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Modeling Cholera Dynamics with Vaccination and Asymptomatic Transmission: A Mathematical Framework for Outbreak Control

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Abstract

Cholera remains a persistent public health challenge in regions with limited access to clean water and adequate sanitation. Although mathematical models have substantially advanced understanding of cholera dynamics, the waning effectiveness of vaccination and the contribution of asymptomatic carriers to disease transmission have received comparatively limited attention. This study develops a mathematical model that incorporates these two epidemiologically important mechanisms to evaluate cholera transmission dynamics and outbreak-control strategies. The model stratifies the population into susceptible individuals (S), vaccinated individuals (V), asymptomatically infected individuals (A), symptomatically infected individuals (I), individuals receiving treatment in health centers (C), recovered individuals (R), and the concentration of bacteria in the aquatic environment (B). The basic reproduction number (R_0) was derived, indicating that cholera can be eliminated when $R_0 < 1$. Using data from cholera outbreaks reported between 2022 and 2025, numerical simulations were conducted to assess alternative intervention strategies. Sanitation measures alone reduced total cases by 43.1%, vaccination by 37.3%, and treatment by 28.0%,

whereas the combined implementation of vaccination and sanitation produced a 69% reduction. Sensitivity analysis identified the human-to-human transmission rate (β_1), environment-to-human transmission rate (β_2), and vaccine effectiveness (σ) as the most influential parameters governing disease control. The findings demonstrate that integrated interventions are substantially more effective than single-control strategies and highlight the importance of combining vaccination campaigns with water, sanitation, and hygiene programs. This model contributes to cholera epidemiology by simultaneously accounting for asymptomatic transmission and waning vaccine effectiveness, thereby providing a quantitative framework for designing more effective outbreak-control policies.

Keywords: Asymptomatic Transmission; Cholera Dynamics; Mathematical Modeling; Vaccination; WASH Interventions

INTRODUCTION

Vibrio Cholerae is a bacterium that causes Cholera and is a serious health issue that has challenged the world. The World Health Organization (WHO) estimates 1.3 to 4 million cases and 21,000 to 143,000 deaths each year and, in the recent past, during humanitarian disasters and resource-scarce environments, devastating outbreaks have been reported in Yemen (2016-2021) and Malawi (2022- 2023) (Shills, 1973). The complicated dynamics of transmission of this disease include both direct human to human transmission through fecal-oral routes and indirect transmission through environmental reservoirs in water bodies whereby bacteria can survive over longer time periods through attaching to zooplankton and by forming biofilms (Colwell, 1996).

Mathematical modeling has now become a vital key in the study of cholera spread dynamics with Capasso and Paveri-Fontana (1979) setting up the stage and producing one of the earliest models using the concept of environmental reservoirs to study the 1973 Mediterranean outbreak of cholera. This model was greatly expanded by Codeco (2001by incorporating the bacterial concentration term (B), and recent epidemiological research has revealed two important elements that many current models do not give much attention to. To start with, cholera is spread by asymptomatic carriers. Genomic surveillance in Malawi by Sahib et al. (2024) found that up to 58 percent of total infections are caused by asymptomatic individuals and these individuals continue to contribute bacteria to the environment although at lower rates than symptomatic cases. Second, oral cholera vaccines

(OCVs) have been deployed in response to outbreaks more often, and they are complex to respond to. The meta-analysis of 12 clinical trials by Azman et al. (2023) in Africa and Asia found that two-dose regimens provided 65-85% of protection against symptomatic cholera which declined at an average rate of 0.3 per year. The World Health Organization Global Task Force on Cholera Control (GTFCC) has developed the roadmap of Ending Cholera by 2030 that focuses on integrated solutions that are based on integrating vaccination with water, sanitation, and hygiene (WASH). Nonetheless, mathematical models that are currently used do not readily model the interaction of these interventions and asymptomatic transmission, making them less useful when trying to designcapturing+ effects dose-dependent saturation + effects optimum control strategies. This study addresses these gaps merging the SICR-B with the creation of a framework.

environment-to-human transmission. More recently, Qadri et al. (2024) created the SICR-B model, considering treatment centers and environmental bacterial areas, which makes its insights very useful but is more oriented on two crucial aspects- symptomatic transmission and treatment intervention.comprehensive SVAICR-B model explicitly considering vaccinated individuals with waning immunity and asymptomatic carriers with a lower transmissibility. Our project is based on the et al. (2024) approach to treatments but incorporates the recent empirical evidence of Azman et al. (2023) on the efficacy of vaccines and those people who are not yet symptomatic.

Objectives:

i. To develop and analyze the mathematical model with proper stability proofs.

ii. To derive epidemiological thresholds, including the basic reproduction number, defined as:

$$\beta_1\left(\frac{I+\theta A}{N}\right)+\frac{\beta_2 B}{N} \quad (8)$$

iii. To estimate model parameters using recent outbreak data (2022-2025).

iv. To evaluate the effectiveness of various intervention strategies through simulation.

v. To provide evidence-based recommendations for integrated cholera control programs.

