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Full Length Research Paper

Transmission dynamics of infectious diseases by immigrants in a vaccinated and temporary immune protected population

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In this paper, a mathematical model of infectious diseases by immigrants in a vaccinated and temporary immune protected population has been investigated. The model incorporates the assumption that immigrant individuals enter in the respective population with an immunity received from either vaccination or recover from the disease. The stability of the system has been analyzed for the existence of the disease-free and endemic equilibrium points, and it has been shown that the disease free equilibrium point is asymptotically stable when an effective reproduction number is less than unity and unstable when an effective reproduction number is greater than unity. From the analysis of the model, it is shown that vaccination coverage is greater than the vaccination; otherwise the disease will persist within the community. It is also shown that the increase of immigrants in a population tends to lower the first dose-vaccination coverage, hence the disease become endemic in the population. Numerical simulations of the model showed that in the absence of the immigrants, the disease can be eradicated in a population with a single-dose vaccination only.

Key words: Immune protection, infectious diseases, infections by immigrants, disease transmission, recovered individuals, vaccinated population.

INTRODUCTION

Raimundo et al. (2007) established and analysed a mathematical model on the effect of temporary immune protection and vaccination against infectious diseases. However, the integration of susceptible immigrants to the population was not incorporated. In this paper, it is intended to analyse a model which incorporate the impact of susceptible immigrants on the disease transmission dynamics. Therefore we study a deterministic model for transmission dynamics of infectious diseases by immigrants in a vaccinated and temporary immune protected population. The model incorporates the assumption that immigrants who enter the respective population are either naïve or already acquired temporary immunity received from vaccination natural recovery from the disease.

Transmission dynamics of infectious diseases occurs when the agent leaves its reservoir or host through a portal of exit, and is conveyed by some mode of transmission, and enters through appropriate portal of entry to infect a susceptible host. The most common modes of transmission of infectious diseases are direct transmission (direct contact and droplets transmissions) and indirect transmission (airborne, vehicle borne, vector borne, biologic and mechanical transmissions) (CDC, 2005).

Population mobility has been reported as the major influence on the spread of infectious diseases (Gushulak and Macpherson, 2003). Global migration has

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characterized population movement since the middle of the twentieth century. This has been caused by unprecedented volume, speed, and geographical range of travel (Collin and Lee, 2003). International migration, or the movement of people between countries, now counts for approximately 130 million people per year. By 2000, up to 185 million people were living outside their country of birth compared with 75 million in 1965 (UNFPA, 2003). At least half of these migrants were living in low- income countries (Cannito et al,, 2004). In the mid 1980s, one billion people, or about one sixth of the world's population, moved within their own countries (Cannito et al., 2004).

There are several reasons why population mobility and incidence and spread of infections are closely linked. The conditions which lead to migration are similar to those which favour the emergence of new infections (Minas, 2003). Mass migration increases the risks of infection if displaced communities are malnourished, have inadequate water and sanitation and are overcrowded. In some cases, this leads to unregulated and inappropriate use of antibiotics, which can contribute to the emergence and drug- resistant organisms (Minas, 2003). Migration also brings people into contact with new microbes and vectors as well as new gene pools, immunological makeup, cultural preferences, behavioural pathogens and technologies (Lee, 2003). All these influence the risks of infection.

The link between infectious diseases and population mobility must be understood in relation to the different forms, conditions and patterns of migration, which have very different influences on the distribution and spread of infectious diseases. For example in low-income countries, economic migration has played a crucial in the evolution of the HIV/AIDS epidemic. However researches show that internal and cross-border migrants, particularly male migrant workers, are at greater risk of HIV infection, and are more likely to spread the disease when they return home (Waldman, 1993). In this paper, therefore it is intended to investigate the transmission dynamics of infectious diseases by immigrants in a vaccinated and temporary immune protected population. It is assumed that the immigrants can either be susceptible or infective, in which infective immigrants take the role of transmitting the disease.

The concealed and apparently unpredictable nature of infectious diseases has been a source of fear and superstition since the first ages of human civilization. The world wide panic following the emergence of severe acute respiratory syndrome (SARS) and avian flu in South–East Asia are recent examples that our feeling of dread increases with our ignorance of the disease (Morens et al., 2004). One of the primary aims of epidemic modelling is helping to understand the spread of diseases in host populations, both in time and space. Indeed, the processes of systematically clarifying indirect model assumptions, interpreting its variables and estimating parameters is invaluable in uncovering precisely the observed patterns.

