0/ND	Scenario 2[b]: $6.12*10^{-5}$ per day	NA
Basic reproduction number	R_0	R/s	Scenario 1: 7.14	NA
Basic reproduction number	R_0	R/s	Scenario 2: 16.0	NA
***R* of cases prior to initiation of control measures**	R	NA	4.22	Estimates likelihood-based estimation procedure(8, 10)
Proportion of the population that is susceptible at outset	s	$V_C(1-V_E{}^c)+s_U{}^d(1-V_C)$	Scenario 1: 0.59	NA
Proportion of the population that is susceptible at outset	s	$V_C(1-V_E{}^c)+s_U{}^d(1-V_C)$	Scenario 2: 0.26	NA
Population size	N	S + E + I + R	32,630	Young Center for Anabaptist and Pietist Studies, Elizabethtown College(14)
Average pre-infectious or latent period	NA	NA	10 days	CDC measles surveillance manual and ACIP recommendations(12, 16)
Average duration of infectiousness	D	NA	9 days	CDC measles surveillance manual and ACIP recommendations(12, 16)
Rate at which individuals become infectious	σ	1/average pre-infectious or latent period	0.1 per day	NA
Recovery rate	γ	1/average duration of infectiousness	0.111 per day	NA

NA, not applicable; V_C, ≥1-dose MMR coverage; V_E, median vaccine effectiveness of 1 dose of MMR; s_U, proportion of unvaccinated individuals that are susceptible; CDC, Centers for Disease Control and Prevention; ACIP, Advisory Committee on Immunization Practices

[a]Assuming ≥1-dose MMR coverage of 14% to calculate s (lower bound) – from a coverage assessment in a subset of affected Amish families(5)

[b]Assuming ≥1-dose MMR coverage of 68% to calculate s (upper bound) –from the literature(13)

[c]VE=93%(12)

[d]unvax.S=67.5% – from household transmission study

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Table 2. Model Predictions of Measles Outbreak Sizes and Durations in an Amish Community in Ohio in 2014, With and Without the Vaccination Campaign[a], and Based on Two Initial Levels (Lower and Upper Bounds) of MMR Coverage Prior to Initiation of Containment Efforts

Assumed MMR coverage[b]	No. of measles case-patients				Duration of outbreak (days)				Absolute Reduction			
	Vaccination campaign included											
	No		Yes		No		Yes					
	No.	90% CI	No.	90% CI	Duration (days)	90% CI	Duration (days)	90% CI	No.	90% CI	Duration (days)	90% CI
14% (lower)	18,978	18,944, 19,003	9,430	9,109, 9,844	213	195, 241	257	201, 308	9,548	9,128, 9,866	−44	−95, 22
68% (upper)	8,472	8,447, 8,489	715	103, 1,338	195	179, 223	128	117, 139	7,757	7,130, 8,365	67	48, 98

[a]County health department clinics offering vaccination were held from day 30 to day 123 of the outbreak; first doses of MMR were delivered to 8,726 unvaccinated individuals

[b]≥1-dose MMR coverage

[c]Values are the medians and 90% confidence intervals (CI) generated from 500 model simulations

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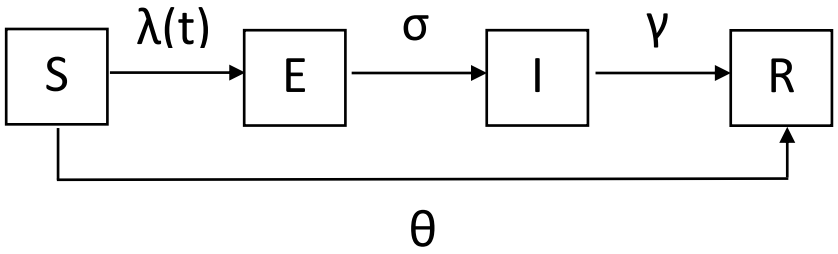

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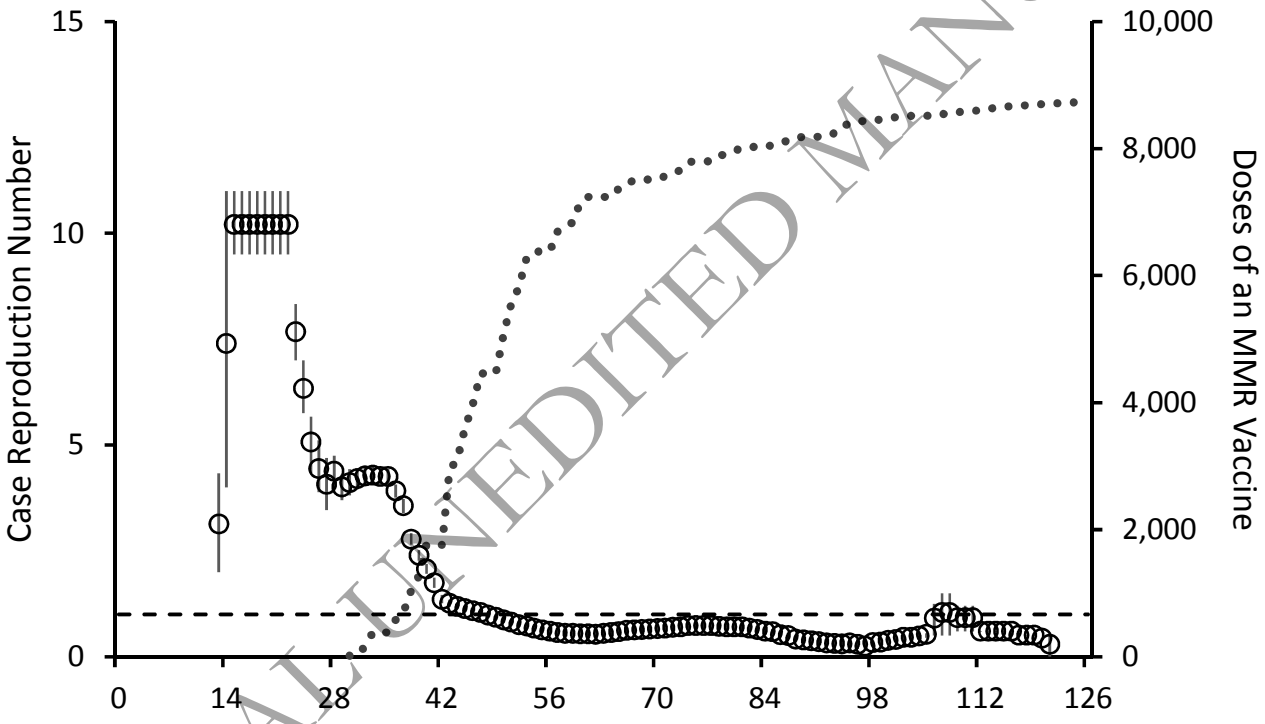