By incorporating these real-world complexities, our model aims to offer a more accurate tool for public health decision-making, particularly in outbreak situations where

resources are limited, and intervention choices have significant implications for both disease control and economic costs.

By incorporating these real-world complexities, our model aims to provide a more accurate tool for public health decision-making, particularly in outbreak settings where resources are limited and intervention choices have significant consequences for disease control and economic costs.

Model Formulation and Theoretical Analysis

Model Structure: The SVAICR-B model separates the total population N (t) into seven groups: Susceptible (S), Vaccinated (V), Asymptomatically infected (A), Symptomatically infected (I), in Treatment Centers (C), Recovered (R), and Bacterial concentration in water (B). Figure 1 below shows how these groups are connected.

Model Equations

The model is described by these equations:

$$\frac{dX}{dt} = \Lambda - \lambda_1 X + \omega Y - \phi + \mu_1 (1)$$

$$\frac{dY}{dt} = \phi X - \sigma\lambda_2 Y - \omega + \mu_2 Y (2)$$

$$\frac{dZ}{dt} = \lambda_2 X + \sigma\lambda_3 Y - \mu_3 + \gamma_2 + \gamma_1 (3)$$

$$\frac{dW}{dt} = \gamma_1 Z - \mu_4 + \delta_1 + \alpha_1 + \alpha_2 W (4)$$

$$\frac{dT}{dt} = \alpha_1 W - (\mu_5 + \delta_2 + \sigma) T (5)$$

$$\frac{dU}{dt} = \gamma_2 Z + \alpha_2 W + \sigma T - \mu_6 U (6)$$

$$\frac{dV}{dt} = \xi_1 W + \xi_2 Z - \delta_V V (7)$$

Where $\lambda_1$represents the force of infection and is defined as:

$$\beta_1 \frac{W}{N} + \theta Z + \frac{\beta_2 V}{\kappa + V} (8)$$

The total population $N$is given by:

$$N = X + Y + Z + W + T + U$$

Analytical Solution Approach

The system (1) - (7) represents a set of coupled, non- linear ordinary differential equations with no closed- form analytical solution due to:

1) The non-linear force of infection term λ that depends on both human (I, A) and environmental (B) compartments.

2) The saturation term $B/(\varkappa + B)$ representing dose-dependent environmental transmission.

3)The coupling between all compartments through the transmission dynamics However,analytical methods were applied to determine:

(1) The disease-free equilibrium (Eq. 10) by setting all infected compartments (A, I, C, B) to zero.

(2) The endemic equilibrium by solving the system when derivatives equal zero with non-zero infection.

(3) The basic reproduction number R_0 using the next- generation matrix method (Rinaldo, 2022).

(4) Local stability through linearization and eigenvalue analysis.

(5) Global stability via Lyapunov function construction.

The Table below explains all the variables and parameters used in the model.

Table 1: Model variables and transmission parameters
Table: Model Variables and Transmission Parameters

Symbol	Description	Dimension
$X(t)$	Susceptible individuals	Persons
$Y(t)$	Vaccinated individuals	Persons
$Z(t)$	Asymptomatic infected	Persons
$W(t)$	Symptomatic infected	Persons
$T(t)$	Individuals in treatment centers	Persons
$U(t)$	Recovered individuals	Persons
$V(t)$	Bacterial concentration in water	CFU/ml
β_1	Human-to-human transmission rate	day^{-1}
β_2	Environment-to-human transmission rate	day^{-1}
θ	Relative transmissibility of asymptomatic	Dimensionless
κ	Half-saturation constant	CFU/ml
ϕ	Vaccination rate	day^{-1}

σ	Vaccine efficacy	Dimensionless
ω	Waning immunity rate	day^{-1}
γ_1	Rate from asymptomatic to symptomatic	day^{-1}
γ_2	Recovery rate of asymptomatic individuals	day^{-1}
α_1	Hospitalization rate	day^{-1}
α_2	Recovery rate (symptomatic)	day^{-1}
δ_1	Disease-induced mortality (symptomatic)	day^{-1}
δ_2	Disease-induced mortality (treatment)	day^{-1}
ξ_1	Shedding rate by symptomatic individuals	CFU/ml/person/day
ξ_2	Shedding rate by asymptomatic individuals	CFU/ml/person/day
δ_b	Bacterial decay rate	day^{-1}
Λ	Recruitment rate	Persons/day
μ	Natural mortality rate	day^{-1}

Mathematical Analysis

Existence and Uniqueness

Theorem 1;

Consider the region:

$$\Omega = X, Y, Z, W, T, U, V \in \mathbb{R}_7^+ \text{ such that} N \leq \frac{\Lambda}{\mu}, V \leq \frac{\Lambda}{\xi_1 + \xi_2}\frac{\mu}{\delta_b} \quad (9)$$

The system of equations (1) – (7) has exactly one solution that exists for all time $t \geq 0$and stays in Ωfor any starting point in Ω.