FORMULATION OF THE MODEL

To formulate the model and set up the related differential equation, we divide the total population (N) into six classes: Namely, the naive susceptible individuals $S_1^{'}$, the vaccinated individuals $V_{,}^{'}$ the primary infectious individuals $I_1^{'}$, the susceptible individuals that developed immune response (by natural infection and primary vaccination) lost after certain period of time and these individuals may need second vaccine doses or may be re-infected $S_2^{'}$, the secondary infectious individuals $I_2^{'}$, and finally the recovered individuals $R_2^{\prime}$. It is assumed that immigrants enter the respective population are either naïve or had already acquired temporary immunity received from vaccination /natural recovery from the disease.

The model will include the vital dynamics, that is the mortality rate μ and the positive and constant recruitment rate μN so that it balances natural deaths, for the total population to be of constant size N. The interaction between the classes will be assumed as follows (Raimundo et al., 2007): The naive susceptible individuals $(S_1^{'})$ are rapidly shifted to the vaccinated class $(V^{'})$ by routine immunization at the rate υ_1, at the same time the naive susceptible individuals $(S_1^{'})$ may also become primary infectious $(I_1^{'})$ following the true mass action incidence (de Jong et al.., 1994). The incidence is the infection rate of susceptible individuals through their contacts with infectives, such that the number of primary infectious individuals $(I_1^{'})$ produced by adequate contacts is $\frac{\beta_1 S_1^{'}(I_1^{'}+I_2^{'})}{N}$, where β_1 is the transmission coefficient of the disease at primary infection.

When individuals are vaccinated, the vaccine induces less protection than does the natural infection itself, and the immunity (induced in response to both vaccination and natural infection) may diminish over time resulting in a different class of susceptible individuals $S_2^{'}$. These susceptible individuals developed immunological memory since they are already had contact with the virus either by vaccination or by disease (wild virus). These susceptible individuals had rid themselves from the antibodies against both wild and vaccination virus but due to their immunological memory they are able to elicit very quickly

an immune response, so their re-infection rate is lower than that of the naive susceptible individuals $S_1^{'}$. In such situation, the number of new infectious produced by adequate contacts is $\frac{\beta_2 S_2(I_1+I_2)}{N}$, where $\beta_2=\sigma\beta_1$ is the transmission coefficient of the disease at re-infection and $0\le\sigma\le1$. The parameter σ illustrates the effect of immunological memory so it is the factor that reduces the risks of re-infection (σ) measures the susceptibility to re-infection. In case $\sigma=0$, both the vaccine and infection are totally effective, the immunological memory developed against re-infection does not wane overtime, and the proposed model reduces to $SIRS$ type model with vaccination. Whereas the $\sigma=1$, implies that both vaccine and infection are totally useless to induce immunological memory. It is now assumed that both vaccination and infection elicit immune responses, but they fail to offer long lasting protection against re-infection now, that is $0<\sigma<1$.

Vaccine-induced and wild virus induced (natural) immunity against infection are assumed to be lost at capita rates ρ_1 and ρ_2, respectively. This means that, ρ_1 is the rate at which the vaccine protection wanes and ρ_2, is the rate at which the natural protection wanes, with $\rho_1>\rho_2$ (Raimundo et al., 2007). The average duration of immune protection (α) (Wodarz, 2003) acquired either by preventive vaccine or infection is $\alpha_1=1/\rho_1$, $\alpha_2=1/\rho_2$ respectively.

The model assumes that both the primary and secondary infectious individuals, I_1 and I_2, recover with the rate constants $\gamma_1>0$ and $\gamma_2>0$ in which $\gamma_1<\gamma_2$. Thus the secondary infected individuals will be more active in cleansing the pathogen than the primary infected individuals because the immunological memory responds faster stronger to new infections.

The recovered individuals (R') move back to class $(S_2^{'})$ by waning protection both to natural infection and re-infection (Grenfell and Anderson, 1989) as shown in the figure below. Because immunological memory was reduced and the immune system can remember the identity of the pathogen, the susceptible $S_2^{'}$ no longer move back to naive class $S_1^{'}$. Lastly, we assume that the individuals in $S_2^{'}$ class may either be revaccinated at the rate ν_2 or become infectious again $(I_2^{'})$. Figure 1 below is the flow diagram of the interaction of the classes in the population (Gomes et al., 2004).

