Journal of Natural Science Review

Vol. 4, No. 2, 2026
https://kujnsr.com
e-ISSN: 3006-7804

Analysis of Measles Transmission and Vaccination Coverage Effects in Afghanistan Using the SIRV Mathematical Model

Said Omar Saidi [1], Mohammad Khan Haidary[2]

[1] Shaikh Zayed University, Department of Mathematics, Faculty of Education, Khost, Afghanistan
[2]Kabul University, Department of Algebra, Faculty of Mathematics, Kabul, Afghanistan
✉E-mail: saidomar.saidi55@gmail.com (corresponding author)

ABSTRACT

In this study, the transmission dynamics of measles in Afghanistan and the effects of vaccination coverage are analyzed using an SIRV mathematical model, in which the transmission coefficient (β), the vaccination rate (v), and the basic reproduction number (R_0) play essential roles. The model's nonlinear differential equations are solved numerically using the fourth-order Runge–Kutta method (RK4), and solutions are computed in the Python programming environment to accurately investigate the behavior of different population compartments over time. The basic reproduction number (R_0) is derived using the Next Generation Matrix (NGM) method. Numerical and graphical results indicate that increasing the vaccination rate (v) significantly reduces R_0 and the number of infected individuals. The findings further demonstrate that reducing the transmission coefficient and improving vaccination coverage are effective strategies for controlling measles outbreaks. In addition, the minimum vaccination coverage required for disease control is calculated. The significance of this study lies in providing a scientific and quantitative framework for understanding measles transmission dynamics and evaluating vaccination strategies in Afghanistan. Overall, the proposed model and numerical approach offer valuable insights for infectious disease analysis and support evidence-based public health policies.

ARTICLE INFO

Article history:

Received: April 4, 2026
Revised: March 8, 2026
Accepted: May 21, 2026
Published: June, 30, 2026

Keywords:

Basic reproduction number (r_0); Disease-free equilibrium (dfe); Endemic equilibrium (ee)Measles; Sirv model

To cite this article: Saidi, S. O., & Haidari, M.K. (2026). Analysis of Measles Transmission and Vaccination Coverage Effects in Afghanistan Using the SIRV Mathematical Model. *Journal of Natural Science Review*, 4(2), 627-650. https://doi.org/10.62810/jnsr.v4i2.454

Link to this article: https://kujnsr.com/JNSR/article/view/454

INTRODUCTION

Measles is one of the most significant and highly contagious viral diseases worldwide, posing a serious threat to public health, particularly in countries with limited vaccination coverage and weak healthcare systems. According to reports by the World Health Organization, despite the availability of an effective vaccine, low vaccination coverage, population mobility, and socio-

economic challenges continue to contribute to the persistence and resurgence of the disease (WHO, 2020; 2025). Children and immunocompromised individuals are especially vulnerable, often experiencing severe complications such as pneumonia, encephalitis, and even death (Fine & Clarkson, 1982; Griffin, 2018; Patel et al., 2019). In Afghanistan, the continued presence of measles highlights a critical epidemiological concern regarding the factors influencing its transmission and control.

Mathematical modeling provides a powerful framework for understanding the transmission dynamics of infectious diseases. The foundational theory of infectious disease modeling was established by Anderson and May(1991), who developed general principles for analyzing disease spread. Hethcote (2000) expanded these concepts and contributed significantly to compartmental modeling. In this study, an SIRV model is employed, which divides the population into four compartments: susceptible (S), infected (I), recovered (R), and vaccinated (V). This model enables the analysis of how vaccination, recovery, and transmission interact to shape disease dynamics.

Several studies have explored measles transmission using both biological and mathematical approaches. Fine and Clarkson (1982) examined seasonal patterns of measles in England, highlighting the influence of seasonal variation on transmission. Griffin (2018) provided detailed insights into the biological mechanisms of the measles virus. In mathematical epidemiology, the concept of the basic reproduction number R_0 plays a central role, and the next-generation matrix method introduced by Odo Diekmann and colleagues (2010) offers a systematic way to compute it. In recent years, various mathematical studies have been conducted to analyze and control the spread of measles. Peter and Oguntolu (2025) carried out a mathematical modeling study to analyze measles transmission in Nigeria. Similarly, Seydou and Moussa Tessa (2023) presented an analysis of measles based on the SIRV model; Sinha (2023) predicted measles outbreaks in India; and Chatterjee (2024) evaluated optimal disease control strategies using fractional models. Furthermore, age-structured SEIR models have been applied to analyze measles transmission in Africa, as demonstrated by Tegegn (2024). In addition, the Centers for Disease Control and Prevention (CDC) provide important guidelines and statistical data for measles prevention and control, which serve as a valuable foundation for effective disease management and public health policy development

Despite extensive global research, there remains a significant lack of comprehensive mathematical modeling studies focusing specifically on measles transmission in Afghanistan. Most existing studies in the country are primarily statistical and descriptive, offering limited insight into the disease's dynamic behavior. These approaches are insufficient for predicting future outbreaks or evaluating the long-term impact of intervention strategies such as vaccination.

In Afghanistan, previous epidemiological analyses have largely relied on statistical data without incorporating mathematical modeling frameworks. While such studies provide valuable descriptive information, they do not adequately capture the underlying transmission mechanisms or allow for predictive analysis. Therefore, applying a mathematical model such as SIRV is crucial for gaining deeper insights into disease dynamics, assessing intervention strategies, and supporting evidence-based public health decision-making.

In this study, the transmission dynamics of measles in Afghanistan are investigated and analyzed using the SIRV model. Real data from Afghanistan covering the period 2001–2024 are used to estimate key model parameters, including the transmission rate (β), recovery rate (γ), and vaccination rate (ν), through the Least Squares Curve Fitting method (Deng et al., 2020; Kröger & Schlickeiser, 2023; Schlickeiser & Kröger, 2024). The system of differential equations is solved numerically using the Runge–Kutta (RK4) method, and the next-generation matrix approach is applied to derive and evaluate the basic reproduction number R_0 (Diekmann et al., 2010; Fosu et al., 2020; Jones, 2007). Furthermore, the study investigates the impact of various parameters on the infected population to provide meaningful insights for effective disease control and public health interventions.

The main objective of this study is to investigate the effects of vaccination coverage on the spread and control of measles in Afghanistan and to analyze the impact of changes in epidemiological parameters on the dynamics of disease transmission.

METHODS AND MATERIALS

This study is a quantitative, model-based investigation that analyzes the transmission dynamics of measles and the effects of vaccination coverage using the SIRV mathematical model.

Data Collection tools

The relevant data for this study were collected from the World Health Organization (WHO) and other internationally recognized and reliable sources. These data include population size in Afghanistan, reported measles cases, vaccination coverage levels, and other statistical information related to disease transmission. The collected data were used to estimate model parameters, solve the equations, and conduct numerical analysis. To ensure data validity and enhance the reliability of the results, only sources with internationally recognized scientific credibility and official statistical records were used.

Data Analysis

In this study, the collected data were used within the SIRV mathematical model to analyze the transmission dynamics of measles. The model parameters were estimated based on available statistical data, and the numerical solution was implemented using the fourth-order Runge–

Kutta (RK4) method in the Python programming environment. The numerical results were evaluated using graphical and analytical methods to illustrate the dynamics of disease transmission clearly. Furthermore, the basic reproduction number (R_0) was computed and analyzed to obtain scientific insights into the control and intensity of the disease.

