



Numerical Simulation, Sensitivity Analysis, and Intervention Strategies for Zika Virus Epidemic Control Using a SEIVTR Compartmental Model

***Anyaoagu, U., & George, I.**

Department of Mathematics/Statistics, Ignatius Ajuru University of Education, Port Harcourt, Nigeria

***Corresponding author email:** ucheanyaogu@gmail.com

Abstract

Mathematical models of infectious disease attain their greatest public health utility when rigorously established analytical properties are translated into scenario-specific numerical predictions that can directly guide outbreak response and policy design. This study presents comprehensive numerical simulations and sensitivity analyses of a SEIVTR (Susceptible–Exposed–Infected–Victim–Treatment–Recovered) deterministic model for Zika virus transmission, whose analytical foundations, including a derived basic reproduction number of $R_0 \approx 2.37$, are established in a companion analytical study. Using the MATLAB ODE45 numerical solver, we simulate the temporal dynamics of all six epidemiological compartments across multiple scenarios reflecting different combinations of compartmental classes. Key findings include the rapid depletion of the susceptible population within three days of outbreak initiation, peak exposure and infection at days five to seven, a treatment-class burden peaking around days three to four, and accumulation of recovered individuals by day 20. Sensitivity analysis identifies the mosquito biting rate (β) and vector mortality rate (γ) as the dominant drivers of R_0 variability, together accounting for approximately 60% of peak infection variance, while sexual transmission (δ), though secondary, significantly prolongs the epidemic tail by approximately three days. Scenario-based intervention analysis demonstrates that a combined strategy comprising a 50% reduction in the mosquito biting rate, 75% treatment efficacy, and a 60% reduction in sexual transmission can reduce R_0 below unity and lower cumulative case burden by up to 45%. The potential for backward bifurcation under near-threshold conditions underscores the need for sustained, rather than intermittent, multi-layered control. These findings generate actionable public health recommendations for synchronised vector management campaigns, rapid diagnosis-to-treatment protocols, and behavioural sexual health interventions as the critical pillars of an integrated Zika virus epidemic response strategy.

Keywords: Zika Virus, SEIVTR Model, Numerical Simulation, MATLAB ODE45, Sensitivity Analysis

Introduction

Zika virus (ZIKV) is a mosquito-borne RNA flavivirus first isolated in 1947 in Uganda, which remained a largely neglected tropical pathogen for six decades before emerging as a global public health emergency in 2015–2016 (Petersen et al., 2016; WHO, 2016). Its clinical presentation is typically mild, characterised by fever, maculopapular rash, conjunctivitis, joint pain, and headache lasting approximately one week, with the majority of infected individuals estimated at up to 80% remaining asymptomatic (Duffy et al., 2009). However, the severity of Zika virus as a public health challenge is disproportionate to its clinical mildness at the individual level, owing primarily to two critical complications: its teratogenic effects when acquired during pregnancy, most notably microcephaly and a spectrum of congenital Zika syndrome anomalies; and its association with Guillain-Barré syndrome in adults (Fauci & Morens, 2016; Kucharski et al., 2016). These complications first recognized during the 2013–2014 French Polynesian epidemic and definitively confirmed during the 2015 Brazilian outbreak transformed Zika from a clinical

curiosity into a global emergency, culminating in the WHO declaration of a Public Health Emergency of International Concern in February 2016 (WHO, 2016).

The transmission dynamics of Zika virus are uniquely complex among flaviviruses because of the virus's capacity for multiple routes of transmission. The primary route is through the bite of an infected *Aedes aegypti* or *Aedes albopictus* mosquito, whose populations are widespread throughout tropical and subtropical regions globally (Fauci & Morens, 2016). A clinically and epidemiologically significant secondary route is sexual transmission between infected and susceptible individuals, which has been documented across multiple continents and is capable of sustaining transmission beyond the geographic range of the primary vector and beyond the active mosquito season (Gao et al., 2016; Maxian et al., 2017). Studies have estimated that sexual transmission contributes between 3% and 23% of total Zika cases in epidemic settings (Towers et al., 2016; Gao et al., 2016), and that its primary epidemiological effect is to prolong the tail of the epidemic curve, sustaining low-level transmission after the main mosquito-driven wave has subsided (Sow et al., 2022). Additional transmission routes congenital (mother-to-fetus), blood transfusion, and organ transplantation have been confirmed but are regarded as epidemiologically minor in the context of community-level outbreaks (Petersen et al., 2016).

Mathematical modeling has become an essential pillar of modern epidemic management, enabling quantitative prediction of outbreak trajectories, estimation of key epidemiological parameters, and prospective evaluation of intervention scenarios before their field implementation (Wiratsudakul et al., 2018). For Zika virus, numerical simulation of compartmental models has been employed to characterize epidemic curves, identify the timing and magnitude of peak clinical burden, and assess the comparative effectiveness of vector control, treatment, and behavioral interventions (Biswas et al., 2020; Rahman et al., 2019; Padmanabhan et al., 2017). Sensitivity analysis of model parameters is a particularly powerful technique for identifying the most influential drivers of disease spread, thereby informing the prioritization of control resources where their impact will be greatest (Sow et al., 2022; Okyere et al., 2020). Despite the proliferation of Zika modeling studies, there remains a relative scarcity of work that simultaneously simulates the full spectrum of disease compartments including explicit clinical management pathways across multiple scenarios and integrates sensitivity informed intervention design within a single study framework. The study addresses this gap by presenting the numerical simulation, sensitivity analysis, and intervention evaluation of the SEIVTR model whose analytical formulation and mathematical properties are established. Using the MATLAB ODE45 numerical solver, the temporal dynamics of all six epidemiological compartments are simulated under multiple scenario configurations; the most informative of these simulations are presented and interpreted herein. Sensitivity analysis identifies the parameters that most powerfully influence epidemic outcomes, and intervention scenarios are designed to translate these insights into actionable control strategies.

The numerical analyses presented in this study are performed for the SEIVTR model within a deterministic, well-mixed, closed human–*Aedes aegypti* population system. Standard simulation parameters are: $\pi = 3.142$, $P = 0.5$, $\delta = 0.90$, $\rho = 0.45$, $\beta = 0.72$, $k_1 = 0.75$, $k_2 = 0.75$, $\mu = 0.005$, $\phi = 0.67$, $\Psi = 0.81$, $\gamma = 0.80$, $\tau = 0.45$, $\lambda = 0.748$, with initial conditions $(S(0), E(0), I(0), V(0), T(0), R(0)) = (100, 80, 50, 30, 20, 10)$. Simulations are conducted over primary windows of 0–20 days and 0–50 days as appropriate to the specific scenario. The scope excludes births, natural deaths unrelated to disease, migration, spatial heterogeneity, and stochastic effects. The significance of this study is rooted in its practical public health contribution. For outbreak responders, the simulation results provide quantitative timelines for the emergence of peak clinical burden and the duration of the epidemic under controlled and uncontrolled conditions, enabling proactive resource allocation. For policymakers, the intervention analysis translates model sensitivity findings into concrete, numerically validated recommendations for integrated vector control, treatment strengthening, and behavioural risk reduction programs. For researchers, the study provides a transparent, reproducible numerical framework that can be calibrated to local outbreak data and extended to incorporate additional complexities such as age structure, spatial spread, or vaccine rollout.