The model is governed by the following system of ordinary differential equations.

$$\begin{cases} \frac{dS_1^{'}}{dt}=\Lambda+(1-P)A-\frac{\beta_1 S_1^{'}(I_1^{'}+I_1^{'})}{N}-(\mu+\nu_1)S_1^{'}, \\ \frac{dV^{'}}{dt}=\nu_1 S_1^{'}+\nu_2 S_2^{'}-(\mu+\rho_1)V^{'}, \\ \frac{dI_1^{'}}{dt}=\frac{\beta_1 S_1^{'}(I_1^{'}+I_2^{'})}{N}-(\gamma_1+\mu)I_1^{'}, \\ \frac{dS_2^{'}}{dt}=PA+\rho_1 V^{'}+\rho_2 R^{'}-\frac{\beta_2 S_2^{'}(I_1^{'}+I_2^{'})}{N}-(\nu_2+\mu)S_2^{'}, \\ \frac{dI_2^{'}}{dt}=\frac{\beta_2 S_2^{'}(I_1^{'}+I_2^{'})}{N}-(\mu+\gamma_2)I_2^{'}, \\ \frac{dR_1^{'}}{dt}=\gamma_2 I_2^{'}+\gamma_1 I_1^{'}-(\rho_2+\mu)R^{'}, \end{cases} \quad (1)$$

with nonnegative initial conditions and $N(0)>0$,

where Λ is the recruitment birth as naive susceptible, A is the Naïve susceptible individuals arriving as immigrants, and P is the proportion of A as immigrants arriving into a population with immunity

The system (1) is well posed, since solutions remain nonnegative for non-negative initial conditions. The demographic equation for the dynamics of the total population is given by

$$\frac{dN}{dt}=A+\Lambda-\mu N$$

Since the population is constant, then $dN/dt=0$, implying that $N=\frac{A+\Lambda}{\mu}$.

Since the model is homogeneous of degree one, the variables can be normalized by setting $S_1=S_1'/N$, $S_2=S_2'/N$, $I_1=I_1^{'}/N$, $I_1^{'}=I_1^{'}/N$, $R=R'/N$ and $a=A/N$.

This leads to the normalized system

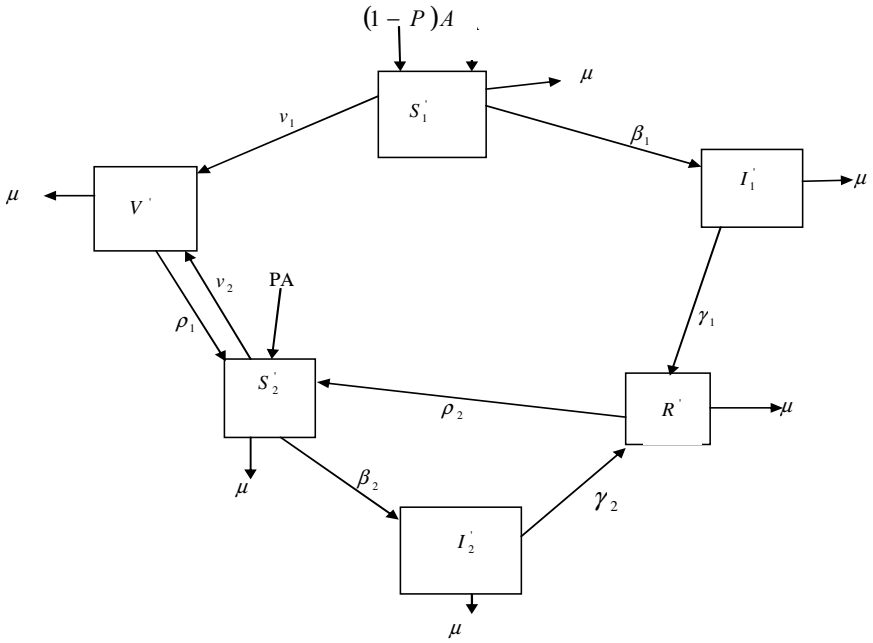


Figure 1. A compartmental model for transmission dynamics of infectious diseases.