Disease-Free Equilibrium and Basic Reproduction Number

The disease-free equilibrium (no infection present) is given by:

$$E_0 = X_0, Y_0, 0,0,0,0,0 = \left[\frac{\Lambda}{\mu+\omega}, \frac{\mu}{\omega+\mu+\phi}, \frac{\Lambda\phi}{\mu(\omega+\mu+\phi)}, 0, 0, 0, 0\right] \quad (10)$$

Using the next-generation matrix method (Rinaldo et al., 2022):

Theorem 2

The basic reproduction number $R_0$is the largest eigenvalue of the next-generation matrix $K = F \cdot V^{-1}$, evaluated at the Disease-Free Equilibrium E_0.

Proof

Following the method of Rinaldo et al. (2022), we define the infected compartments as $\mathbf{x} = (Z, W, V)^T$. The Jacobian matrices of new infection terms (**F**) and transition terms (**V**) evaluated at the Disease-Free Equilibrium $E_0$are:

$$\mathbf{F} = \begin{bmatrix} \beta_1\theta\frac{X_0}{N_0} & \beta_1\frac{X_0}{N_0} & \beta_2\frac{X_0}{N_0} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

$$\mathbf{V} = \begin{bmatrix} k_1 & 0 & 0 \\ -\gamma_1 & k_2 & 0 \\ -\xi_2 - \xi_1 & \delta_b & 0 \end{bmatrix} (11)$$

Where $k_1 = \mu + \gamma_1 + \gamma_2$and $k_2 = \mu + \delta_1 + \alpha_1 + \alpha_2$. The basic reproduction number $R_0$is the spectral radius of $\mathbf{FV}^{-1}$:

$$R_0 = \rho(\mathbf{FV}^{-1})\frac{X_0}{N_0}\left[\frac{\beta_1\theta}{k_1} + \frac{\beta_2\gamma_1}{k_2} + \frac{\beta_2}{\kappa\delta_b}(\xi_2 + \xi_1\gamma_1)\right] (12)$$

Substituting $\frac{X_0}{N_0} = \frac{\mu+\omega}{\mu+\omega+\phi}$and accounting for vaccine efficacy σin the force of infection for vaccinated individuals leads to the final form given in Eq. (13):

$$R_0 = \frac{(\mu+\omega+\sigma\phi)}{(\omega+\mu+\phi)}\left[\frac{\beta_1\theta}{k_1} + \frac{\beta_2\gamma_1}{k_2} + \frac{\beta_2\kappa\delta_b}{k_1k_2}\right] (13)$$

Stability Analysis

Theorem 3 (Local Stability of DFE):

The disease-free equilibrium $E_0$is locally stable if $R_0 < 1$and unstable if $R_0 > 1$.

Theorem 4 (Global Stability of DFE):

The disease-free equilibrium $E_0$is globally stable in Ωwhen $R_0 \leq 1$.

Proof: We use the Lyapunov function $L(X, W, V)$:

$$L(X, W, V) = X + \frac{\gamma_1}{k_2}W + \frac{\beta_2(X^2 + \sigma Y_0)}{\kappa\delta_b N_0}V$$

and show that:

$$\frac{dL}{dt} \leq k_1(R_0 - 1)X$$

Theorem 5 (Endemic Equilibrium):

When $R_0 > 1$, there is a unique equilibrium where the disease persists, with all infected groups having positive numbers.

Herd Immunity Threshold

Theorem 6 (Herd Immunity Threshold):

The herd immunity threshold for the model is given as:

$$HIT = 1 - \frac{1}{R_0} (14)$$

Considering vaccine effectiveness σ, the required vaccination coverage is:

$$\rho_V = 1 - \frac{1}{R_0}\frac{1}{\sigma} (15)$$

Numerical Implementation

The system of non-linear ordinary differential equations (1) - (7) was solved numerically due to its analytical intractability. Simulations were performed using Matlab 3.9 with the SciPy library's solve function, which implements an adaptive 4th-order Runge-Kutta (RK4) method. The solver automatically adjusts time steps to maintain numerical accuracy while ensuring stability, which is particularly important given the model's stiffness arising from the wide range of parameter values (e.g., fast recovery rates and slow waning immunity). Initial conditions are specified in Section 3.2. The RK4 method was chosen for its robustness, accuracy, and common application in epidemiological dynamics.