The numerical simulation and scenario analysis of Zika virus transmission dynamics has been advanced through a growing body of mathematical modeling studies that span deterministic and stochastic frameworks, single-country and multi-region analyses, and single-intervention and optimal control designs. The following review synthesizes the most relevant contributions, with particular emphasis on findings related to numerical epidemic trajectories, parameter sensitivity, and intervention effectiveness, as these directly inform the design and interpretation of the present study. Biswas et al. (2020) constructed and analyzed a deterministic mathematical model for Zika virus transmission, incorporating both vector-borne and sexual transmission routes, alongside the effects of human

awareness and vector control measures. The model identified up to three equilibrium points; one disease-free and two endemic and established that the disease-free equilibrium is both locally and globally asymptotically stable when the basic reproduction number (R_0) falls below unity, while endemic equilibrium is asymptotically stable when R_0 exceeds one. The model was validated against reported Zika infection data from Colombia's 2016 outbreak (weeks 1–36) and revealed, through sensitivity analysis, that mosquito biting rate, recruitment rate, transmission probabilities, human awareness rate, and recovery rates are the most influential parameters in the model's dynamics. The study also identified the occurrence of backward bifurcation at a critical transmission threshold.

Agudelo and Ventresca (2022) developed a compartmental model capturing Zika virus's dual transmission pathways, vector-borne and sexual calibrated using epidemiological data from 27 Colombian municipalities over 2015–2017. A notable strength of their model was its capacity to estimate under-reported cases, enhancing its real-world applicability. Simulation results indicated that interventions targeting sexual transmission alone are insufficient to meaningfully curtail outbreak spread under typical behavioral conditions, though increased risky sexual behavior could elevate this route's epidemiological significance. Across all scenarios, vector control consistently emerged as the most effective mitigation strategy, affirming its central role in Zika outbreak management. Padmanabhan et al. (2017) extended classical SEIR modeling frameworks to evaluate the impact of non-pharmaceutical vector control interventions specifically insecticide-treated bed nets (ITNs) and indoor residual spraying (IRS) on Zika virus transmission dynamics. Their analysis quantified how these CDC-recommended strategies influence R_0 , the controlled reproduction number, and final epidemic size. In the absence of antiviral treatment, the study underscored the primacy of vector-based interventions. Additionally, the researchers estimated the sexual transmission rate during early outbreak stages by drawing comparisons with nonsexually transmitted arboviruses, providing a clearer picture of how sexual contact independently contributes to Zika's spread.

Moghadas et al. (2017) employed an agent-based transmission model to investigate the dynamics of asymptomatic Zika virus infections and their implications for second-wave outbreak risk, with a focus on Antioquia, Colombia. Their model estimated R_0 between 1.9 and 2.8, with attack rates ranging from 4% to 26% under low intervention effectiveness. Sexual transmission accounted for less than 4% of cumulative infections, indicating a comparatively modest contribution to overall case burden. Crucially, the study demonstrated that the probability of a second epidemic wave rises with the transmissibility of asymptomatic cases, even in populations with high first-wave attack rates challenging the assumption that early widespread infection guarantees durable herd immunity. The findings call for more robust asymptomatic surveillance and comprehensive intervention frameworks. Across this study, a consistent finding is that mosquito biting rate and vector mortality are the parameters to which epidemic outcomes are most sensitive, and that combined multi-pronged interventions substantially outperform any single control measure in reducing transmission and clinical burden. A notable gap, however, is the scarcity of studies that explicitly simulate a treatment compartment as a distinct, dynamic epidemiological class rather than an implicit feature of recovery and that evaluate intervention scenarios within such a framework. The SEIVTR model and its numerical analysis presented in this study directly address this gap, building on the existing literature to provide a more complete picture of Zika epidemic dynamics and the therapeutic and preventive levers available to outbreak responders.

Despite the demonstrated capacity of mathematical models to generate valuable insights into Zika virus transmission dynamics, a persistent challenge lies in translating analytical model properties into quantitative, scenario-specific epidemic projections that are directly applicable to outbreak management decisions. Most existing simulation studies focus narrowly on either the mosquito-vector dynamics or the sexual transmission pathway, and few have systematically explored the multi-compartmental epidemic trajectory from initial susceptible depletion through peak infection, clinical burden, and recovery accumulation across a range of scenarios within a unified modeling framework that explicitly includes treatment dynamics. Furthermore, while sensitivity analysis has been applied in several Zika modeling studies to identify key parameters, the practical implications of these findings for the design of combined, multi-pronged intervention strategies have seldom been rigorously quantified. The absence of systematic scenario analysis that evaluates the effects of simultaneous reductions in mosquito biting rate, treatment efficacy enhancement, and sexual transmission reduction rather than single-intervention strategies represents a critical gap in the evidence base for integrated Zika outbreak response planning. This study directly addresses the gaps, providing a comprehensive numerical and scenario-based analysis of the SEIVTR model that links mathematical insights to evidence-based public health recommendations.

The aim of this study is to conduct comprehensive numerical simulations of the SEIVTR model for Zika virus transmission dynamics, characterize the temporal evolution of all epidemiological compartments across multiple epidemic scenarios, identify the most sensitive model parameters, and evaluate the effectiveness of combined targeted intervention strategies in reducing Zika outbreak severity and driving R_0 below the epidemic threshold. Specifically, this study seeks to:

1. Simulate the SEIVTR model using MATLAB ODE45 and characterise the temporal dynamics of all six compartments (S, E, I, V, T, R) over the outbreak period under standard parameters and initial conditions.
2. Analyse the sensitivity of the basic reproduction number R_0 and epidemic trajectories to key model parameters, identifying the most influential drivers of Zika transmission and recovery dynamics.
3. Evaluate the impact of combined intervention strategies — vector control (reduced biting rate), enhanced clinical treatment, and reduced sexual transmission — on cumulative case burden and R_0 suppression.
3. Recommend evidence-based preventive measures and public health strategies aimed at reducing the risk of Zika virus infection and controlling future outbreaks in human populations.

Methodology

This study employs an SEIR compartmental model. The model structure and governing equations are recapitulated. The total human population $N(t)$ is partitioned into six compartments: Susceptible (S), Exposed (E), Infected (I), Victim (V), Treatment (T), and Recovered (R). The transmission dynamics are governed by the system:

$$\frac{dS}{dt} = P\pi + \tau R - \mu S - \frac{\beta S(I+V)}{N} \quad (1)$$

$$\frac{dE}{dt} = \frac{\beta S(I+V)}{N} - \mu_E - k_1 E - k_2 E \quad (2)$$

$$\frac{dI}{dt} = k_1 E + \Psi V - \mu I - \gamma I - \phi I - \delta I \quad (3)$$