$$\begin{cases} \frac{dS_1}{dt} = \mu - Pa - \beta_1 S_1(I_1 + I_2) - (\mu + v_1)S_1 \\ \frac{dV}{dt} = v_1 S_1 + v_2 S_2 - (\mu + \rho_1)V \\ \frac{dI_1}{dt} = \beta_1 S_1(I_1 + I_2) - (\gamma_1 + \mu)I_1 \\ \frac{dS_2}{dt} = \mathrm{P}a + \rho_1 V + \rho_2 R - \beta_2 S_2(I_1 + I_2) - (v_2 + \mu)S_2 \\ \frac{dI_2}{dt} = \beta_2 S_2(I_1 + I_2) - (\mu + \gamma_2)I_2 \\ \frac{dR}{dt} = \gamma_2 I_2 + \gamma_1 I_1 - (\rho_2 + \mu)R \end{cases} \quad (2)$$

with $N = S_1 + V + I_1 + S_2 + I_2 + R$, $N = 1$ and $dN/dt = 0$.

ANALYSIS OF THE MODEL

The system (2) will be qualitatively analyzed so as to find the conditions for existence and stability of disease free equilibrium points. Analysis of the model allows us to determine if increasing the number of immigrants into a population tends to lower the first dose-vaccination coverage or not. Also on finding the reproductive number R_0, one can determine if the disease become endemic in a population. The reproductive number R_0 introduced by Ross (1909), is defined in epidemiological modelling as the average number of infected individuals produced by one infected immigrant in a population which is completely susceptible. If $R_0 < 1$, the disease vanishes, and if $R_0 > 1$, the disease spreads and goes to the endemic level. For a disease that confers immunity in which the susceptible population is vaccinated, it has been found that under certain conditions there is a dependence of the reproductive number on the vaccination rate. In such a case the reproduction ration R_{vac}, which is the basic reproduction ration R_0 modified by vaccination, must be reduced to below one in order to ensure that the disease vanishes (Raimundo et al., 2007). If there is no vaccination, then $R_{vac} = R_0$

Disease free equilibrium point

For system (2), always there exists a disease-free or trivial equilibrium point (DFE) $E_0^* = (S_1^*, V^*, 0, S_2^*, 0, 0)$, with

$$\begin{cases} S_1^* = \dfrac{\mu - Pa}{\mu + v_1} \\ V^* = \dfrac{1}{\rho_1 + \mu}\left[\dfrac{v_1(\mu - Pa)}{v_1 + \mu} + \dfrac{v_2 v_1 \rho_1}{(v_1 + \mu)(v_2 + \rho_1 + \mu)} + \dfrac{v_2 Pa}{v_1 + \mu}\right] \\ S_2^* = \dfrac{\rho_1 v_1}{(v_1 + \mu)(v_2 + \rho_1 + \mu)} + \dfrac{Pa}{v_1 + \mu} \end{cases} \quad (3)$$

The Jacobian matrix of the system (3) evaluated at the DFE is

$$\mathbf{A}_0 = \begin{bmatrix} a_{11} & 0 & -\beta_1 S_1^* & 0 & -\beta_1 S_1^* & 0 \\ v_1 & -(\rho_1 + \mu) & 0 & v_2 & 0 & 0 \\ \beta_1(I_1^* + I_2^*) & 0 & a_{22} & 0 & \beta_1 S_1^* & 0 \\ 0 & \rho_1 & \beta_2 S_2^* & a_{33} & \beta_2 S_2^* & \rho_2 \\ 0 & 0 & \beta_2 S_2^* & \beta_2(I_1^* + I_2^*) & a_{44} & 0 \\ 0 & 0 & \gamma_1 & 0 & \gamma_2 & -(\rho_2 + \mu) \end{bmatrix}, \quad (4)$$

where
$$a_{11} = -(v_1 + \mu)$$
$$a_{22} = \beta_1 S_1^* - (\gamma_1 + \mu)$$
$$a_{33} = \beta_2(I_1^* + I_2^*) - (v_2 + \mu)$$
$$a_{44} = \beta_2 S_2^* - (\gamma_2 + \mu).$$