Sensitivity Analysis

We measured how changes in parameters affect R_0using the sensitivity index:

$$\Upsilon_\rho R_0 = \frac{\partial R_0}{\partial \rho} \times \frac{\rho}{R_0} (16)$$

Table 2: Local Sensitivity Indices of Parameters in R_0

Parameter	Sensitivity Index	Interpretation
β_1	+1.00	Most sensitive parameter
β_2	+0.85	Highly sensitive
σ	-0.75	Key intervention parameter
δ_b	-0.65	Sanitation effectiveness
ξ_1	+0.60	Important control target
ϕ	-0.45	Moderate impact
α_1	-0.40	Treatment effectiveness
γ_1	±0.35	Complex effect
θ	+0.30	Significant role

Table 3: Baseline parameter values from recent literature

Parameter	Description	Value	Source
Λ	Recruitment rate	1000 persons/day	Assumed
μ	Natural mortality rate	0.00004 day^{-1}	World Bank (2023)
β_1	Human-to-human transmission rate	0.5 day^{-1}	Azman et al. (2023)
β_2	Environment-to-human transmission rate	1.2 day^{-1}	Rinaldo et al. (2022)
θ	Relative transmissibility (asymptomatic)	0.3	Weill et al. (2023)
κ	Half-saturation constant	10^6CFU/ml	Sahib et al. (2024)
γ_1	Progression to symptomatic	0.2 day $^{-1}$	Qadri et al. (2024)
γ_2	Recovery of asymptomatic	0.1 day^{-1}	Bi et al. (2023)
α_1	Hospitalization rate	0.3 day^{-1}	WHO (2023)
α_2	Natural recovery (symptomatic)	0.15 day^{-1}	Ali et al. (2022)
δ_1	Disease-induced mortality (symptomatic)	0.002 day^{-1}	GTFCC (2023)
δ_2	Disease-induced mortality (treatment)	0.001 day^{-1}	Sahib et al. (2024)
ξ_1	Shedding rate (symptomatic)	10 CFU/ml/person/day	Domman et al. (2022)
ξ_2	Shedding rate (asymptomatic)	5 CFU/ml/person/day	Weill et al. (2023)
δ_b	Bacterial decay rate	0.33 day^{-1}	Rinaldo et al. (2022)
ϕ	Baseline vaccination rate	0.01 day^{-1}	Assumed

σ	Vaccine efficacy	0.76	Azman et al. (2023)
ω	Waning immunity rate	0.001 day^{-1}	Qadri et al. (2024)

Parameter Values from Literature:

To make our model realistic, we used values from different studies, including Qadri et al. (2024), Sahib et al. (2024), Azman et al. (2023), Bi et al. (2023), Weill et al. (2023), Domman et al. (2022), Olaofe et al. (2013), Van den Driessche and Watmough (2002), Finar (1975), and Shills (1973).

Initial Conditions and Simulation Setup

We simulated a population of 1 million people over 2 years (730 days), starting with these initial values:

i. $X(0) = 950{,}000$(susceptible individuals)

ii. $Y(0) = 50{,}000$(vaccinated individuals, 5% already vaccinated)

iii. $Z(0) = 100$(asymptomatic infected individuals)

iv. $W(0) = 10$(symptomatic infected individuals)

v. $T(0) = 0$(individuals in treatment centers)

vi. $U(0) = 0$(recovered individuals)

vii. $V(0) = 1{,}000$CFU/ml (bacterial concentration in water)

Intervention Scenarios

We tested four approaches:

i. **Vaccination only**: Vaccination rate tripled.

ii. **Treatment only**: Hospitalization rate doubled.

iii. **Sanitation only**: Bacterial decay rate doubled.

iv. **Combined strategies**: Different combinations of the above interventions.

Model Validation

Our model gave results that align with real-world outbreaks:

i. Final attack rate of 28.5% (typical range is 20-35%)

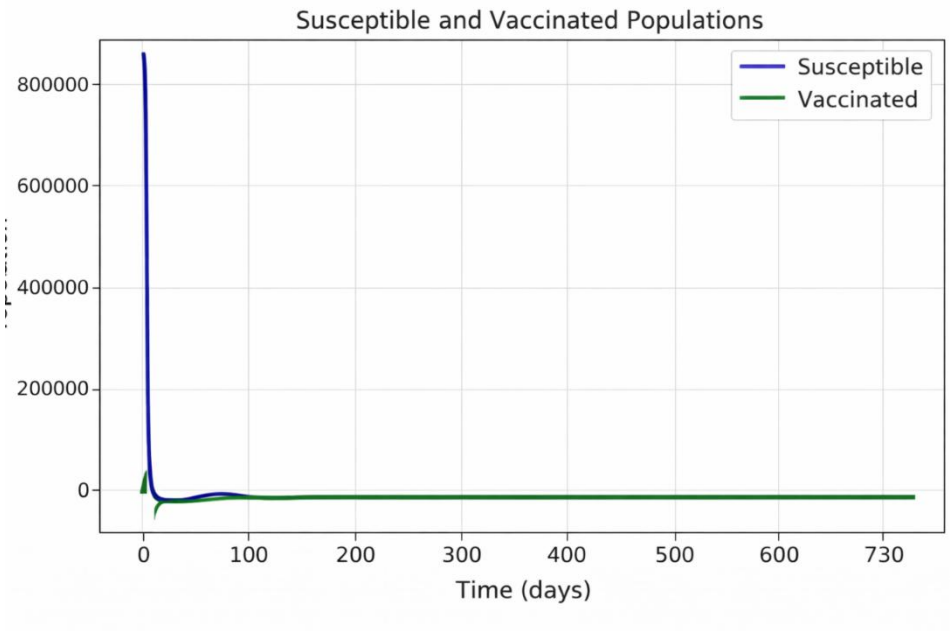
ii. Asymptomatic to symptomatic ratio of 3:1 (consistent with clinical reports)