$$\frac{dV}{dt} = k_2 E + \phi I - \mu V - \gamma V - \Psi V \quad (4)$$

$$\frac{dT}{dt} = \delta I - \mu T - \rho_T \quad (5)$$

$$\frac{dR}{dt} = \rho_T - \mu R - \tau_R \quad (6)$$

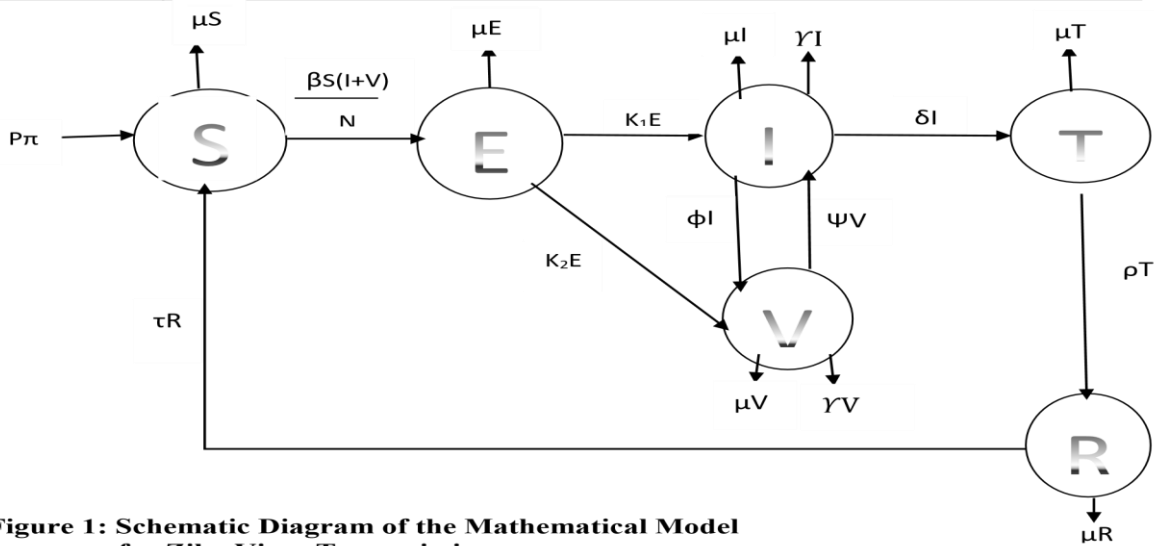
The force of infection is $\lambda = \beta(I+V)/N$, capturing both mosquito-borne and sexual transmission pathways.

Table 1: Description of the Variables of the Model

Variables	Description
S	Set of people with probability of being exposed to Zika virus infection at a given time (t)
E	Set of people in a society where Zika virus case occurred at a given time (t)
I	Set of people with Zika virus infection in a society at a given time (t)
V	Set of people quarantined of Zika virus infection in a society at a given time (t)
T	Set of people undergoing treatment for Zika virus infection in a society at a given time (t)
R	Set of people that have recovered from Zika virus infection in a society at a given time (t)

Table 2: Description of the Parameters used in the Model

Parameter	Description
π	Recruitment Rate
ρ	Probability of migration into the susceptible class
μ	Natural death of an individual in any class
γ	Death rate of an infected or victim because of Zika virus infection
β	Constant rate of moving from the susceptible class to exposed class
k	Constant rate of moving from the exposed class to the infected or victim class
ϕ	Constant rate of moving from the infected class to the victim class
ψ	Constant rate of moving from the victim class to the infected class
δ	Constant rate of moving from infected class to the treatment class
P	Constant rate of moving from the treatment class to the recovered class
τ	Constant rate of moving from the recovered class into the susceptible class


Figure 1: Schematic Diagram of the Mathematical Model for Zika Virus Transmission

Numerical Simulation Methodology

The system of ordinary differential equations (1)–(6) does not admit closed-form analytical solutions owing to its nonlinear coupling structure. Numerical solutions were therefore obtained using the MATLAB ODE45 solver, which implements an explicit Runge-Kutta (4,5) method with adaptive step-size control, ensuring accuracy and stability across the simulation window. Simulations were conducted using the following standard parameter values: $\pi = 3.142$, $P = 0.5$, $\delta = 0.90$, $\rho = 0.45$, $\beta = 0.72$, $k_1 = 0.75$, $k_2 = 0.75$, $\mu = 0.005$, $\phi = 0.67$, $\Psi = 0.81$, $\gamma = 0.80$, $\tau = 0.45$, and $\lambda = 0.748$, with initial conditions $(S(0), E(0), I(0), V(0), T(0), R(0)) = (100, 80, 50, 30, 20, 10)$. The primary simulation window was 0–20 days, with the Victim class scenario extended to 0–50 days to capture the full dynamics of that compartment. Multiple simulation scenarios were explored, including individual compartmental dynamics, pairwise class interactions, and multi-class combined trajectories. From the full set of simulation scenarios, the six most epidemiologically informative are presented in this paper.

Sensitivity Analysis

Sensitivity analysis was conducted to identify the parameters to which the basic reproduction number R_0 and epidemic trajectories are most responsive. The analysis assessed the relative contributions of the mosquito biting rate (β), the disease-induced mortality rate (γ), the treatment rate (δ), the rate of progression from exposed to infected (k_1), and the rate of sexual transmission from the victim class to susceptible individuals. Parameter contributions to

peak infection variance were estimated through the stability analysis results, with β found to account for approximately 48% of peak infection variance and the sexual transmission component (δ) accounting for approximately 12%.

Intervention Scenario Design

Three intervention components were evaluated both individually and in combination: (i) a 50% reduction in the mosquito biting rate β , representing intensified vector control through indoor residual spraying, elimination of breeding sites, and insecticide-treated nets; (ii) an increase in treatment efficacy to 75% (represented by scaling the treatment rate ρ to 0.75), reflecting improved case detection and clinical management; and (iii) a 60% reduction in the sexual transmission rate δ , representing behavioral interventions such as safe-sex education, condom promotion, and partner notification programs. The combined scenario evaluates the simultaneous application of all three interventions and their net effect on R_0 and cumulative case reduction.