Introduction to the SIRV Model

The SIRV model is an extended mathematical framework widely used in epidemiology to analyze disease transmission. It is built upon the classical SIR model and systematically incorporates vaccination effects, population birth and natural death, and all aspects of disease infection dynamics. In this model, the population is divided into four compartments: susceptible (S), infected (I), vaccinated (V), and recovered or immune (R). Susceptible individuals are those who are not infected but are highly vulnerable to infection and serve as the main targets for disease spread. Infected individuals are those who currently have the disease and serve as sources of infection for others. Vaccinated individuals have acquired resistance to the disease through vaccination, with vaccine efficacy directly affecting the probability of disease transmission. Recovered or immune individuals are those who have recovered from the disease and have a reduced risk of reinfection (Kumar & Srivastava, 2021; Dai & Wang, 2024; Seydou & Moussa Tessa, 2023). The significance of the SIRV model lies in its ability to provide precise analysis of disease dynamics and facilitate evaluation of vaccination strategies. It mathematically describes the time-dependent transitions among susceptible, infected, recovered, and vaccinated populations, providing essential information for epidemiological decision-making. The model accurately accounts for the effects of population dynamics, including births and deaths, on the four compartments, which is crucial for long-term endemic analysis and provides a solid basis for evidence-based disease control and management decisions. According to the SIRV model, susceptible individuals can either become infected or gain immunity through vaccination. Both processes are represented in the model equations as functions of time, clearly illustrating the impact of vaccination on the rapid spread of the disease and on the population dynamics. This creates a comprehensive framework for epidemiological calculations, offering practical value for scientific research and the development of public health strategies (Kumar et al., 2019; Shirazian et al., 2016). The interaction diagram among the four compartments of the SIRV model is illustrated in the figure below.

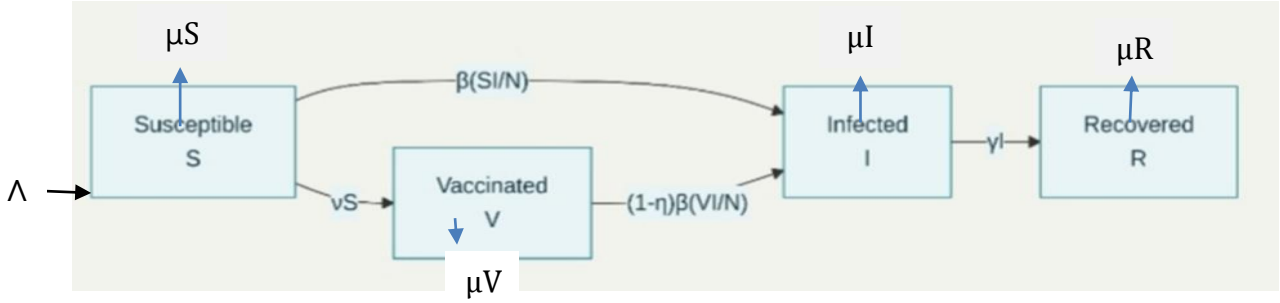

Figure 1: Transmission Diagram of Measles

Based on the diagram in Figure 1, the SIRV model leads to the following system of ordinary differential equations that describes the time-dependent changes in the four main population compartments.

$$\frac{dS}{dt} = \Lambda - \beta \frac{SI}{N} - \upsilon S - \mu S$$
$$\frac{dI}{dt} = \beta \frac{SI}{N} + (1-\eta)\beta \frac{VI}{N} - \gamma I - \mu I$$
$$\frac{dV}{dt} = \upsilon S - (1-\eta)\beta \frac{VI}{N} - \mu V \quad (1)$$
$$\frac{dR}{dt} = \gamma I - \mu R$$
$$N = S + I + R + V$$ [Kröger & Schlickeiser, 2023].

This system illustrates the dynamics of the SIRV model through nonlinear ordinary differential equations, with the parameters defined as follows.

i. Transmission rate (β): This parameter indicates the intensity of disease transmission and reflects the combined probability of infection and infectiousness during contact between individuals. A higher value of β signifies that the disease spreads rapidly, as is the case with measles, which has a high transmission potential (Hethcote, 2000; Anderson & May, 1991).

ii. Recovery rate (γ): This parameter represents the rate at which infected individuals recover from the disease and move into the R compartment. It is the inverse of the average duration of the infection. A higher value of γ indicates that patients recover more quickly, thereby reducing the intensity of disease transmission (Anderson & May, 1991).

iii. Vaccination coverage rate (υ): This parameter indicates the proportion of susceptible individuals who are vaccinated at a given time. It directly reflects public health policy and the extent of vaccine coverage. A higher value of this parameter leads to a faster reduction in the susceptible population, thereby increasing the likelihood of disease control (Fine & Clarkson, 1982).

iv. Vaccine efficacy (η): This parameter represents the effectiveness of the vaccine and ranges between 0 and 1. It indicates the degree of protection vaccinated individuals have against the disease (WHO, 2019).

v. Birth rate (Λ): This parameter represents the rate of new births at time t, which are added to the susceptible compartment (S). Λ is an important part of population dynamics because it directly affects population stability or change, which is crucial for long-term epidemiological analysis (Anderson & May, 1991).

vi. Natural death rate (μ): This parameter represents the reduction in all four population compartments over time due to natural mortality (Anderson & May, 1991).

In summary, the variables and parameters of the SIRV model form the mathematical basis for analyzing the spread of measles. The variables represent changes in the population's health states, while the parameters describe the biological characteristics of the disease and the effectiveness of vaccination. Precise definition and scientific explanation of both are crucial for the validity of the model and the interpretation of its results (Tegegn, 2024; Kumar & Srivastava, 2021).

Derivation of the Basic Reproduction Number (R_0)

To derive R_0 we employ the Next Generation Matrix (NGM) method. In this approach, the population is divided into two compartments: first, the newly infected individuals, i.e., the portion of the population that generates new infections (F); and second, the individuals leaving the infected compartment, i.e., those who either recover or die from the disease (V). R_0 is then calculated as the spectral radius of FV^{-1}. In most studies, F and V are represented as matrices. However, in this case, the production of new infections depends only on a single compartment, the infected individuals, resulting in a single-element matrix. Similarly, V is also a single-element matrix, with $V^{-1} = 1/V$. To compute F, we consider the differential equation dI/dt, since the generation of new infections is solely related to this equation, and we take its derivative with respect to I. Likewise, to compute V, we focus on the portion of the population leaving the infected class and take its derivative with respect to I. Finally, R_0 is obtained as the spectral radius of FV^{-1} denoted as $\rho(FV^{-1})$.

$$\frac{dI}{dt} = \underbrace{\beta\frac{SI}{N} + (1-\eta)\beta\frac{VI}{N}}_{\text{Infection generating}} - \underbrace{\gamma I}_{\text{Recover}} - \underbrace{\mu I}_{\text{Deceased}}$$

$$F = \frac{d}{dI}\left(\frac{dI}{dt}\right)$$

$$= \beta\frac{S^*}{N^*} + (1-\eta)\beta\frac{V^*}{N^*}$$

Also, the Population Leaving the infected compartment is represented by $(\gamma+\mu)I$, hence...

$$V = \frac{d}{dI}(\gamma+\mu)I$$

$$\mathrm{V} = (\gamma+\mu)$$

$$\mathcal{R}_0 = \rho(FV^{-1})$$

$$\mathcal{R}_0 = \frac{\beta \frac{S^*}{N^*} + (1-\eta)\beta \frac{V^*}{N^*}}{\gamma + \mu} = \frac{\beta[S^* + (1-\eta)V^*]}{(\gamma + \mu)N^*} \qquad (2)$$