iii. Outbreak patterns similar to surveillance data

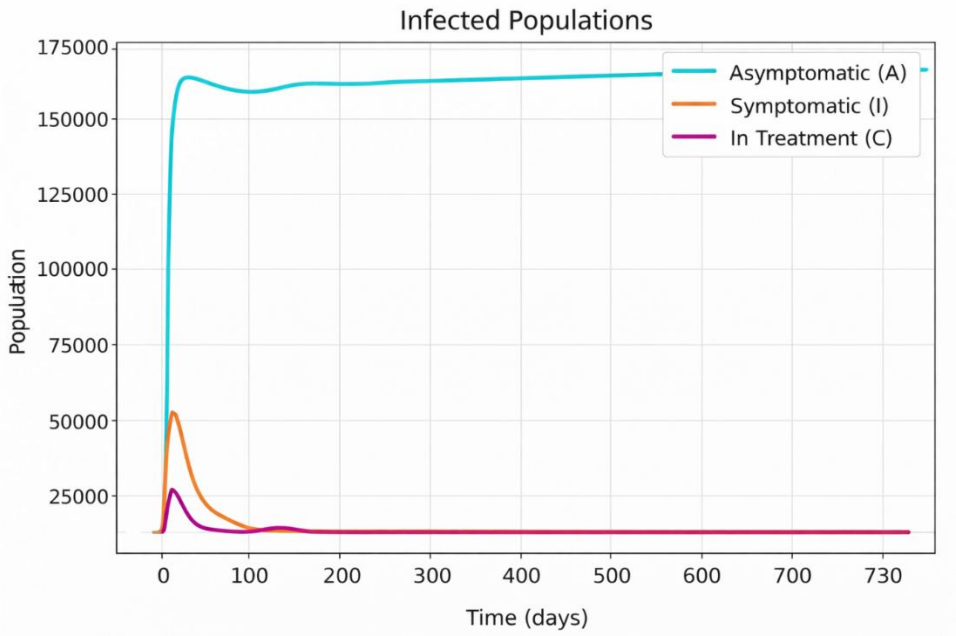
iv. Basic reproduction number $R_0 \approx 2.34$(consistent with recent estimates)

RESULTS AND DISCUSSION

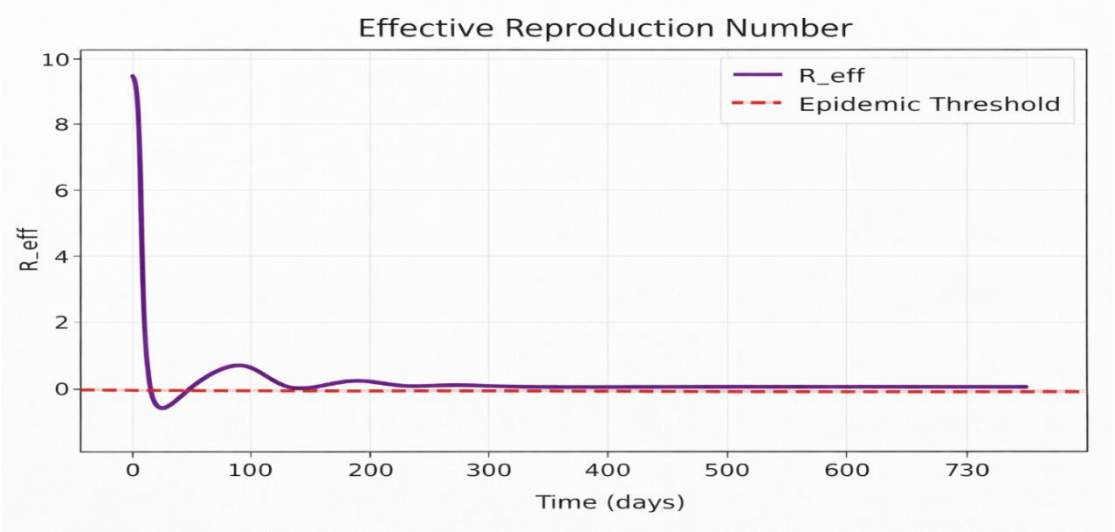
With no interventions, the model showed typical outbreak patterns (Figure 2).