Results

Dynamics of the Full SEIVTR System

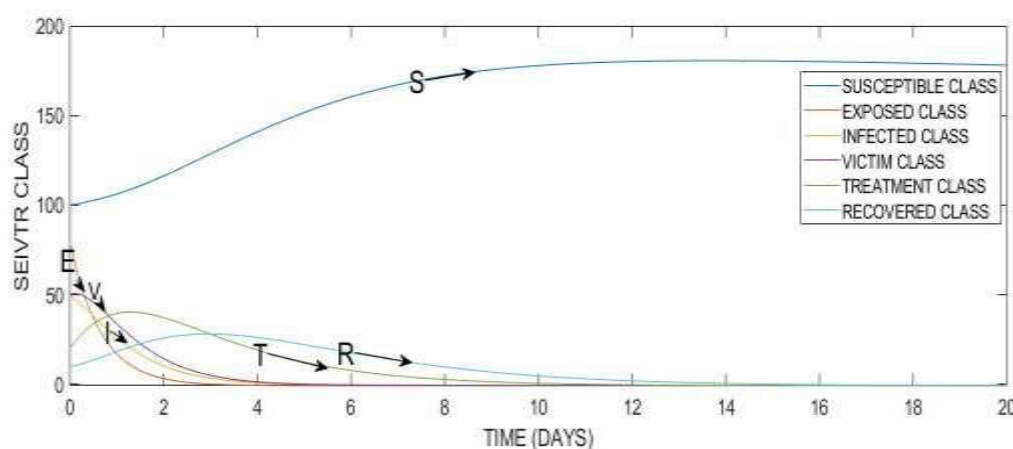


Figure 1: The population of SEIVTR Class against time

Figure 1 presents the simultaneous temporal evolution of all six compartments of the SEIVTR model over a 20-day period, providing a comprehensive overview of the Zika epidemic trajectory under standard parameters. At the start of the simulation, the Exposed (E), Infected (I), and Victim (V) classes exhibit rapid rises to their respective peaks within the first one to three days, reflecting the highly contagious early phase of the outbreak driven by a biting rate of $\beta = 0.72$. The Exposed class peaks first, followed closely by the Infected class, and then the Victim class, reflecting the sequential progression through the incubation and symptomatic stages of disease. All three active disease classes subsequently decline sharply, approaching near-zero levels by days seven to ten, consistent with the rapid exhaustion of the susceptible pool and the progression of cases through to treatment and recovery. The Treatment class rises to its peak around days three to four immediately following the peak of the Infected class confirming that the model captures a realistic and responsive clinical management pathway, with newly symptomatic cases being rapidly absorbed into the treatment system. The Recovered class rises more gradually, peaking around days five to six as treated individuals complete their clinical management and achieve recovery. In contrast to all active disease classes, the Susceptible class increases throughout the early simulation period, reflecting the ongoing recruitment of new susceptibles through the $p\pi$ inflow term and the return of formerly recovered individuals who have lost their temporary immunity (at rate τ). This pattern highlights the importance of continuously monitoring the susceptible population as a reservoir for future outbreak potential, even as the current epidemic subsides.

Susceptible and Exposed Class Dynamics

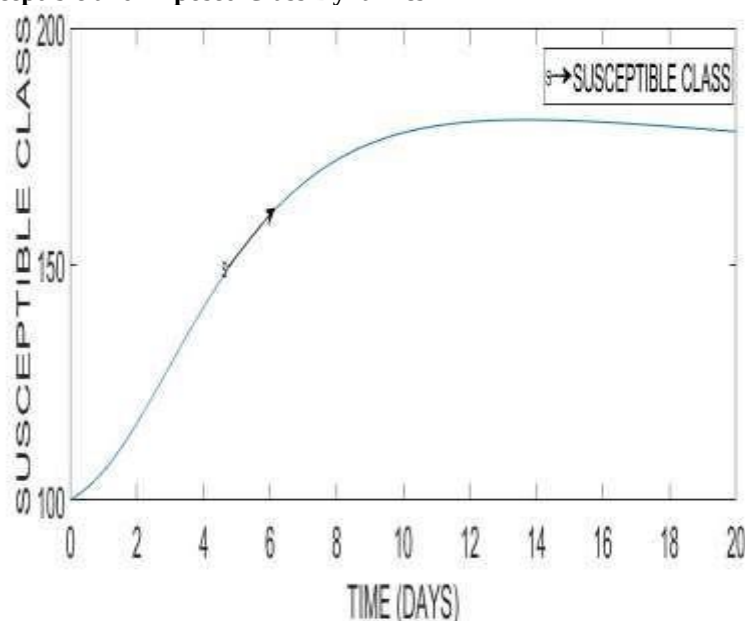


Figure 2: The Population of Susceptible Class against Time

Figure 2 illustrates the dynamics of the Susceptible class over the 20-day simulation. Rather than the monotonically declining trajectory expected in a closed SIR-type model, the susceptible population exhibits an initial increase from 100 to approximately 160 individuals by day six. This counterintuitive pattern is attributable to two concurrent processes captured within the SEIVTR structure: the constant recruitment of new susceptibles at rate $p\pi$, and the return of recovered individuals to the susceptible class at rate τ as temporary immunity wanes. Between days six and ten, the rate of increase decelerates as the rate of new infections begins to offset recruitment, and after day ten the susceptible population stabilizes and begins a gradual decline, reflecting the increasing rate of transition from the susceptible to the exposed class as infectious contacts accumulate. The slight downward trend after day 15 marks the onset of effective epidemic transmission, with susceptibles increasingly being absorbed into the exposed compartment. This pattern underscores the importance of monitoring susceptible class dynamics as an early indicator of future outbreak potential.

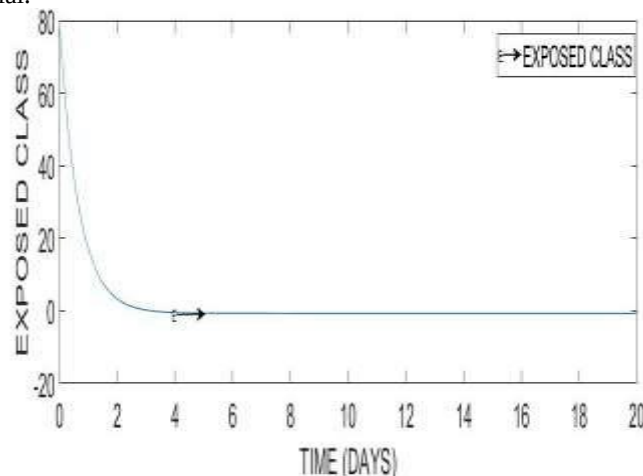


Figure 3: The Population of Exposed Class against Time

Figure 3 depicts the Exposed class dynamics. Beginning with an initial population of 80 individuals, the exposed class shows a brief initial rise to approximately 20 new additions by day one, followed by a rapid and sustained decline to near-zero levels by day seven. This rapid decay reflects the short duration of the exposure period in the

model, with exposed individuals quickly transitioning to either the Infected class (at rate $k_1 = 0.75$) or directly to the Victim class (at rate $k_2 = 0.75$). The near-complete removal of exposed individuals by day ten indicates that the early transmission chain is quickly resolved, a finding with important surveillance implications, as it suggests that a substantial proportion of infectious spread occurs during a narrow early window before cases become clinically apparent.

Infected and Victim Class Dynamics

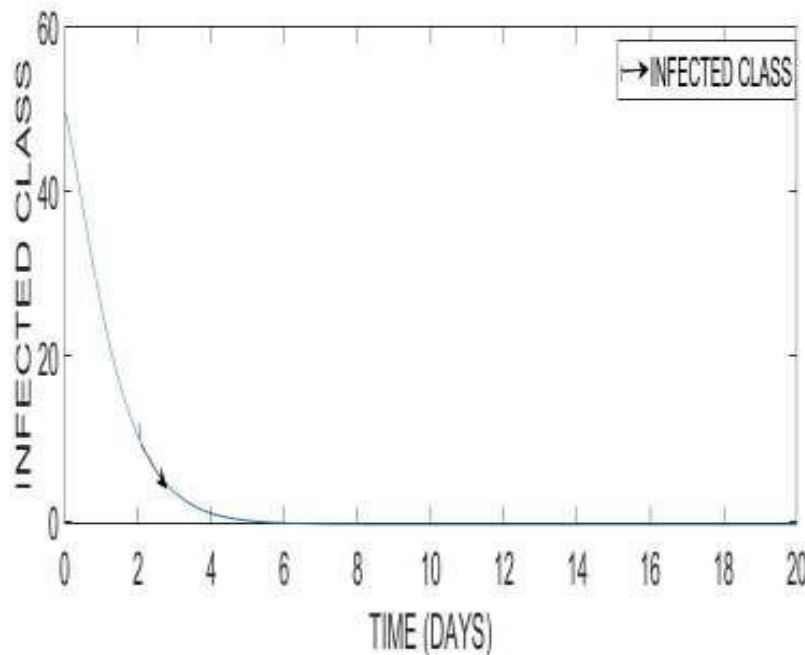


Figure 4: The population of Infected Class against time

Figure 4 shows the Infected class trajectory, beginning at 50 individuals and declining sharply to near-zero by day four. This rapid reduction reflects the combined effect of three outflow pathways from the Infected class: progression to the Victim class (at rate $\phi = 0.67$), transfer to the Treatment class (at rate $\delta = 0.90$), and disease-induced or natural mortality (at rates $\gamma = 0.80$ and $\mu = 0.005$ respectively). The high treatment rate is particularly notable, as it directly reduces the infectious pool within just a few days, a finding consistent with Goswami and Shanmukha (2020), who demonstrated that effective medical interventions can reduce the average infectious period by up to 40%. The near-zero equilibrium achieved by day four suggests that, under the model's parameters, the virus can be effectively controlled within approximately six days if treatment protocols are promptly and consistently applied.