Two of the eigenvalues of $\mathbf{A}_0$ are straightforward determined as $\lambda_1 = -(v_1 + \mu)$ and $\lambda_2 = -(\rho_2 + \mu)$. The other four are expressed as the roots of the equation;

$$\mathbf{A}_{22}\left\{\begin{vmatrix} \beta_1 S_1^* - (\gamma_1 + \mu) - \lambda & \beta_1 S_1^* \\ \delta\beta_1 S_2^* & \delta\beta_1 S_2^* - (\gamma_2 + \mu) - \lambda \end{vmatrix} = 0\right. \quad (5)$$

where $\mathbf{A}_{22} = \begin{vmatrix} -(\rho_1 + \mu) - \lambda & v_2 \\ \rho_1 & -(v_2 + \mu) - \lambda \end{vmatrix}$

Since $\text{trace}(\mathbf{A}_{22} < 0)$, and $\det(\mathbf{A}_{22} > 0)$, $\mathbf{A}_{22}$ has two negative eigenvalues. The other two eigenvalues associated with the second degree of Equation (5) are negative when

$$R_{vac} = R_0 \times q < 1. \quad (6)$$

where R_{vac} is the reproduction ratio which is the basic reproduction number R_0 modified by vaccination.

$$R_0 = \frac{\beta_1}{\gamma_1 + \mu}, \quad (7)$$

$$q = \frac{\mu + Mv_1 + PaL}{v_1 + \mu}, \quad (8)$$

$$M = \frac{\delta\rho_1(\gamma_1 + \mu)}{(\gamma_2 + \mu)(v_2 + \rho_1 + \mu)}, \quad (9)$$

$$L = \frac{\delta(\gamma_1 + \mu)}{(\gamma_2 + \mu)} - 1. \quad (10)$$

Since $\gamma_2 > \gamma_1$, $\rho_1 > \rho_2$ and $0 < \delta < 1$ we have $L < 0$ and $M < 1$, therefore $q < 1$. Hence, the DFE (3) is asymptotically stable when the condition (6) holds. Setting $R_{vac} = 1$ and solving for Equation (6) for v_1, the threshold vaccination rate is found to be

$$v_1^c(v_2) = \frac{\mu(R_0 - 1) + R_0 PaL}{1 - R_0.M}. \quad (11)$$

Hence, for $R_0 < 1$ the DFE is stable. For $R_0 > 1$, $v_1^c(v_2)$ is positive if and only if $M < 1/R_0$. In this case, the disease is eradicated when, $v_1 > v_1^c(v_2)$, otherwise when $v_1 < v_1^c(v_2)$ the disease stays in the community.

From Equation (9), if the vaccine has no effects, then $\rho_1 \to \infty$, meaning that $M \to \frac{\delta(\gamma_1 + \mu)}{(\gamma_2 + \mu)} < \delta$. If the vaccine induces lifelong immunity, then $\rho_1 = 0$ and the disease eradication is attainable with single –dose vaccination.

For $M > 1/R_0$ a single vaccine dose will not eradicate the disease when $\rho_1 \to \infty$ or $0 < \delta \le 1$. Under these circumstances, a second dose must be administered only when $\rho_1 > 0$.

The basic problem is to find out when the first dose loses effectiveness so that a second dose becomes necessary to eradicate the disease. To find the critical value of ρ_1, one sets $v_2 = 0$. If $v_1 \to \infty$ the conditions for disease eradication are $q = M$ and $R_{vac} = M \times R_0 < 1$. Setting $M \times R_0 = 1$ one gets

$$\rho_1^c = \frac{(\gamma_2+\mu)(\nu_2+\mu)}{\beta_2-(\gamma_2+\mu)}, \quad (12)$$

and the disease can be eradicated with a single dose vaccination if $\rho_1 < \rho_1^c$. For weak reinfection, $\beta_2 < (\gamma_2+\mu)$, implies that $\rho_1^c < 0$ and the disease can be eradicated with a single vaccination dose. Finally, for $\rho_1 > \rho_1^c$, condition (6) becomes necessary for two dose vaccination program to be successful.