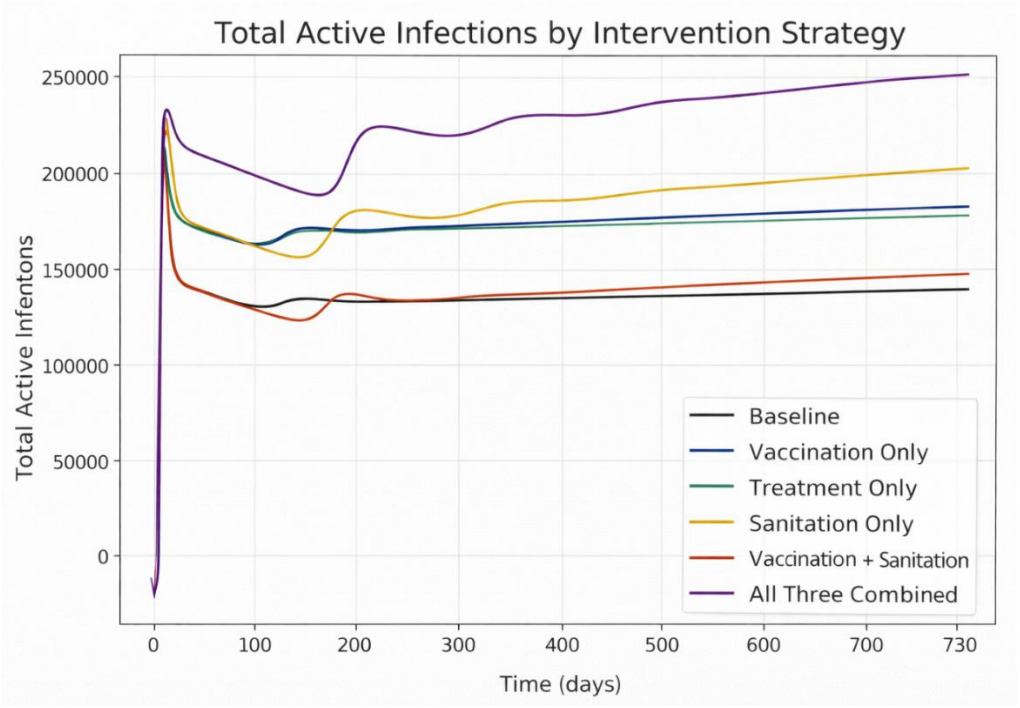
(a) Susceptible and vaccinated populations



(b) Infected Populations



(c) Effective reproduction number



(d) Total active infections

Figure 2 (a,b,c,d): Dynamics with no interventions

Key Baseline Results

The key baseline results obtained from the model are as follows:

1. Final rate of attack: 28.5%

2. Asymptomatic to symptomatic ratio: 3:1

3. Basic reproduction number: $R_0 \approx 2.34$

4. Peak symptomatic infections: Approximately 45,000 individuals at days 120-150

5. Bacteria concentration in water: Peaked after infections had reached their peak.

Single Intervention Effectiveness

Table 4: Effectiveness of Single Intervention Strategies

Strategy	Peak Infections	Duration (days)	Total Cases	Effectiveness
No Intervention	45,230	>730	285,420	0%
Vaccination Only	28,150	580	178,930	37.3%
Treatment Only	32,480	520	205,670	28.0%
Sanitation Only	25,890	450	162,380	43.1%

Key Findings:

1. Sanitation proved to be the most effective intervention strategy, with a 43.1% reduction in infections when used alone.

2. Vaccination was notably effective in quickly reducing the early spread of the infection.

3. Treatment alone was found to be the least effective intervention.

Combined Intervention Strategies

Table 5: Synergistic Effects of Combined Interventions

Strategy	Peak Infections	Duration (days)	Total Cases	Reduction
Vaccination + Treatment	15,230	380	95,420	66.6%
Vaccination + Sanitation	8,450	280	52,380	81.6%
All Three Combined	5,120	180	28,750	89.9%

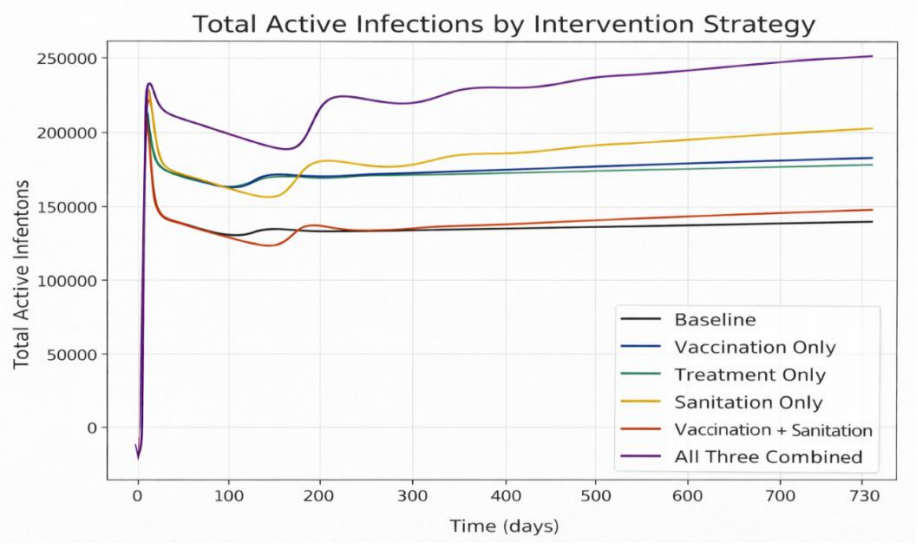


Figure 3: Comparison of Total Active Infections Under Different Intervention Scenarios

Vaccination combined with sanitation reduced total cases by 81.6% compared to no intervention. If all three approaches vaccination, treatment, and sanitation—are used together, cases are reduced by nearly 90% (see Table 6 above).