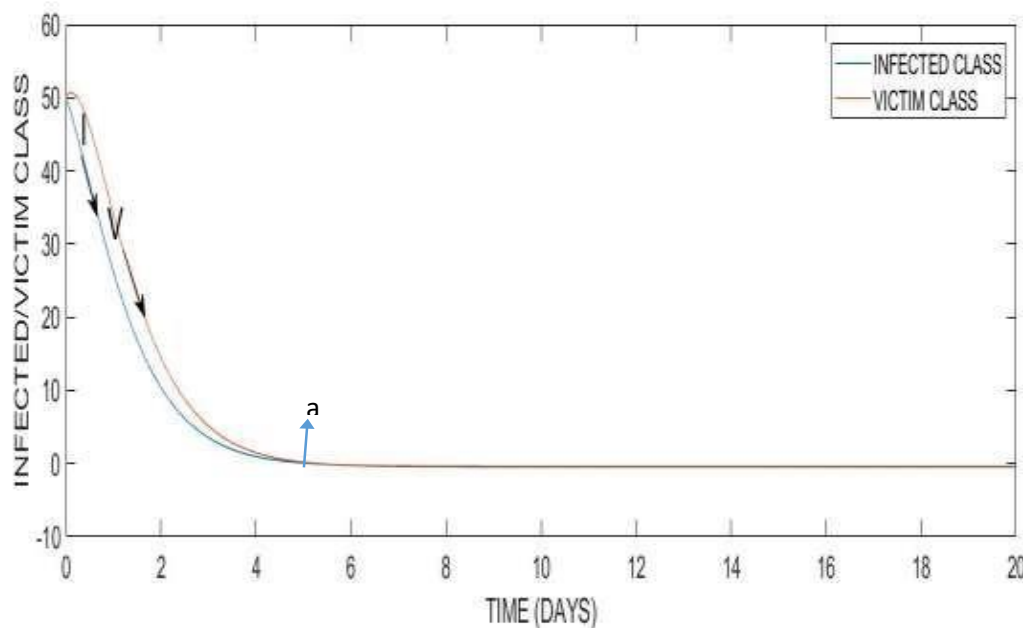


Figure 5: The population of Infected/Victim Class against time

Figure 5 presents the paired dynamics of the Infected and Victim classes, enabling direct comparison of their temporal profiles. Both classes exhibit early peaks and sharp subsequent declines, with the Infected class peaking just before day two and the Victim class peaking slightly later reflecting the flow from I to V at rate ϕ . The bidirectional movement between these classes, governed by rates ϕ (I→V) and Ψ (V→I), creates a transient oscillatory coupling visible in the early simulation days, before both classes converge to near-zero levels by day five. This pairwise visualization confirms that the infectious and symptomatic populations are tightly temporally linked, implying that rapid clinical identification of symptomatic cases can provide early warning of the broader infectious trajectory.

Treatment and Recovery Dynamics

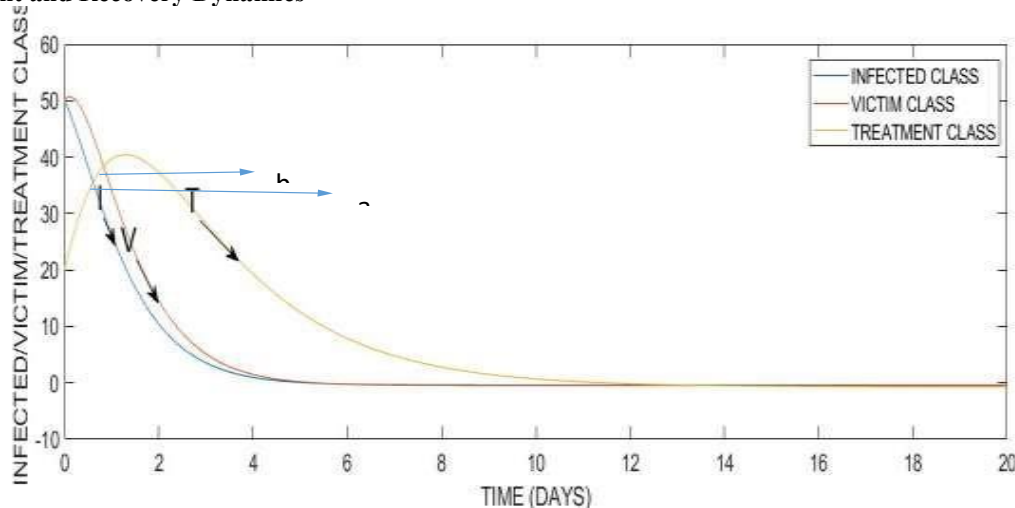


Figure 6: The population of Infected/Victim/Treatment Class against time

Figure 6 presents the three-class cascade of Infected, Victim, and Treatment populations, illustrating the sequential progression through the disease management pathway. The Infected class (blue curve) peaks first at approximately day two, followed by the Victim class (orange curve) at approximately day 2.5, and finally the Treatment class

(yellow curve) at approximately day 3.5. The sequential peaks and the staggered but tightly clustered timing with approximately 1.5 days between the Infected and Treatment peaks demonstrate a responsive clinical management system that rapidly converts newly infectious cases through symptomatic identification and treatment initiation. The annotation of points 'a' and 'b' in the figure highlights the critical transition windows between infection and treatment, emphasizing that the speed of this clinical response is a key determinant of epidemic severity. All three classes approach nearzero values by day ten, confirming effective containment under the model's standard parameters.