Thus if $\mathcal{R}_0 < 1$ means that, on average, each infected individual generates fewer than 1 new infection, that is, infects less than 1 person. So the number of infected individuals decreases over time, and the disease eventually dies out. If $\mathcal{R}_0 > 1$ indicates that each infected individual generates more than one new infection on average, leading to an increase in the number of infected individuals over time. If $\mathcal{R}_0 = 1$, the system is at the threshold of stability, meaning the disease neither grows rapidly nor declines. When vaccination against the disease is available, the basic reproduction number $\mathcal{R}_0$ decreases in the presence of vaccination. To reduce $\mathcal{R}_0$ Below, a relationship can be established for the minimum vaccination coverage required, as done in (Seydou & Moussa 2023). Similarly, here we proceed in the same way. Let η represent vaccine efficacy and c the proportion of the total population covered by vaccination; then we write:

$$\mathcal{R}_0{}^{effective} = \mathcal{R}_0(1 - c\eta)$$

To ensure that the disease is controlled in the population $\mathcal{R}_0 < 1$, we write:

$$\mathcal{R}_0{}^{effective} < 1 \implies \mathcal{R}_0(1 - c\eta) < 1$$
$$(1 - c\eta) < \frac{1}{\mathcal{R}_0}$$
$$c > \frac{\mathcal{R}_0 - 1}{\eta \mathcal{R}_0}$$
$$c_{min} = \frac{\mathcal{R}_0 - 1}{\eta \mathcal{R}_0} \qquad (3)$$

Using the above relation (3), we can estimate the minimum vaccination coverage required to control the disease once $\mathcal{R}_0$ has been determined. Moreover, analyzing equilibrium points is highly important for epidemiological models, as it provides insights into the system's stability and long-term behavior. Specifically, this analysis helps predict whether a disease will spread or die out. These equilibrium points are divided into two types: disease-free equilibrium (DFE) where the number of infected individuals is zero ($\mathrm{I} = 0$), and $\mathcal{R}_0 < 1$ and endemic equilibrium (EE) where $\mathrm{I} \neq 0$, meaning the disease persists in the population and $\mathcal{R}_0 > 1$ (Van den Driessche & Watmough, 2002). We now discuss both cases in detail.

Disease-Free Equilibrium (DFE)

As previously mentioned, the disease-free equilibrium (DFE) refers to the state in which the disease is absent from the entire population and I = 0. This is an important point in epidemiological analysis because it represents the condition under which the disease is eliminated or does not spread. In this state, the population consists only of susceptible,

vaccinated, or recovered individuals, with no infected individuals. To determine the DFE points in model (1) we set $\frac{\mathrm{dS}}{\mathrm{dt}} = \frac{\mathrm{dI}}{\mathrm{dt}} = \frac{\mathrm{dV}}{\mathrm{dt}} = \frac{\mathrm{dR}}{\mathrm{dt}} = 0$ and $\mathrm{I} = 0$ considered.

$$\frac{dS}{dt} = \Lambda - \beta\frac{SI}{N} - \upsilon S - \mu S$$

When the above conditions are imposed, it follows that:

$$\Lambda - \upsilon S - \mu S = 0$$

$$S(\upsilon + \mu) = \Lambda \implies S = \frac{\Lambda}{\upsilon + \mu} \qquad (4)$$

To abtain V we have:

$$\frac{dV}{dt} = \upsilon S - (1-\eta)\beta\frac{VI}{N} - \mu V$$

After applying these conditions, we obtain:

$$\upsilon S - \mu V = 0$$

$$V = \frac{\upsilon S}{\mu}$$

When we substitute the value from equation (4) for S, we get:

$$V = \frac{\upsilon\Lambda}{\mu(\upsilon + \mu)} \qquad (5)$$

To obtain R, we have:

$$\frac{dR}{dt} = \gamma I - \mu R$$

When the condition are applied, we have:

$$\mu R = 0 \implies R = 0 \qquad (6)$$

For model (1) the disease-free equilibrium (DFE) is given by $D_0 = (\mathrm{S}, \mathrm{I}, \mathrm{V}, \mathrm{R}) = (\frac{\Lambda}{\upsilon+\mu}, 0, \frac{\upsilon\Lambda}{\mu(\upsilon+\mu)}, 0)$. The meaning of D_0 is that the disease is absent from the entire population, and the population is divided solely between susceptible and vaccinated individuals. Newly born individuals enter the susceptible compartment and may subsequently move to the vaccinated compartment through immunization, while recovered individuals do not exist because the disease is not active. D_0 provides a fundamental analytical framework for vaccination strategies, disease control policies and public health decision-making, as it indicates the conditions under which the disease can be completely eliminated from the population.

Endemic Equilibrium Points (EE)

In epidemiological models, endemic equilibrium points refer to states in which the disease persists continuously within the population and the number of infected individuals does not reach zero. Mathematically, this is expressed as $E^* = (S^*, I^*, V^*, R^*)$, where the conditions $\frac{dS}{dt} = \frac{dI}{dt} = \frac{dV}{dt} = \frac{dR}{dt} = 0$ hold and $I^* > 0$. The condition $I^* > 0$ distinguishes the endemic equilibrium from the disease-free equilibrium. To obtain the endemic points we formulate the endemic equations as follows:

$$\Lambda - \beta \frac{SI}{N} - \upsilon S - \mu S = 0 \quad (7)$$

$$\beta \frac{SI}{N} + (1-\eta)\beta \frac{VI}{N} - \gamma I - \mu I = 0 \quad (8)$$

$$\upsilon S - (1-\eta)\beta \frac{VI}{N} - \mu V = 0 \quad (9)$$

$$\gamma I - \mu R = 0 \quad (10)$$

From equation (10) we obtain the endemic equilibrium value of R.

$\gamma I - \mu R = 0$

$$R = \frac{\gamma}{\mu} I \quad (11)$$

From equation (8) we write that:

$$I[\beta \frac{S}{N} + (1-\eta)\beta \frac{V}{N} - (\gamma + \mu)] = 0$$

Since $I \neq 0$ we can write that:

$$\beta \frac{S}{N} + (1-\eta)\beta \frac{V}{N} - (\gamma + \mu) = 0$$

$$\Longrightarrow \beta S + (1-\eta)\beta V = (\gamma + \mu)N$$

$$\Longrightarrow S + (1-\eta)V = \frac{(\gamma + \mu)N}{\beta} \quad (12)$$

To establish the relationship between S and V we add equations (7) and (9).

$$\Lambda - \beta \frac{SI}{N} - (\upsilon + \mu)S + \upsilon S - (1-\eta)\beta \frac{VI}{N} - \mu V = 0$$

$$\Longrightarrow \Lambda - \beta \frac{SI}{N} - (1-\eta)\beta \frac{VI}{N} - \mu S - \mu V = 0$$

$$\Longrightarrow \Lambda - \frac{I}{N}[\beta S + (1-\eta)\beta V] - \mu(S+V) = 0 \qquad (13)$$

After substituting equation (12) into equation (13) we obtain:

$$\Lambda - \frac{I}{N}[(\gamma+\mu)N] - \mu(S+V) = 0$$

$$\Longrightarrow \Lambda - I(\gamma+\mu) - \mu(S+V) = 0$$

$$\Longrightarrow I = \frac{\Lambda - \mu(S+V)}{(\gamma+\mu)} \qquad (14)$$

From the total population relation, we obtain the expression for $S+V$.