The impact of immigrants in the process of vaccination can be determined by the relationship $R_{vac} = R_0 \times q < 1$. We need to find out the minimum number of immigrants necessary for the disease eradications using the vaccination program. Setting

$$R_{vac} = 1$$

we have

$$R_{vac} = R_0 \times q = 1,$$

or

$$\frac{R_0 \times (\mu + M\nu_1 + PaL)}{(\nu_1+\mu)} = 1.$$

Solving for Pa as immigrants, one gets

$$Pa = \frac{\nu_1(1-R_0M)+\mu(1-R_0)}{R_0 L}.$$

But

$M = \frac{\delta\rho_1(\gamma_1+\mu)}{(\gamma_2+\mu)(\nu_2+\rho_1+\mu)}$ and $L = \frac{\delta(\gamma_1+\mu)}{(\gamma_2+\mu)}$, so that

$$Pa = \frac{\nu_1\left(1-\frac{R_0\delta\rho_1(\gamma_1+\mu)}{(\gamma_2+\mu)(\nu_2+\rho_1+\mu)}+\mu(1-R_0)\right)}{R_0\left(\frac{\delta(\gamma_1+\mu)}{\gamma_2+\mu}-1\right)}, \quad (13)$$

If $\delta \to \infty$, $L > 1$. Therefore the disease cannot be eradicated in the community by using single-dose vaccination only. Under this condition the second-dose vaccination must be administered.

If $\delta \to 0$, $L < 1$ and the disease eradication is attainable with a single-dose vaccination only.

In the absence of immigrants, $Pa = 0$. Consequently

$$R_0 = \frac{(\gamma_2+\mu)(\nu_1+\mu)(\nu_2+\rho_1+\mu)}{\nu_1\delta\rho_1(\gamma_1+\mu)+\mu(\gamma_2+\mu)(\nu_2+\rho_1+\mu)}. \quad (14)$$

Hence if $R_0 < 1$, the disease can be eradicated by a single dose vaccination.

Endemic equilibrium points

When the population has a disease, one has $I^* \neq 0$, In this case there may be several critical points when $I^* \neq 0$. These are the endemic equilibrium points (EEP) of the model. These points will be denoted by $E_e = (S_1^*, V^*, I_1^*, S_2^*, I_2^*, R^*)$ which are determined from the system (2) as follows;

$$\begin{cases} \mu - Pa - (\nu_1+\mu)S_1^* - (\gamma_1+\mu)I_1^* = 0, \\ \nu_1 S_1^* + \nu_2 S_2^* - (\rho_1+\mu)V^* = 0, \\ \beta_1 S_1^*(I_1^*+I_2^*) - (\gamma_1+\mu)I_1^* = 0, \\ Pa + \rho_1 V^* + \rho_2 R^* - (\nu_2+\mu)S_2^* - (\gamma_2+\mu)I_2^* = 0, \\ \gamma_1 I_1^* + \gamma_2 I_2^* - (\rho_2+\mu)R^* = 0, \\ \gamma_1 I_1^* + \gamma_2 I_2^* - (\rho_2+\mu)R^* = 0. \end{cases} \quad (15)$$

From the first, second and the fifth equations, one gets

$$\begin{cases} S_1^* = \frac{\mu - Pa - (\gamma_1+\mu)I_1^*}{\nu_1+\mu}, \\ V^* = \frac{\nu_1 S_1^* + \nu_2 S_2^*}{\rho_1+\mu}, \\ R^* = \frac{\gamma_1 I_1^* + \gamma_2 I_2^*}{\rho_2+\mu}. \end{cases} \quad (16)$$

The negative values of the variables have no biological meaning. Thus one needs

$$S_1^* > 0 \Leftrightarrow I_1^* < \frac{\mu - Pa}{\gamma_1 - \mu}. \quad (17)$$

Substituting expressions of V^* and R^* in (16) to the fourth equation of (15), one gets

$$S_2^* = \frac{\rho_1 + \mu}{\mu(\rho_1 + \nu_2 + \mu)}\left(K_0 + K_1 I_1^* - K_2 I_2^*\right), \tag{18}$$

where

$$\begin{cases} K_0 = \dfrac{\rho_1 \nu_1 \mu}{(\rho_1 + \mu)(\nu_1 + \mu)} + \dfrac{Pa\mu(\rho_1 + \nu_1 + \mu)}{(\rho_1 + \mu)(\nu_1 + \mu)}, \\ K_1 = \dfrac{\rho_2 \gamma_1}{\rho_2 + \mu} - \dfrac{\rho_1 \nu_1 (\gamma_1 + \mu)}{(\rho_1 + \mu)(\nu_1 + \mu)}, \\ K_2 = \dfrac{\mu(\rho_2 + \gamma_2 + \mu)}{\rho_2 + \mu}. \end{cases} \tag{19}$$