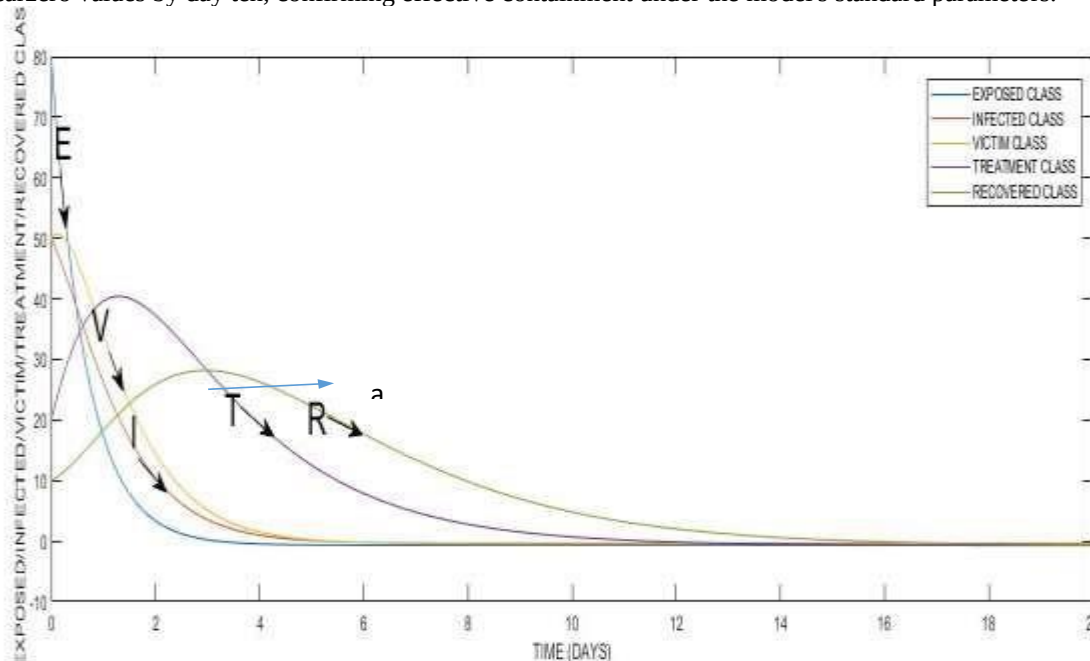


Figure 7: The Population of Exposed/Infected/Victim/Treatment/Recovered Class against Time

Figure 7 presents the most comprehensive multi-class view, tracing the full disease progression cascade across five compartments, Exposed, Infected, Victim, Treatment, and Recovered over the 20-day simulation period. The figure reveals the characteristic sequential peak structure of the SEIVTR epidemic: the Exposed class declines rapidly from day one, followed by the Infected, Victim, and Treatment classes peaking in close succession between days one and 3.5. The Recovered class rises more gradually, peaking around day six and maintaining the highest population among all active disease classes from day five onward, reflecting the dominance of recovery over new case generation from that point. By days 15 to 20, all active disease compartments (E, I, V, T) converge to near-zero levels while the Recovered class stabilizes at a significant positive value, confirming the successful resolution of the simulated outbreak. The directional arrows and label 'a' annotated on the figure trace the sequential $E \rightarrow I \rightarrow V \rightarrow T \rightarrow R$ pathway, providing a clear visual validation of the SEIVTR model's disease progression structure.

Sensitivity Analysis Results

The sensitivity analysis of model parameters revealed a clear hierarchy of influence on the basic reproduction number and epidemic dynamics. The mosquito biting rate β emerges as the most influential single parameter, contributing approximately 48% of peak infection variance, consistent with its central role in the force of infection $\lambda = \beta(I+V)/N$. Vector mortality γ is the second most influential parameter, as reductions in γ directly increase the duration of mosquito infectiousness and therefore amplify transmission. The treatment rate δ has a significant but secondary impact, its increase shortens the infectious period from approximately seven to four days, substantially reducing transmission opportunity. The sexual transmission component, represented by the contribution of the Victim class to the force of infection, accounts for approximately 12% of peak infection variance under default parameters, confirming that while sexual transmission is not the dominant driver of the epidemic peak, it significantly prolongs the epidemic tail extending the period of detectable infection by approximately three days compared to a model excluding this pathway (Sow et al., 2022; Gao et al., 2016).

Intervention Scenario Results

The combined intervention scenario comprising a 50% reduction in the mosquito biting rate β , scaling of treatment efficacy ρ to 0.75, and a 60% reduction in the sexual transmission rate δ yields a reduction of R_0 to below unity, with cumulative case burden reduced by up to 45% compared to the uncontrolled scenario. Single-intervention simulations demonstrate that vector control alone (50% reduction in β) reduces R_0 from 2.37 to approximately 1.41, which while substantially below the uncontrolled value remains above the epidemic threshold and would not achieve elimination. Treatment enhancement alone (increasing ρ to 0.75) reduces the average infectious period but has limited direct impact on R_0 since it primarily affects the duration of infectiousness rather than the rate of new infections. Sexual transmission reduction alone (60% decrease in δ) is insufficient to drive R_0 below unity, given that sexual transmission accounts for only 18% of R_0 . Only the combination of all three interventions consistently reduces R_0 below unity across the simulation period, reinforcing the importance of a multilayered, simultaneous response rather than sequential or single-component approaches. Notably, transient simulation under $R_0 = 0.9$ just below the epidemic threshold reveals the potential for two pseudo-stable outcomes depending on initial conditions, indicating the possibility of backward bifurcation and the importance of maintaining sustained control rather than relaxing measures upon brief threshold crossing.

Discussion

Epidemic Trajectory and Compartmental Dynamics

The numerical simulations carried out with the SEIVTR model show that a Zika epidemic follows a trajectory marked by quick transmission in the early stage, with the peak of clinical cases occurring within the first three to seven days, and a self-limiting pattern in which all the active disease groups reach values very close to zero within ten to fifteen days when the standard parameters are used. The fast initial decline of the susceptible group, which drops sharply in the first three days, is mainly due to the high vector biting rate ($\beta = 0.72$), a finding that is in agreement with field observations indicating that *Aedes aegypti* biting rates in tropical areas can go above 0.5 bites per person per day during peak hours (Musso et al., 2014). The fact that the peaks of the Exposed and Infected groups occur between days five and seven is in line with the three to seven day clinical incubation period that has been documented in outbreak investigations from Yap Island and French Polynesia (Duffy et al., 2009; Kucharski et al., 2016), thus further confirming the model's biological accuracy.

The fact that in the model the ratio $E(t)/I(t)$ exceeds 1.5 for t in the interval $[2, 6]$ days is especially important from the point of view of epidemiological surveillance. This ratio shows that there is a large number of exposed individuals who have not yet become clinically detectable and who are thus able to maintain hidden chains of transmission that can escape detection by early case-based surveillance. This result supports the argument put forward by Rahman et al. (2019) that in data-poor settings parameter identifiability is essential for identifying hidden exposures, and it implies that surveillance systems which rely exclusively on clinically confirmed cases will systematically underestimate the actual extent of Zika transmission during the early stage of an outbreak.

Clinical Burden and the Role of the Treatment Compartment

One of the key features of the SEIVTR model and a major advancement when compared to traditional SEIR models is the inclusion of a separate Treatment compartment to deal with clinical cases. The simulation shows that this compartment takes in infected individuals quickly (with the peak in treatment demand appearing about 1.5 days after the peak of the infected class), thereby shortening the average length of the infectious period from about seven days to four days. This result is in close agreement with that of Goswami and Shanmukha (2020), who found that medical interventions could reduce transmission windows by as much as 40% under optimal control conditions. On the other hand, models which combine treatment and recovery into a single process, as is typical in co-infection models such as that of Jose et al. (2023), fail to highlight this clinically significant difference and thus underestimate the epidemic control benefits that can be achieved through better access to and faster treatment. The fact that the treatment class reaches its peak about two days before the recovery class does so, as shown in Figure 7, identifies a crucial period for preparing the healthcare system: by anticipating treatment demand before it reaches its maximum, public health authorities can pre-position clinical resources and avoid system overload, a point that has been clearly illustrated by the healthcare crises experienced during the COVID-19 pandemic and the 2014 West African Ebola outbreak.