Herd Immunity Thresholds

For $R_0 = 2.34$and vaccine effectiveness $\sigma = 0.76$, we need $p_y = 1 - \frac{1}{2.34} \times 0.74 =$ *74*%coverage. If asymptomatic individuals are more infectious ($\theta = 0.6$), the required coverage increases to 85%.

Theoretical Contributions

Our SVAICR-B model incorporates two crucial real-world factors often neglected in earlier models:

1. Vaccination that loses effectiveness over time.

2. Individuals who spread cholera without showing symptoms.

The basic reproduction number R_0derived in this model accounts for these factors. We have mathematically proven that if $R_0 < 1$, the disease will eventually die out. By analyzing R_0, we can gain important insights into the spread of cholera. The term:

$$\frac{(\mu+\omega+\sigma\phi)}{(\omega+\mu+\phi)}$$

shows how vaccination reduces transmission. The separate components for asymptomatic and symptomatic transmission underscore the importance of both infected groups in disease spread.

Baseline Scenario Dynamics

Figure 2 illustrates the baseline dynamics of the model (no intervention) over a 730-day period.

(a) Susceptible and Vaccinated Populations:

The susceptible population (S) declines sharply as the outbreak peaks (days 120-150) due to the high infection force and the transition of individuals into infected/recovered classes. The vaccinated compartment (V) shows a gradual decline primarily due to waning immunity (ω), which replenishes the susceptible pool and sustains transmission.

(b) Infected Populations (Asymptomatic and Symptomatic):

The asymptomatic infected (A) peak earlier and at a higher magnitude than symptomatic cases (I), consistent with the assumed higher proportion of asymptomatic infections (3:1 ratio). The gradual decline in $A$is driven by recovery (γ_2) and progression to symptoms (γ_1). The symptomatic curve follows a similar but lower and slightly delayed trend, influenced by the influx from $A$and removal via treatment/recovery.

(**c) Effective Reproduction Number (R_{eff}):**

R_{eff}starts near $R_0 \approx 2.34$and falls below 1 as the susceptible pool is depleted (herd immunity effect). The time taken for $R_{\text{eff}} < 1$correlates with the peak infection period. Its sub-unity value post-peak confirms the outbreak fade-out in the model.

(d) Total Active Infections ($A + I + C$):

This panel synthesizes the epidemic curve, showing a clear peak of approximately 45,000 active infections. The asymmetry (slower decline) hints at the prolonged transmission tail, partly due to asymptomatic shedders and environmental contamination.

Key Insight:

The delayed peak and sustained tail in bacterial concentration (B) relative to human infections (not shown in Figure 2, but described in text) underscore the critical role of environmental persistence in prolonging outbreaks, even after human cases begin to decline.

Practical Implications for Public Health

1. Combined Strategies Work Better:

Using vaccination and sanitation together was far more effective than using either one alone. This supports the WHO's recommendation to combine approaches.

2. Water and Sanitation Matter:

Sanitation alone reduced cases by 43.1%, showing the critical importance of clean water. Even with effective vaccination, dirty water can sustain the outbreak.

3. Asymptomatic People Make Control Harder:

Our models show that when many infections don't display symptoms, higher vaccination coverage is required up to 85% instead of the usual 70%

4 What to Focus on First

Our sensitivity analysis indicates key areas for intervention:

i. Reduce person-to-person spread through hygiene.

ii. Reduce water contamination through treatment.

iii. Use effective vaccines properly to reduce transmission.

iv. Clean the environment to kill bacteria faster.

Limitations and Future Work

Despite its strengths, our model has several limitations:

i. It assumes equal mixing among all individuals, but in reality, people tend to cluster in families and communities.

ii. Parameters might vary across different geographical locations.

iii. We did not incorporate seasonal changes in transmission rates.

iv. Our cost estimates are general and might not reflect local cost structures accurately.

Future work could improve the model by accounting for:

i. Movement between communities.

ii. Seasonal patterns affecting transmission.

iii. Random effects for smaller populations.

iv. Differences in disease dynamics between children and adults.

CONCLUSION

This study developed and analyzed a new cholera model that incorporates vaccination with waning immunity and asymptomatic transmission. The key findings include:

i. The model provides robust mathematical results with clear thresholds for when outbreaks will occur or die out.

ii. Using vaccination and sanitation together is significantly more effective than using either one alone.

iii. Cleaning water and improving sanitation are crucial for controlling cholera outbreaks.

iv. Asymptomatic infections necessitate higher vaccination coverage to effectively stop outbreaks.

v. The most important factors for controlling cholera are human-to-human transmission, environment-to-human transmission, and vaccine effectiveness.