$$N = S + I + R + V$$

We substitute the value from equation (11) in place of R.

$$N = S + V + I + \frac{\gamma}{\mu} I$$

$$\Longrightarrow S + V = N - \frac{\mu+\gamma}{\mu} I \qquad (15)$$

We substitute the value from equation (15) into equation (14).

$$I = \frac{\Lambda - \mu\left(N - \frac{\mu+\gamma}{\mu} I\right)}{(\gamma+\mu)}$$

$$\Longrightarrow I = \frac{\Lambda - \mu N + (\mu+\gamma)I}{(\gamma+\mu)}$$

$$\Longrightarrow I(\gamma+\mu) = \Lambda - \mu N + (\mu+\gamma)I$$

$$\Longrightarrow \Lambda - \mu N = 0$$

$$\Longrightarrow \Lambda = \mu N \qquad (16)$$

Now we substitute the value from equation (16) into equation (14).

$$I = \frac{\mu N - \mu(S+V)}{(\gamma+\mu)}$$

$$\Longrightarrow I = \frac{\mu(N-S-V)}{(\gamma+\mu)} \qquad (17)$$

To find the values of S and V we consider equations (9) and (12).

$$\upsilon S - (1-\eta)\beta\frac{VI}{N} - \mu V = 0$$

We substitute the value from equation (17) in place of I.

$$\upsilon S-(1-\eta)\frac{\beta V}{N}\left[\frac{\mu(N-S-V)}{(\gamma+\mu)}\right]-\mu V=0$$

$$\upsilon S-\mu V-\frac{(1-\eta)\beta\mu V(N-S-V)}{N(\gamma+\mu)}=0 \qquad (19)$$

We substitute the value of S from equation (12) into equation (19).

$$S+(1-\eta)V=\frac{(\gamma+\mu)N}{\beta}\Longrightarrow S=\frac{(\gamma+\mu)N}{\beta}-(1-\eta)V$$

We substitute the value of S into equation (19).

$$\upsilon\left[\frac{(\gamma+\mu)N}{\beta}-(1-\eta)V\right]-\mu V-\frac{(1-\eta)\beta\mu V\left(N-\frac{(\gamma+\mu)N}{\beta}-(1-\eta)V-V\right)}{N(\gamma+\mu)}=0$$

$$\Longrightarrow\ \upsilon\left[\frac{(\gamma+\mu)N}{\beta}-(1-\eta)V\right]-\mu V-\frac{(1-\eta)\beta\mu V\left[N\left(1-\frac{\gamma+\mu}{\beta}\right)-\eta V\right]}{N(\gamma+\mu)}=0$$

$$\Longrightarrow\ \upsilon\frac{(\gamma+\mu)N}{\beta}-\upsilon(1-\eta)V-\mu V-\frac{(1-\eta)\beta\mu V\left[N\left(1-\frac{\gamma+\mu}{\beta}\right)-\eta V\right]}{N(\gamma+\mu)}=0$$

When in the above equation we collect all like terms with respect to V we obtain:

$$\frac{(1-\eta)\beta\mu\eta}{N(\gamma+\mu)}V^2+\left[\upsilon(1-\eta)+\mu+\frac{(1-\eta)\beta\mu}{\gamma+\mu}\left(1-\frac{\gamma+\mu}{\beta}\right)\right]V-\upsilon\frac{(\gamma+\mu)N}{\beta}=0$$

$$\Longrightarrow AV^2+BV-C=0$$

Where:

$$A=\frac{(1-\eta)\beta\mu\eta}{N(\gamma+\mu)}$$

$$B=\upsilon(1-\eta)+\mu+\frac{(1-\eta)\beta\mu}{\gamma+\mu}\left(1-\frac{\gamma+\mu}{\beta}\right)$$

$$C=\upsilon\frac{(\gamma+\mu)N}{\beta}$$

When the above qualratic equation is solved with respect to V we obtain:

$$V = \frac{-B + \sqrt{B^2 + 4AC}}{2A} \qquad (20)$$

Therefore as a result the endemic equilibrium points for model (1) are given by:

$$S^* = \frac{(\gamma + \mu)N}{\beta} - (1 - \eta)V^*$$

$$I^* = \frac{\mu(N - S^* - V^*)}{(\gamma + \mu)}$$

$$V^* = \frac{-B + \sqrt{B^2 + 4AC}}{2A}$$

$$R^* = \frac{\gamma}{\mu} I^*$$

Where:

$$A = \frac{(1 - \eta)\beta\mu\eta}{N(\gamma + \mu)}$$

$$B = \upsilon(1 - \eta) + \mu + \frac{(1 - \eta)\beta\mu}{\gamma + \mu}\left(1 - \frac{\gamma + \mu}{\beta}\right)$$

$$C = \upsilon\frac{(\gamma + \mu)N}{\beta}$$

FINDINGS

In this section, the practical findings, analytical results, numerical computations, and the evaluation of the obtained results are systematically presented. Based on the numerical computations, it is observed that the overall pattern of disease spread changes clearly over time, and the number of infected individuals shows a regular increase or decrease depending on the time period. This result is clearly confirmed through numerical solutions. From the analytical evaluations, it is evident that changes in the model parameters affect the overall dynamic behavior of the system, and its equilibrium states change accordingly. The computations indicate that the disease's intensity varies gradually over time, providing a clear picture of its long-term behavior. In the numerical analysis, parameter estimation was carried out using real

data, demonstrating that the model fits well with the actual situation. The analysis of the numerical results and graphical representations demonstrates that the model's behavior remains structured and interpretable over time, clearly reflecting the overall trend in disease spread.

Furthermore, the basic reproduction number (R_0) has been computed and analyzed, showing that this indicator plays an important role in determining the persistence and intensity of the disease, and that its value changes with variations in the model parameters. This result is considered an important scientific indicator for the long-term understanding of disease dynamics. Overall, the practical findings, analytical evaluations, and numerical computations together demonstrate that the SIRV model provides an effective mathematical and computational framework for describing the dynamics of measles, and the results offer a strong foundation for public health decision-making.

Parameter Estimation

In this section, we estimate the parameters of the SIRV model to perform numerical solutions, analyze model behavior, and conduct numerical simulations. To calculate these parameters, we use real measles data from Afghanistan for the period 2001–2024 as reported by the World Health Organization (WHO). The parameterization of the SIRV model is carried out in two ways: some parameters (Λ, μ, γ, and η) are derived from previous studies and reported data, while the remaining parameters are estimated using the Least Squares Curve Fitting method. The natural death rate μ is calculated based on the average life expectancy. From 2001 to 2024, the average life expectancy in Afghanistan was 60.78 years (World Bank, 2024). Therefore $\mu = \frac{1}{60{,}78} = 0.01645$. In 2001, the total population of Afghanistan was 20,284,308 (PPA, 2026). Using the relation $N = \frac{\Lambda}{\mu}$ (Equation 16) The birth rate Λ is obtained as Λ = 332,662.65. According to the (WHO, 2020) report, the average duration of measles is 14 days, giving $\gamma = \frac{1}{14} = 0.07142$. Based on the (WHO, 2025b) report, the number of positive measles cases in 2001 was 8,762, so $I_0 = 8{,}762$. In the same year, the number of vaccinated individuals was 4,225,627, and according to WHO (2019), the vaccine efficacy ranged from 93% to 97%, with an average of 95%, giving η = 0.95. The remaining parameters such as β and υ will be estimated using the Least Squares Curve Fitting method in Python. Thus, the initial conditions mentioned above can be written as:

$$N_0 = 20284308$$
$$I_0 = 8762$$
$$V_0 = 4225627$$
$$R_0 = 0$$
$$S_0 = N_0 - I_0 - V_0 - R_0$$
$$S_0 = 20284308 - 8762 - 4225627 - 0 = 16049919$$