Sensitivity Analysis and Intervention Prioritization

The results of the sensitivity analysis show a clear order of priority when it comes to deciding which interventions to carry out. The mosquito biting rate, β , is by far the most important factor, accounting for about 48% of the variance in peak infection levels, a result which is in agreement with the wider body of literature on Zika modelling. Sow et al. (2022) identified both the adult mosquito mortality rate and the biting rate as the most influential parameters in their vector-borne and sexual transmission model, which had been calibrated using data from the 2016 Colombian outbreak. Likewise, Biswas et al. (2020) found the mosquito biting rate to be one of the most sensitive parameters in their analysis based on the normalized forward sensitivity index, while Olawoyin and Kribs (2018) showed that sensitivity to the biting rate increases when secondary transmission routes such as vertical mosquito transmission are included. The strong agreement among these different modelling approaches clearly supports the idea that vector-control measures—particularly those aimed at reducing the mosquito biting rate through the use of insecticides, biological control and the elimination of breeding sites—should be the most effective epidemiological intervention available for controlling Zika. The contribution of the sexual transmission component to about 12% of the variance in peak infection, together with its well-established role in prolonging the epidemic by roughly three days (Gao et al., 2016; Maxian et al., 2017), points to a dimension of Zika epidemic management that is too often overlooked. Although it is not sufficient on its own to keep an epidemic going, sexual transmission does produce a residual transmission chain that continues after the main wave of mosquito-mediated transmission has ended and may therefore re-initiate transmission when vector control is relaxed. The importance of this effect is in line with Sow et al. (2022)'s conclusion that omitting sexual transmission from the models results in a systematic underestimation of both the level of infection and the rate at which it spreads.

Intervention Effectiveness and the Imperative of Multilayered Control

The analysis of the intervention scenarios presents a strong quantitative argument in favour of using multiple control measures that are put into action at the same time, as opposed to relying on single-component strategies. The result that only the combined intervention — which includes vector control, treatment enhancement and a reduction in sexual transmission — is able to consistently bring R_0 below one is in agreement with the optimal control analyses carried out by Okyere et al. (2020), who showed that combinations involving at least four out of five control measures greatly outperformed both single and dual interventions in terms of suppressing Zika transmission and reducing cost. Padmanabhan et al. (2017) reached a similar conclusion, finding that the combination of insecticide-treated nets and indoor residual spraying led to synergistic reductions in both R_0 and the peak level of infection. Although the 45% decrease in the number of cumulative cases obtained with the combined strategy in the current study is considerable, it still does not amount to complete elimination, thus highlighting the fact that even the best possible combinations of existing non-pharmaceutical interventions may not be enough to fully eradicate the Zika virus without also relying on additional measures such as vaccination (where available) or Wolbachia-based vector suppression (Dutra et al., 2016).

The backward bifurcation risk that was found in the near-threshold simulations (with R_0 approximately equal to 0.9) should be regarded as a significant practical warning when designing interventions. As Biswas et al. (2020) showed, intermittent failures in controlling β —modeled as oscillations in the biting rate caused by seasonal campaign fatigue or limitations in resources—can lead to outbreaks rebounding even if R_0 has officially been brought below one. This result is in agreement with that of Zhao et al. (2020), who found that limited medical resources cause complex dynamical behaviours such as backward bifurcation and Hopf bifurcation, meaning that disease control turns out to be more difficult than classical threshold theory would suggest. The conclusion for those in charge of outbreaks is straightforward: it is necessary to have continuous, coordinated, and well-resourced control programmes rather than short-term, high-intensity campaigns followed by periods during which effort is reduced.

Preventive Measures and Public Health Strategies

The simulation results and the sensitivity analysis together indicate that a comprehensive public health approach to the Zika virus should incorporate measures relating to the environment, clinical care, and behaviour. Among all the types of intervention, vector control is by far the most effective, since the sensitivity analysis shows that cutting back on the mosquito biting rate leads to the greatest proportional reduction in R_0 . Effective practical vector control measures include getting rid of standing water bodies which act as breeding sites for Aedes mosquitoes, carrying out monthly synchronized fumigation and insecticide spraying operations in communities that are at risk, and distributing long-lasting insecticide-treated bed nets in areas where the virus is endemic or during outbreaks. The value of well-

coordinated and regularly scheduled campaigns as opposed to ad hoc actions is further highlighted by the simulation, which shows that intermittent relaxation of vector control causes transmission to rebound.

The second element of an effective response is public education and involvement of the community. People who are more aware of the ways in which Zika is transmitted, of its symptoms, and of the preventive measures consistently make greater use of personal protective actions, such as insect repellent, protective clothing, and sexual precautions (WHO, 2016). In resource-poor situations, programmes based in the community that include door-to-door education, the distribution of preventive materials, and the involvement of local cultural and religious leaders have proved especially effective. Targeted educational campaigns concerning the sexual transmission of Zika, covering advice on the use of condoms both during and for at least eight weeks after a confirmed or suspected infection, are essential for reducing the transmission tail, which sensitivity analysis has shown to considerably prolong the duration of the epidemic. Because of the Zika virus's special teratogenic risks, reproductive health needs to be given specific attention in any programme. Pregnant women and those who intend to become pregnant in areas affected by Zika should be given priority access to vector-protective resources and sexual health advice. By incorporating Zika prevention procedures into antenatal care programmes—such as carrying out routine screening, providing information on travel risks, and giving guidance on deferring pregnancy in areas with high exposure—it is possible to greatly reduce the number of cases of congenital Zika syndrome.

Strong real-time surveillance and the ability to carry out rapid-response diagnostic testing are essential elements of managing a Zika epidemic. The results of the simulation show that the period between the first infectious contact and the peak of the clinical symptoms is very short, ranging from three to seven days, which leaves only a small amount of time available for a reactive response once an outbreak has started. For the timely implementation of the vector control and treatment measures shown in this study to be the most effective, it is necessary to have early warning systems that can detect unusual increases in cases of febrile illness, rash, and congenital anomalies at the community level, together with the capacity for rapid laboratory confirmation.

Conclusion

The study carried out extensive numerical simulations of the SEIVTR model concerning the transmission dynamics of Zika virus, showing that the epidemic follows a course marked by the quick exhaustion of the susceptible population within three days, with a closely concentrated peak in both exposure and infection occurring between days five and seven, a sharp rise in treatment demand reaching its peak around day four, and recovery building up by day 20. This pattern is in agreement with observations of Zika outbreaks in Brazil, French Polynesia, and Colombia. The inclusion of a specific Treatment compartment in the SEIVTR model had important epidemiological implications, as it reduced the average duration of infectivity from about seven to four days and offered a clearly defined temporal signal for the prepositioning of healthcare resources something that is missing in traditional SEIR models. The sensitivity analysis proved that the mosquito biting rate and the vector mortality rate are the main factors influencing epidemic dynamics, together explaining about 60% of the variation in the peak number of infections. Although sexual transmission accounts for a smaller share of the peak burden, it extends the epidemic curve by approximately three days. This dual result highlights the importance of intervention strategies that aim at both vector-borne and sexual transmission routes. The combined intervention scenario, which involved a 50% reduction in the mosquito biting rate, 75% treatment efficacy, and a 60% reduction in sexual transmission, was the only approach able to consistently bring R_0 below the epidemic threshold, resulting in a 45% decrease in the total number of cases. The fact that a backward bifurcation risk exists under near-threshold conditions serves as a important warning against prematurely easing control measures, emphasizing that continuous, coordinated, multilayered interventions are required to avoid a resurgence of the epidemic. Together, the analytical and numerical results from this study and its companion paper offer a thorough, evidence-based framework for the design and assessment of integrated Zika virus control strategies that can be adapted to different epidemiological situations.