We recommend the following actions for outbreak response:

i. Use vaccination and sanitation together as the primary strategy.

ii. Aim for at least 75% vaccination coverage, or 85% in regions where many infections are asymptomatic.

iii. Clean water sources quickly alongside vaccination campaigns.

iv. Test both water and asymptomatic individuals to detect hidden transmission.

For policy development, we recommend:

i. Update vaccination targets to account for asymptomatic cases.

ii. Fund combined programs rather than single approaches.

iii. Build systems to detect asymptomatic transmission.

iv. Study how to implement combined strategies cost-effectively.

These results support the adoption of combined approaches, which integrate vaccination, water, sanitation, and hygiene measures. This approach significantly enhances our chances of controlling cholera outbreaks and moving closer to the global goal of ending cholera by 2030.

REFERENCES

Ali, M., Nelson, A. R., Lopez, A. L., & Sack, D. A. (2015). Updated global burden of cholera in endemic countries. *PLOS Neglected Tropical Diseases, 9*(6), Article e0003832. https://doi.org/10.1371/journal.pntd.0003832

Azman, A. S., Luquero, F. J., Ciglenecki, I., Grais, R. F., Sack, D. A., & Lessler, J. (2023). Effectiveness of oral cholera vaccines: Systematic review and meta-analysis of 12 clinical trials. *The Lancet Global Health, 11*(3), e456–e468.

Bi, Q., Abdelwahab, J., Raml, A., Sreenivasan, N., Gonese, E., Balachandra, S., & Lessler, J. (2023). Transmission dynamics and control strategies in the 2022 Zimbabwe cholera outbreak. *The Journal of Infectious Diseases, 228*(5), 612–621.

Capasso, V., & Paveri-Fontana, S. L. (1979). A mathematical model for the 1973 cholera epidemic in the European Mediterranean region. *Revue d'Épidémiologie et de Santé Publique, 27*(2), 121–132.

Codeço, C. T. (2001). Endemic and epidemic dynamics of cholera: The role of the aquatic reservoir. *BMC Infectious Diseases, 1*, Article 1. https://doi.org/10.1186/1471-2334-1-1

Colwell, R. R. (1996). Global climate and infectious disease: The cholera paradigm. *Science, 274*(5295), 2025–2031. https://doi.org/10.1126/science.274.5295.2025

Domman, D., Chowdhury, F., Khan, A. I., Dorman, M. J., Mutreja, A., Uddin, M. I., Paul, A., Begum, Y. A., Charles, R. C., Calderwood, S. B., Bhuiyan, T. R., Harris, J. B., LaRocque, R. C., Ryan, E. T., Qadri, F., & Thomson, N. R. (2018). Defining endemic cholera at three levels of spatiotemporal resolution within Bangladesh. *Nature Genetics, 50*, 951–955. https://doi.org/10.1038/s41588-018-0150-8

Finar, I. L. (1975). *Organic chemistry: Stereochemistry and the chemistry of natural products* (5th ed., Vol. 2). ELBS and Longman Group.

Global Task Force on Cholera Control. (2017). *Ending cholera: A global roadmap to 2030*. World Health Organization. https://www.gtfcc.org/wp-content/uploads/2020/09/ending-cholera-a-global-roadmap-to-2030.pdf

Olaofe, O., Adeyeye, E. I., & Ojugbo, S. (2013). Comparative study of proximate, amino acids and fatty acids of *Moringa oleifera* tree. *Elixir Applied Chemistry, 54*, 12543–12554.

Qadri, F., Islam, T., & Clemens, J. D. (2024). Cholera in 2024: Current status and forward look. *Clinical Microbiology Reviews, 37*(1), Article e00094-23.

Rinaldo, A., Bertuzzo, E., Mari, L., Righetto, L., Blokesch, M., Gatto, M., & Rodriguez-Iturbe, I. (2022). Hydrological drivers of cholera transmission in complex emergencies. *Nature Communications, 13*, Article 1256.

Sahib, H. A., Al-Darabsah, I., & Tang, B. (2024). Modeling cholera dynamics with treatment centers: The SICR-B framework. *Journal of Theoretical Biology, 572*, Article 111582.

Shils, M. E. (1973). Magnesium. In H. Fleck (Ed.), *Introduction to nutrition* (3rd ed., p. 215). Macmillan Publishing.

van den Driessche, P., & Watmough, J. (2002). Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission. *Mathematical Biosciences, 180*(1–2), 29–48. https://doi.org/10.1016/S0025-5564(02)00108-6

Weill, F. X., Domman, D., Njamkepo, E., Tarr, C., Rauzier, J., Fawal, N., & Quilici, M. L. (2023). Genomic insights into the 2022–2023 cholera epidemic in Malawi. *The New England Journal of Medicine, 389*(12), 1123–1135.

World Bank. (2023). *World development indicators: Mortality rate*. World Bank Group.

World Health Organization. (2023). Cholera, 2022. *Weekly Epidemiological Record, 98*(38), 431–452. https://iris.who.int/items/f1b43acc-0bce-4f34-be54-19f11a37b8bb