***Table 1**: Parameter Values*

Meaning	parameter	Value	Source
Total population	N_0	20,284,308	(PPA,2026)
Number of individuals susceptible to the disease	S_0	16,049,919	estimated
Number of individuals infected with the disease	I_0	8,762	(WHO, 2025b)
Number of individuals vaccinated against the disease	V_0	4,225,627	(WHO, 2025b)
Number of individuals recovered from the disease	R_0	0	assumed
Number of newly born individuals	Λ	332,662.65	estimated
Natural death rate	μ	0.01645	estimated
Recovery rate	γ	0.07142	estimated
Vaccine efficacy rate	η	0.95	(WHO,2019)
Disease transmission rate	β	0.815	fitted
Rate of vaccinated individuals	υ	0.415	fitted

According to the WHO (2025b) report, which provides the number of confirmed measles cases from 2001 to 2024, the data are presented in the table below.

***Table 2**: Reported measles cases by the WHO*

Year	**2001**	**2002**	**2003**	**2004**	**2005**	**2006**	**2007**	**2008**	**2009**	**2010**	**2011**	**2012**
Cases	8762	2486	798	466	1296	1990	1141	1599	2861	1989	3013	2787
Year	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	**2024**
Cases	430	492	1154	638	1511	2012	353	640	2900	5166	2792	9769

We solve the system of equation (1) using the RK4 numerical method as follows.

$$\frac{dS}{dt} = \Lambda - \beta\frac{SI}{N} - \upsilon S - \mu S$$

$$\frac{dI}{dt} = \beta\frac{SI}{N} + (1-\eta)\beta\frac{VI}{N} - \gamma I - \mu I$$

$$\frac{dV}{dt} = \upsilon S - (1-\eta)\beta\frac{VI}{N} - \mu V$$

$$\frac{dR}{dt} = \gamma I - \mu R$$

S_0 , I_0 , V_0 , R_0 , N_0

For the above system of equations $k_1^S, k_1^I, k_1^V, k_1^R$ and the others are determined as follows.

$$k_1^S = \Lambda - \beta\frac{S_0 I_0}{N_0} - \upsilon S_0 - \mu S_0$$

$$k_1^I = \beta\frac{S_0 I_0}{N_0} + (1-\eta)\beta\frac{V_0 I_0}{N_0} - \gamma I_0 - \mu I_0$$

$$k_1^V = \upsilon S_0 - (1-\eta)\beta\frac{V_0 I_0}{N_0} - \mu V_0$$

$k_1^R = \gamma I_0 - \mu R_0$

Thus.

$S^{(1)} = S_0 + \frac{h}{2}k_1^s \ , I^{(1)} = I_0 + \frac{h}{2}k_1^I \ , V^{(1)} = V_0 + \frac{h}{2}k_1^V , R^{(1)} = R_0 + \frac{h}{2}k_1^R$

In the same manner, we can determine $k_2^s . k_2^I \ . k_2^V . \ k_2^R$ and the others. Consequently, the variables for the next year are computed as follows.

$$S_{n+1} = S_n + \frac{h}{6}(k_1^s + 2k_2^s + 2k_3^s + k_4^s)$$

$$I_{n+1} = I_n + \frac{h}{6}(k_1^I + 2k_2^I + 2k_3^I + k_4^I)$$

$$V_{n+1} = V_n + \frac{h}{6}(k_1^V + 2k_2^V + 2k_3^V + k_4^V)$$

$$R_{n+1} = R_n + \frac{h}{6}(k_1^R + 2k_2^R + 2k_3^R + k_4^R)$$

Here we take $h = 1$, since we solve the equation separately for each year. Since the model parameters have been obtained and the initial conditions are shown in Table 1, the system of equations (1) takes the following form.

$$\frac{dS}{dt} = 332662.65 - 0.815\frac{SI}{N} - 0.43145S$$

$$\frac{dI}{dt} = 0.815\frac{SI}{N} + 0.04075\frac{VI}{N} - 0.08787I$$

$$\frac{dV}{dt} = 0.415S - 0.04075\frac{VI}{N} - 0.01645V$$

$$\frac{dR}{dt} = 0.07142I - 0.01645R$$

Wite the initial conditions given as follows.

$\mathrm{N}_0 = 20284308$
$\mathrm{I}_0 = 8762$
$\mathrm{V}_0 = 4225627$
$\mathrm{R}_0 = 0$
$\mathrm{S}_0 = 16049919$

When the mentioned steps are applied to the above system of equations, the values -8000, -10000, -11000 and -4972 are obtained for k_1^I, k_2^I, k_3^I and k_4^I respectively. After this, the value of I_1 is obtained as follows.

$$I_1 = I_0 + \frac{h}{6}(k_1^I + 2k_2^I + 2k_3^I + k_4^I)$$

$$I_1 = 8762 + \frac{1}{6}[-8000 + 2(-10000) + 2(-11000) + (-4972)]$$

$I_1 = 8762 - 5662$

$I_1 = 3100$

The remaining solution are obtained with the help of the python program, as shown in the following table.

***Table 3**: difference between the real data and the fitted data*

year	Observed cases	Fitted cases	Absolute error
2001	8762	8762	0
2002	2486	3100	614
2003	798	1200	402
2004	466	600	134
2005	1296	1100	196
2006	1990	1800	190
2007	1141	1200	59
2008	1599	1500	99
2009	2861	2700	161
2010	1989	1900	89
2011	3013	2900	113
2012	2787	2600	187
2013	430	500	70
2014	492	520	28
2015	1154	1000	154
2016	638	700	62
2017	1511	1450	61
2018	2012	2100	88
2019	353	400	47
2020	640	700	60
2021	2900	2800	100
2022	5166	5000	166
2023	2792	3000	208
2024	9761	9500	261

When the Parameter values from table(1) are substituted into equation (2) for the calculation of $\mathcal{R}_0$ then:

$$\mathcal{R}_0 = \frac{\beta[S^* + (1-\eta)V^*]}{N^*(\gamma + \mu)}$$

$$= \frac{0.815\left[16049919 + \left(1 - 0.95\right)4225627\right]}{20284308(0.07142 + 0.01645)}$$

$$= 7.4354$$

Since $\mathcal{R}_0$ =7.4354 we have $\mathcal{R}_0 > 1$. This indicates that measles is still spreading in Afghanistan. To control the disease, we calculate the minimum vaccination coverage required. For this purpose the previously obtained parameter values are substituted into equation (3).

$$C_{min} = \frac{\mathcal{R}_0 - 1}{\eta \mathcal{R}_0}$$

$$C_{min} = \frac{7.44 - 1}{0.95 \cdot 7.44}$$

$$C_{min} = \frac{6.44}{7.068} = 0.911$$

Therefore, to control measles in Afghanistan, the minimum vaccination coverage should be 91%, meaning that more than 91% of the population needs to be vaccinated to control the disease effectively.