Since all parameters are positive, from Equation (18), we shall always have $S_2^* \neq 0$, if $K_0 > K_1 I_1^* - K_2 I_2^*$. Let us find the expressions for I_1^* and I_2^* that satisfy system (15), and satisfy $S_1^* > 0$ and $S_2^* > 0$. Replacing the expression for S_1^* in the third equation of (15) one obtain the expression of I_1^* as

$$\left(I_1^*\right)^2 + BI_1^* + C = 0, \tag{20}$$

Where

$$B = \frac{\mu}{\gamma_1 + \mu}\left[\frac{Pa}{\mu} + \frac{(\gamma_1 + \mu)I_2^*}{\mu} + \frac{\nu_1 + \mu}{\mu R_0} - 1\right], \tag{22}$$

$$C = \left[\frac{Pa}{\gamma_1 + \mu} - \frac{\mu}{\gamma_1 + \mu}\right] I_2^*. \tag{23}$$

Lets write Equation (20) as

$$AI_1^2 + BI_1 + C = 0 \tag{24}$$

Assume that the quadratic Equation (24) has two positive real solutions denoted by I^* and I^{**}, where I^{**} is the smaller and higher value of I_1^* respectively. When $I^* < \frac{\mu - Pa}{\mu + \gamma_1}$ and $I^{**} > \frac{\mu - Pa}{\mu + \gamma_1}$, a unique EEP exists, which is biologically viable. When $I^* > \frac{\mu - Pa}{\mu + \gamma_1}$ and $I^{**} > \frac{\mu - Pa}{\mu + \gamma_1}$, neither endemic equilibrium points are biologically viable, and the unique equilibrium point is the DFE. In this case, the system (2) presents one of the following (a) only the DFE which is locally asymptotically stable; (b) the unstable DFE; a smaller positive EEP which is locally asymptotically stable; and a higher positive EEP which is unstable; and (c) the stable DFE which is locally asymptotically stable plus two positive (smaller and higher) endemic equilibrium points which are not biologically viable, and therefore unstable. It follows that for $R_{vac} > 1$, the system (2) has a unique EEP which is locally asymptotically stable and for $R_{vac} < 1$ it has a stable DFE. Therefore, if there exists a nontrivial equilibrium which is biologically viable, $E_e = \left(S_1^*, V^*, I_1^*, S_2^*, I_2^*, R^*\right)$, then it is unique, locally asymptotically stable and also exhibits a backward bifurcation.

NUMERICAL SIMULATION

In order to verify the theoretical predictions of the model, the numerical simulations were done using the theoretical fixed values of the parameters of the model, as indicated in the Table 1.

The rate of loss of vaccine-induced immunity (ρ_1) and the rate of recovery from primary infection (γ_1) are chosen to represent measles (Raimundo et al., 2007). We explore the implications of variable vaccination coverage (ν_1, ν_2) and transmission coefficients (β_1, β_2). The parameters δ, $\rho_2 (< \rho_2)$ and $\gamma_2 (> \gamma_1)$ are chosen for simulation purposes only. However, these parameters are theoretical and may (or may not) be biologically feasible.

Figure 2 illustrates the variation of the population under the presence of the immigrants. The susceptible individuals are seen to decline as a result of the vaccination programs. Some of the individuals are shifted to vaccinated class at the rates of ν_1 and ν_2. However, the number of infected individuals from S_1 is higher than number of individuals in S_2, the reason been that the individuals in S_1 responds quickly to infectious diseases due to the lack of immunological memories which they can fight against pathogen. While the individuals from S_2 have an immunological memories which can fight against pathogens, the individuals in both infected classes are not recovering permanently. After certain period, they start losing their immunity and go back to S_2 as susceptible individuals different from S_1 which may undergo re-infections. Also the constant flow of the naive

Table 1. Parameter values used in simulations.