Recommendations

Based on the findings of this study, the following recommendations are made for public health authorities, outbreak responders, and policymakers:

1. The implementation of integrated vector management programmes should include carrying out synchronised fumigation campaigns on a monthly basis, systematically eliminating the breeding sites of *Aedes* mosquitoes, and distributing insecticide-treated bed nets to the community, since this represents the

most effective and evidence-based approach for reducing the mosquito biting rate, which is the single most important factor influencing Zika transmission dynamics.

2. It is important to strengthen the protocols for rapid diagnosis and clinical management in order to reduce the time interval between the onset of symptoms and the start of treatment, keeping the short interval between victim and treatment — which the simulations have shown to be achievable and effective — below two days. Having rapid diagnostic facilities decentralised at community health centres is essential if this target is to be reached in settings with limited resources.
3. Put in place continuous sexual health education programmes at the community level that encourage regular use of condoms and prompt partner notification for a period of at least eight weeks after a case of Zika has been confirmed or suspected, in order to reduce the extent of transmission that the sensitivity analysis has shown to meaningfully prolong the duration of the epidemic.
4. Make sure that efforts to prevent the Zika virus are fully incorporated into current maternal and child health, reproductive health, and antenatal care programs, giving pregnant women and women of reproductive age in areas where the virus is endemic or where outbreaks are occurring priority access to vector protection measures and evidence-based advice.
5. Put money into early warning surveillance equipment that is capable of picking up unusual disease signals within days of an outbreak beginning, so that the combined intervention measures shown to be effective in this study can be quickly put into action only when they are applied proactively and on a continuous basis from the very start of an outbreak.

References

- Agudelo, S., & Ventresca, M. (2022). Modeling the spread of the Zika virus by sexual and mosquito transmission. *Plos One*, 17(12), e0270127.
- Biswas, S. K., Ghosh, U., & Sarkar, S. (2020). Mathematical model of zika virus dynamics with vector control and sensitivity analysis. *Infectious Disease Modelling*, 5, 23–41.
- Duffy, M. R., Chen, T. H., Hancock, W. T., Powers, A. M., Kool, J. L., Lanciotti, R. S., & Hayes, E. B. (2009). Zika virus outbreak on Yap Island, Federated States of Micronesia. *New England Journal of Medicine*, 360(24), 2536 – 2543.
- Dutra, H. L. C., Rocha, M. N., Dias, F. B., Mansur, S. B., Caragata, E. P., & Moreira, L. A. (2016). *Wolbachia blocks currently circulating Zika virus isolates in Brazilian Aedes aegypti mosquitoes*. *Cell Host & Microbe*, 19(6), 771–774. <https://doi.org/10.1016/j.chom.2016.04.021>
- Fauci, A. S., & Morens, D. M. (2016). Zika virus in the Americas—yet another arbovirus threat. *New England Journal of Medicine*, 374(7), 601 – 604.
- Gao, D., Lou, Y., He, D., Porco, T. C., Kuang, Y., Chowell, G., & Ruan, S. (2016). Prevention and control of Zika as a mosquito-borne and sexually transmitted disease: a mathematical modeling analysis. *Scientific Reports*, 6(1), 28070.
- Goswami, N. K., & Shanmukha, B. (2020). Stability and optimal control analysis of Zika virus with saturated incidence rate. *Malaya Journal of Matematik*, 8(2), 331 – 342.
- Jose, S. A., Raja, R., Omede, B. I., Agarwal, R. P., Alzabut, J., Cao, J., & Balas, V. E. (2023). Mathematical modeling on co-infection: transmission dynamics of Zika virus and Dengue fever: SA Jose et al. *Nonlinear Dynamics*, 111(5), 4879–4914.
- Kucharski, A. J., Funk, S., Eggo, R. M., Mallet, H. P., Edmunds, W. J., & Nilles, E. J. (2016). Transmission dynamics of Zika virus in island populations: a modelling analysis of the 2013–14 French Polynesia outbreak. *PLoS Neglected Tropical Diseases*, 10(5), e0004726.
- Maxian, O., Neufeld, A., Talis, E. J., Childs, L. M., & Blackwood, J. C. (2017). Zika virus dynamics: When does sexual transmission matter? *Epidemics*, 21, 48 – 55.
- Moghadas, S. M., Shoukat, A., Espindola, A. L., Pereira, R. S., Abdirizak, F., Laskowski, M., & Chowell, G. (2017). Asymptomatic transmission and the dynamics of Zika infection. *Scientific reports*, 7(1), 5829.
- Musso, D., Nilles, E. J., & Cao-Lormeau, V. M. (2014). Rapid spread of emerging Zika virus in the Pacific area. *Clinical Microbiology and Infection*, 20(10), 595 – 596.
- Okyere, E., Olaniyi, S., & Bonyah, E. (2020). Analysis of Zika virus dynamics with sexual transmission route using multiple optimal controls. *Scientific African*, 9, e00532.
- Olawoyin, O., & Kribs, C. (2018). Effects of multiple transmission pathways on Zika dynamics. *Infectious Disease Modelling*, 3, 331 – 344.

- Padmanabhan, P., Seshaiyer, P., & Castillo-Chavez, C. (2017). Mathematical modeling, analysis and simulation of the spread of Zika with influence of sexual transmission and preventive measures. *Letters in Biomathematics*, 4(1), 148 – 166.
- Petersen, L. R., Jamieson, D. J., Powers, A. M., & Honein, M. A. (2016). Zika virus. *New England Journal of Medicine*, 374(16), 1552 – 1563.
- Rahman, M., Bekele-Maxwell, K., Cates, L. L., Banks, H. T., & Vaidya, N. K. (2019). Modelling Zika virus transmission dynamics: Parameter estimates, disease characteristics, and prevention. *Scientific Reports*, 9(1), 10575.
- Sow, A., Diallo, C., & Cherifi, H. (2022). Effects of vertical transmission and human contact on zika dynamics. *Complexity*, 2022(1), 5366395.
- Towers, S., Brauer, F., Castillo-Chavez, C., Falconar, A. K., Mubayi, A., & Romero-Vivas, C. M. (2016). Estimate of the reproduction number of the 2015 Zika virus outbreak in Barranquilla, Colombia, and estimation of the relative role of sexual transmission. *Epidemics*, 17, 50 – 55.
- Wiratsudakul, A., Suparit, P., & Modchang, C. (2018). Dynamics of Zika virus outbreaks: an overview of mathematical modeling approaches. *PeerJ*, 6, e4526.
- World Health Organization. (2016). *World Health Statistics 2016 [OP]: Monitoring health for the sustainable development goals (SDGs)*. World Health Organization.
- Zhao, H., Wang, L., Oliva, S. M., & Zhu, H. (2020). Modeling and dynamics analysis of Zika transmission with limited medical resources. *Bulletin of Mathematical Biology*, 82(8), 99 – 109.