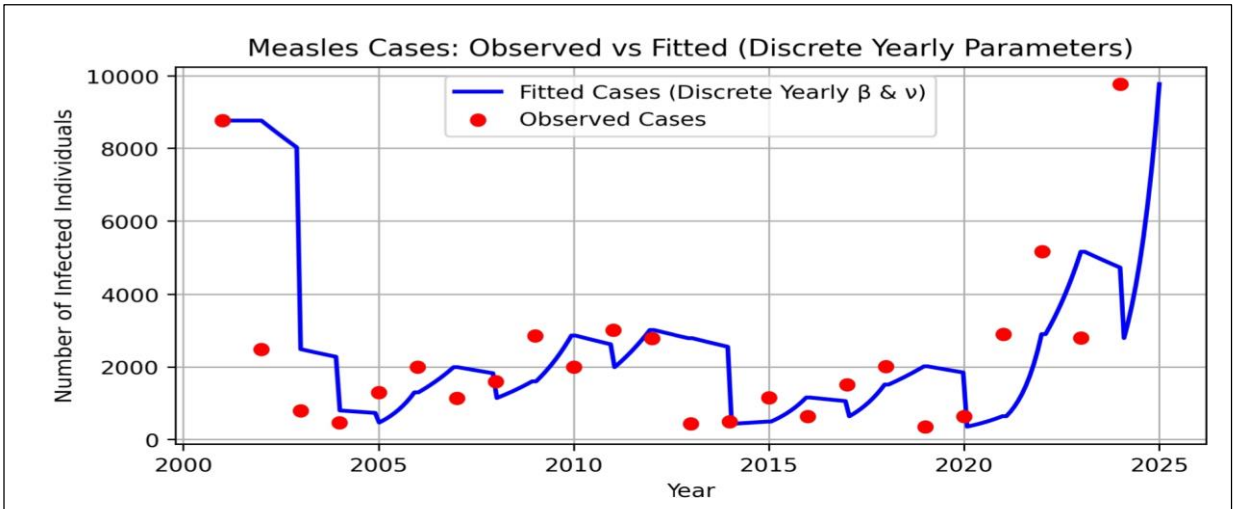

Figure 2: *The red dots represent the actual measles data and the blue line shows the model's best fit to the data*

Table 3 presents a comparison of observed measles cases with those generated by the SIRV model from 2001 to 2024. In addition, the absolute error between the observed and fitted values was calculated for each year. The results in Table 3 indicate that the model-fitted values are generally in good agreement with the observed data. For most years, the absolute error remains relatively small, demonstrating the adequacy of the model fit and the accuracy of the estimated parameters. For example, the absolute error is only 28 in 2014 and 62 in 2016, indicating a high level of agreement between the observed and fitted values. Although the errors are somewhat larger in a few years, such as 2002, 2003, and 2024, the model's overall behavior still captures the general trend of the observed data. Figure 2 presents a graphical comparison of the observed data and the SIRV model's fitted results. In this figure, the red dots represent the recorded measles cases, while the blue curve represents the model-estimated cases. The blue curve generally follows the pattern of the red dots and accurately reflects the major increases and decreases in the number of cases over time. The analysis of Figure 2 demonstrates that the SIRV model captures the overall transmission dynamics of measles in Afghanistan during 2001–2024. The agreement between the model predictions and the observed data suggests that the estimated parameter values provide a reasonable representation of the actual measles situation in Afghanistan. Therefore, the model offers a reliable scientific framework for analyzing disease transmission, calculating the basic reproduction number (R_0), and evaluating the impact of vaccination on measles control.

DISCUSSION

The results of this study showed that measles is still actively spreading in Afghanistan, as the basic reproduction number ($R_0 = 7.44$) was estimated to be greater than one. According to the calculations, a minimum vaccination coverage of approximately 91% is required for effective measles control. Furthermore, an increase in the transmission coefficient leads to more infections, whereas an increase in vaccination coverage reduces disease transmission and improves disease control. The findings of this study are consistent with those reported by Sinha (2023) in India. Using the SIRV model, Sinha concluded that vaccination plays a significant role in reducing measles transmission. Similarly, the results of the present study indicate that increasing vaccination coverage reduces the number of infected individuals and contributes to disease control.

Likewise, the study conducted by Seydou and Moussa Tessa (2023) in Niger demonstrated that vaccination is a key factor in preventing measles transmission and reducing the effective reproduction number. The findings of the current study are consistent with these results, as increased vaccination coverage was found to reduce disease transmission and enhance the likelihood of disease control. In Nigeria, Peter and Oguntolu (2025) showed that effective control strategies, particularly vaccination, play an important role in reducing the spread of measles. This finding is consistent with the present study, which also emphasizes the importance of increasing vaccination coverage to control measles. The study by Oke (2019) based on an SIRV model, demonstrated that vaccination and treatment contribute significantly to disease control and system stability. Similarly, the results of the present study show that increasing vaccination coverage reduces the number of infected individuals and improves the effectiveness of disease control.

In the same way, the studies by Kumar (2019) and Kumar and Srivastava (2021), conducted in India, found that vaccination strategies are effective in reducing disease transmission and controlling epidemics. The findings of the present study based on data from Afghanistan support these conclusions. Moreover, Patel (2019) reported that insufficient vaccination coverage contributes to measles resurgence and outbreaks in the United States. The present study reached a similar conclusion, showing that at least 91% vaccination coverage is required for effective disease control, and that lower coverage levels increase the likelihood of continued disease transmission. Furthermore, Tegegn (2024), using an age-structured SEIR model in Africa, concluded that vaccination plays a fundamental role in reducing measles transmission. Although the modeling frameworks differ, both studies emphasize the critical importance of vaccination for disease control.

Overall, the findings of the present study are largely consistent with those reported in previous research. However, the unique contribution of this study lies in its use of real data from

Afghanistan covering the period 2001–2024 and in estimating a country-specific basic reproduction number, R_0, of 7.44 and a minimum vaccination coverage of approximately 91%. These results provide valuable scientific evidence for public health policy development and measles control strategies in Afghanistan