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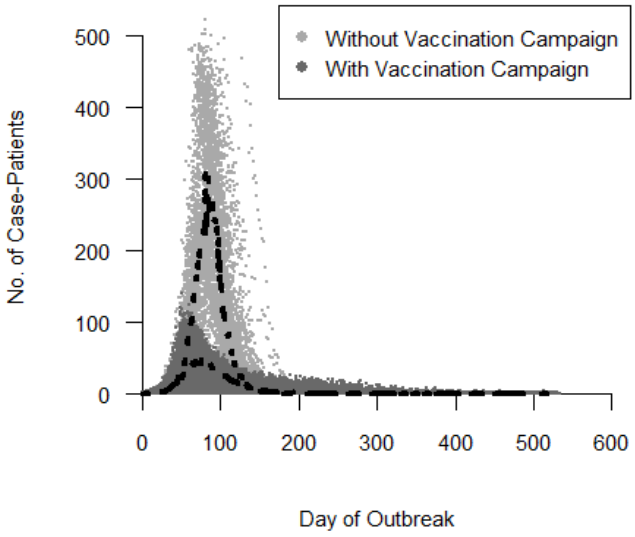

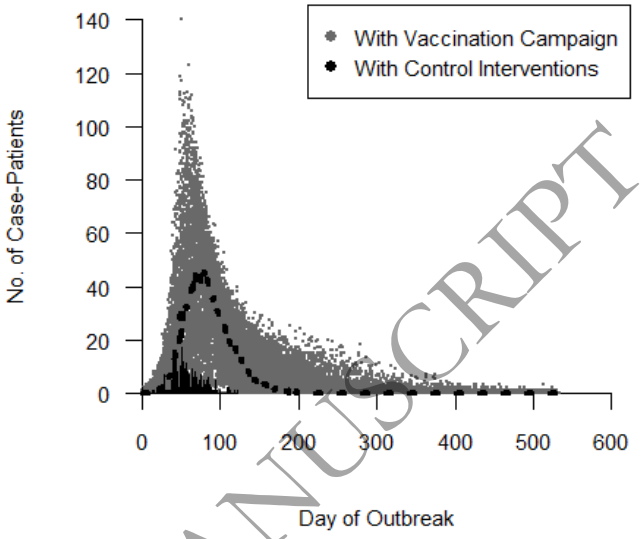

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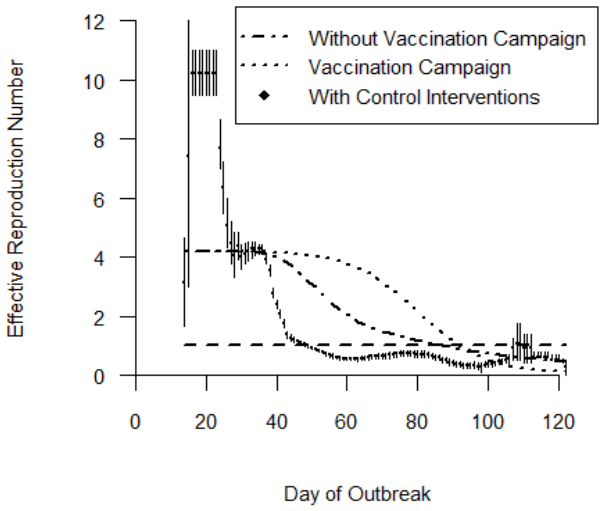

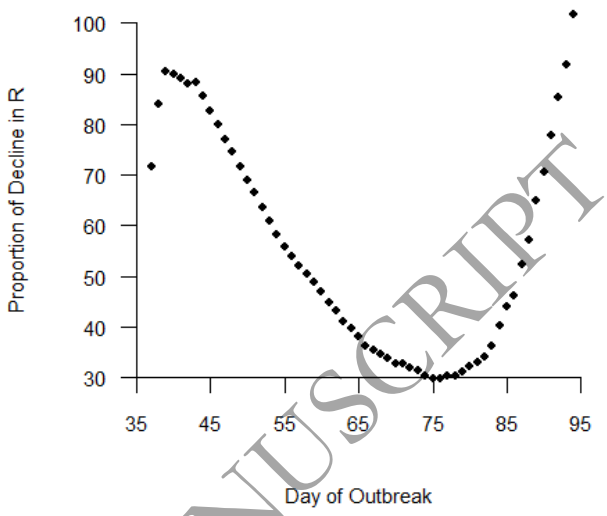

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