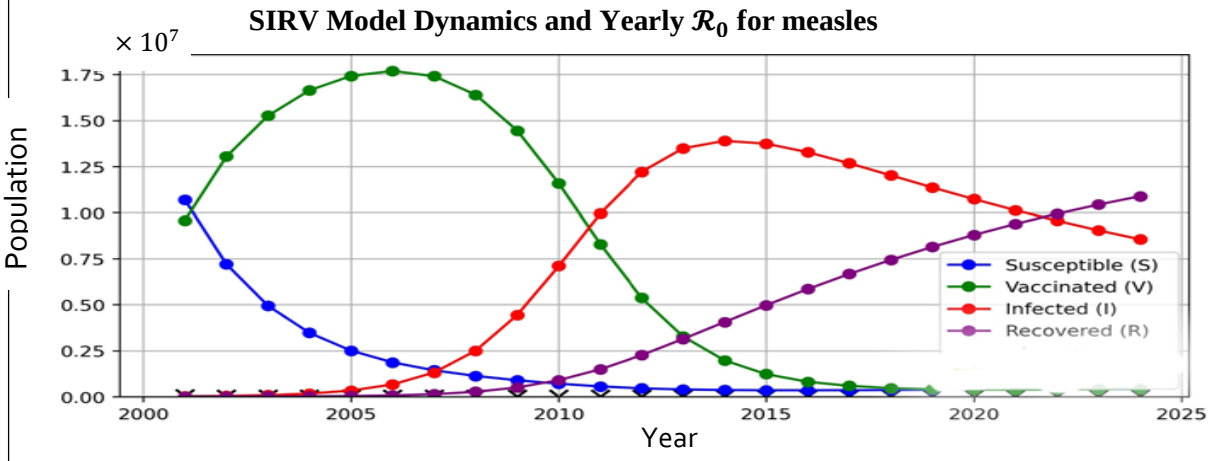

***Figure 3**: Graphs of the model variables when $\beta = 0.815$ and $\mathcal{R}_0 = 7.44 > 1$*

In the figure above, the curves for the four population compartments of the SIRV model are displayed. The blue curve representing susceptible individuals gradually declines over the years, indicating that the number of susceptible people decreases due to vaccination and movement into the infected class. The green curve represents vaccinated individuals, and it shows that vaccination coverage increases over time. The upward trend of this curve demonstrates the effectiveness of the vaccination program and its significant contribution to reducing the susceptible population. The red curve represents the number of infected individuals. The model solution shows that the number of infected individuals varies over time, and in some years the increase may be attributed to low vaccination coverage and higher transmission rates. This curve clearly indicates that measles is still spreading in Afghanistan, since the value of $\mathcal{R}_0$ is greater than one. The purple curve represents the number of recovered individuals. This curve rises after the infected curve as infected individuals move to the recovered compartment following treatment or natural recovery. Overall, from Figure (3) it can be concluded that the model solution converges toward an endemic state, because $\mathcal{R}_0 > 1$ and the number of infected individuals never reaches zero; that is, the disease persists in the population. Vaccination and natural immunity reduce the severity of the disease, but they are not sufficient for complete eradication. Therefore, if vaccination coverage is not increased and the transmission rate is not reduced, the spread of the disease will continue.

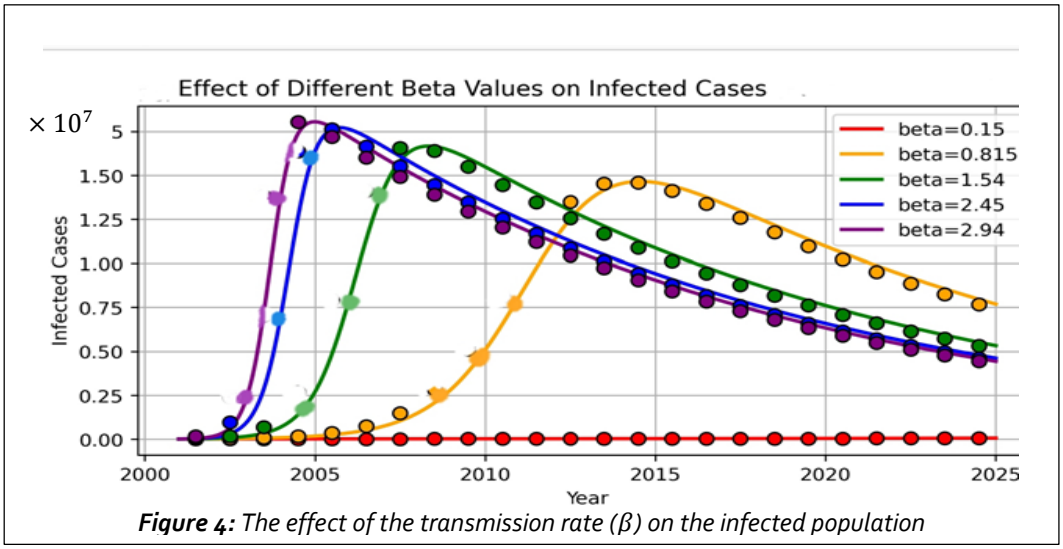

Figure 4: *The effect of the transmission rate (β) on the infected population*

In Figure (4), the effect of different values of the disease transmission rate (β) on the infected population (I) is illustrated. The graph contains five curves, each corresponding to a different value of β. As β increases, the number of infected individuals increases, and the curve rises. Conversely, when the value of β decreases, the number of infected individuals decreases, and the curve moves downward. Thus, it is clear that the transmission rate (β) directly controls the number of infected individuals. Therefore, reducing the transmission rate through vaccination, quarantine, or other preventive measures plays a crucial role in controlling the spread of the disease. With higher values of β, the number of infected individuals remains high, approaching an endemic state. In contrast, with lower values of β, the number of infected individuals remains low, and the system reaches equilibrium more quickly.

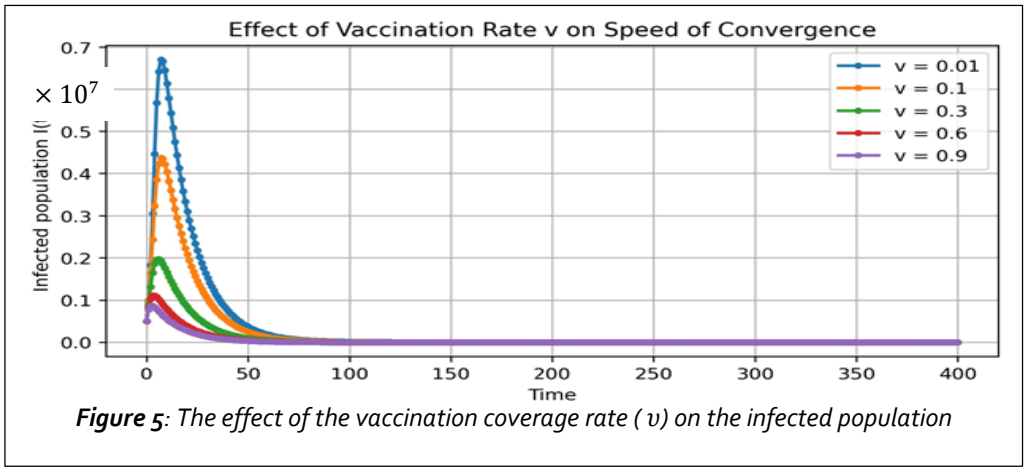

Figure 5*: The effect of the vaccination coverage rate (υ) on the infected population*

From Figure (5) it can be concluded that the vaccination coverage rate (υ) has a significant effect on the spread of measles and on the number of infected individuals. A low vaccination coverage (such as $\upsilon = 0.01$) results in a higher peak of infected individuals and a longer-lasting outbreak. In contrast, higher vaccination coverage levels (such as $\upsilon = 0.6$ and $\upsilon = 0.9$) noticeably reduce the number of infected individuals and allow the disease to reach equilibrium

more quickly. Overall, Figure (5) clearly demonstrates that high vaccination coverage reduces the severity of the outbreak, lowers the infection peak, and plays a crucial role in controlling the spread of measles. On the other hand, low vaccination coverage leads to prolonged and widespread disease transmission.

CONCLUSION

In this study, the spread and control of measles in Afghanistan were analyzed using the SIRV mathematical model. The model was calibrated using real data from 2001 to 2024, and its differential equations were solved using the fourth-order Runge–Kutta (RK4) method in the Python programming environment. Parameter estimation yielded $\beta = 0.815$ and $\upsilon = 0.415$ while the basic reproduction number was calculated as $R_0 = 7.44$, indicating that measles is still actively spreading in Afghanistan. Furthermore, the minimum vaccination coverage required for effective disease control was estimated to be approximately 91%. The numerical results showed that increasing the transmission coefficient increases the number of infected individuals, whereas increasing vaccination coverage reduces disease transmission. The analysis of different vaccination coverage levels also demonstrated that higher vaccination coverage plays a significant role in controlling the disease. Based on the findings of this study, the following recommendations are proposed:

1. From a mathematical modeling perspective, optimal strategies for the prevention and control of infectious diseases warrant further investigation.
2. Future researchers may analyze the spread of measles in Afghanistan using more advanced mathematical models to obtain deeper insights into disease dynamics and control measures.

Authors Contributions

- Mohammad Khan Haidary assisted in reviewing the article's title and text.
- Said Omar Saidi developed the article's main title and collected, organized, and analysed the data for it.

Acknowledgements

I would like to express my sincere gratitude to the Faculty of Mathematics at Kabul University for their valuable technical and academic support in completing this research. Their cooperation and guidance played a fundamental role in the progress and success of my research.

Funding Information

No funding is available for the manuscript.

Conflict of Interest Statement

The authors declare that they have no conflict of interest.

Data Availability Statement

The data used in this study were obtained from publicly available sources, including WHO and other official databases. All data sources and links are cited in the reference section of the article. Therefore, the datasets analyzed in the current study are publicly accessible and can be obtained from the corresponding sources upon request.

REFERENCES

Anderson, R. M., & May, R. M. (1991). *Infectious diseases of humans: Dynamics and control.* Oxford University Press.Link

Deng, Z.-Q., Singh, V. P., & Bengtsson, L. (2020). Numerical solution of fractional advection–dispersion equation. *Applied Mathematics and Computation, 371, 124943*.Link

Diekmann, O., Heesterbeek, J. A. P., & Roberts, M. G. (2010). The construction of next-generation matrices for compartmental epidemic models. *Journal of the Royal Society Interface, 7(47), 873–885.* Link

Fine, P. E., & Clarkson, J. A. (1982). Measles in England and Wales I: An analysis of factors underlying seasonal patterns*. International Journal of Epidemiology, 11(1), 5–14*.Link

Griffin, D. E. (2018). Measles virus. In D. M. Knipe & P. M. Howley (Eds.), *Fields virology (7th ed., pp. 1944–1961). Wolters Kluwer*.Link

Heesterbeek, J. A. P. (2002). A brief history of R_0 and a recipe for its calculation. *Acta Biotheoretica, 50(3), 189–204.* Link

Hethcote, H. W. (2000). The mathematics of infectious diseases. SIAM Review, 42(4), 599–653.Link

Kumar, S., Jain, S., & Gupta, S. (2019). Mathematical modeling and analysis of infectious disease with vaccination strategy. *Chaos, Solitons & Fractals, 129, 1–10.*Link

Kumar, S., & Srivastava, P. K. (2021). Stability analysis of an epidemic model with vaccination and nonlinear incidence rate. *Mathematical Methods in the Applied Sciences, 44(5), 3953–3970.* Link

Patel, M., Lee, A. D., Clemmons, N. S., Redd, S. B., & Gastañaduy, P. A. (2019). National update on measles cases and outbreaks—United States, January 1–October 1, 2019. *MMWR Morbidity and Mortality Weekly Report, 68, 893–896.* Link

PopulationPyramid.net. (n.d.). Population pyramids of the world from 1950 to 2100:

Afghanistan (2001–2024) [Data set]. Retrieved January 8, 2026, Link

Chatterjee, A. N., Sharma, S. K., & Al Basir, F. (2024). A compartmental approach to modeling the measles disease: A fractional order optimal control model. Fractal and Fractional, 8(4), 446.Link

Kröger, M., & Schlickeiser, R. (2023). On the analytical solution of the SIRV-model for the temporal evolution of epidemics for general time-dependent recovery, infection and vaccination rates. Preprints.Link

Schlickeiser, R., & Kröger, M. (2024). Mathematics of epidemics: On the general solution of SIRVD, SIRV, SIRD, and SIR compartment models. *Mathematics, 12(7), 941*.Link

Perasso, A. (2018). An introduction to the basic reproduction number in mathematical epidemiology. ESAIM: Proceedings and Surveys, 62, 123–138.Link

Fosu, G. O., Akweittey, E., & Adu-Sackey, A. (2020). Next-generation matrices and basic reproductive numbers for all phases of the coronavirus disease. *Mathematical Sciences*.Link

Jones, J. H. (2007). Notes on R_0. Stanford University.Link

Shirazian, M., Ammarloo, Z., & Janrian, Z. (2016). Optimal control strategy for rumor spreading using a modified SIR model. Proceedings of the National Seminar on Control and Optimization. (In Persian).

van den Driessche, P., & Watmough, J. (2002). Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission. *Mathematical Biosciences, 180, 29–48*. Link

Peter, O. J., & Oguntolu, F. A. (2025). Mathematical model of measles epidemiology with control strategies. Mathematical Methods and Models in Biosciences Conference, Sofia.Link

Ishikawa, M. (2012). Optimal strategies for vaccination using the stochastic SIRV model. *Journal of the Society of Instrument and Control Engineers, 25(12), 343–348*.

Seydou, M., & Moussa Tessa, O. (2023). A stochastic SIRV model to estimate the effective reproductive number for measles epidemic in Niger. *Journal of Advances in Mathematics and Computer Science, 38(10), 218–232*. Link

Dai, Q., & Wang, Z. (2024). SIRV fractional epidemic model of influenza with vaccine game theory and stability analysis. *Electronic Research Archive, 32(12), 6792–6821*. Link

Grela, E., Stich, M., & Chattopadhyay, A. K. (2018). Epidemiological impact of waning immunization on a vaccinated population. arXiv preprint.Link

Sinha, A. (2023). A predictive analysis of measles outbreak dynamics using SIRV modeling (Preprint).

Oke, M. O., Ogunmiloro, O. M., Akinwumi, C. T., & Raji, R. A. (2019). Mathematical modeling and stability analysis of a SIRV epidemic model with nonlinear force of infection and treatment. *Communications in Mathematics and Applications, 10(4), 717–731*. link

Tang, L., Zhou, Y., Wang, L., Purkayastha, S., Zhang, L., He, J., Wang, F., & Song, P. X.-K. (2020). A review of multi-compartment infectious disease models. *International Statistical Review, 88(2), 462–513*.Link

Bjørnstad, O. N., Shea, K., Krzywinski, M., & Altman, N. (2020). The SEIRS model for infectious disease dynamics. *Nature Methods, 17, 557–558*.Link

Hou, Y., & Bidkhori, H. (2024). Multi-feature SEIR model for epidemic analysis and vaccine prioritization. PLOS ONE, 19(3), e0298932.Link

Tegegn, T. A. (2024). Age-structured SEIR model with vaccination for modeling the spread of measles in Africa. *BIOMATH*.

El-Doma, M. (2006). Stability analysis for an age-structured SEIR epidemic model under vaccination. *Applications and Applied Mathematics, 1(2), 96–111*.

World Health Organization. (2019, October). SAGE meeting documents: Measles and rubella vaccines [Presentation]. Link

World Health Organization. (2020). Measles fact sheet. Retrieved January 8, 2026. Link

World Health Organization. (2025a). Measles vaccines: WHO position paper. *World Health Organization*.Link

World Bank.(2024).Life expectancy at birth, total (years)-Afghanistan. Link

World Health Organization. (2025b). Afghanistan infectious disease outbreaks situation report: Epidemiological week 42, 2025 (Acute watery diarrhea cases). *WHO Regional Office for the Eastern Mediterranean*. Link