Parameter	Definition	Value
μ	Death and birth rate	$1/45$ years $^{-1}$
β_1	Coefficient of transmission	Variable
β_2	Coefficient of transmission	Variable
v_1	Vaccination coverage (first dose)	Variable
v_2	Vaccination coverage (second dose)	Variable
ρ_1	Rate of waning immunity induced by vaccination	$1/20$ years $^{-1}$
ρ_2	Rate of waning immunity induced by infection	$1/25$ years $^{-1}$
γ_1	Rate of recovery from primary infection	26(14 days)
γ_2	Rate of recovery from re-infection	36.5(10days)
Λ	Recruitment birth as naive susceptible	Variable
a	Number of Immigrant	Variable
P	Proportion of a as immigrants individuals with an immunity	Variable

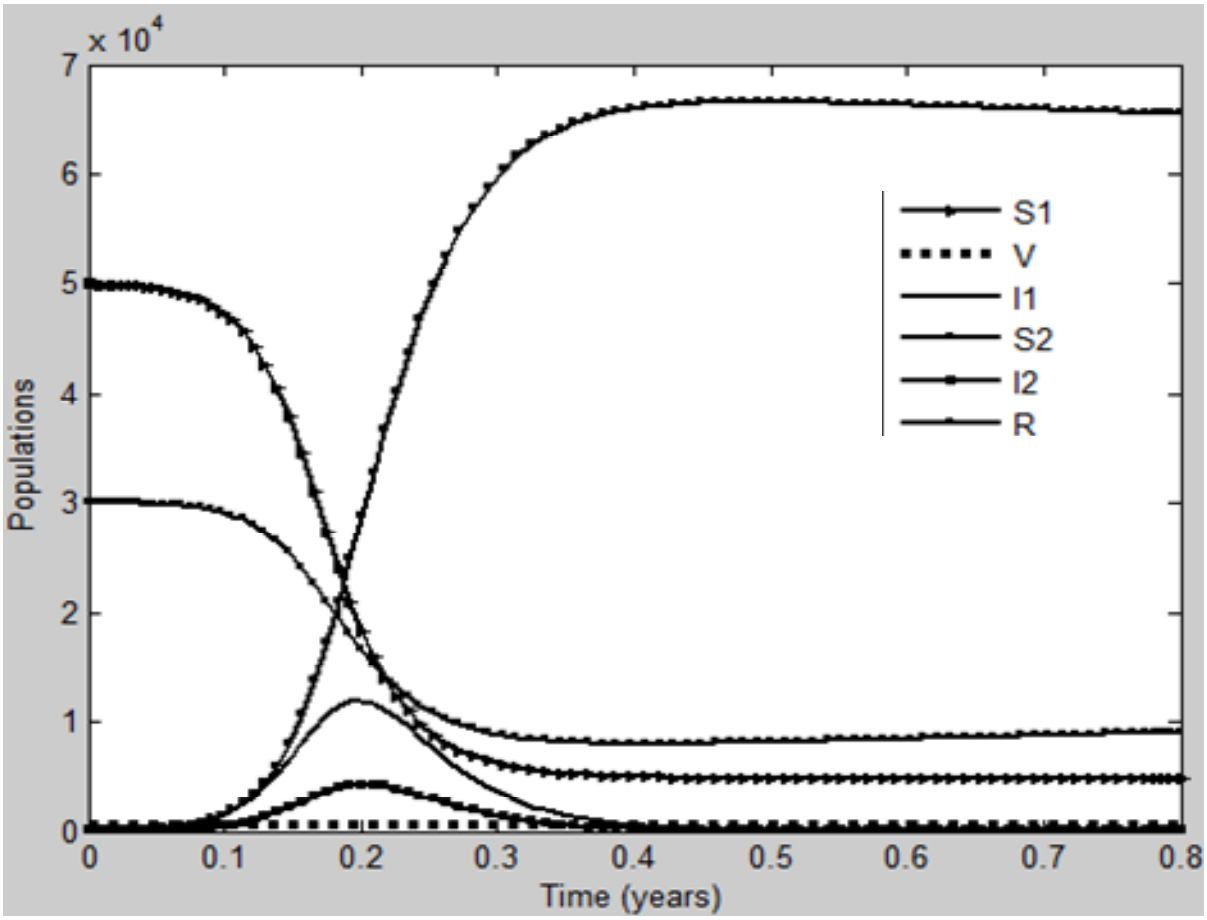


Figure 2. The variation of population at different classes for, $v_1 = 0.095$, $v_2 = 0.015$, $A = 800$, $P = 0.5$ and $\Lambda = 100$.

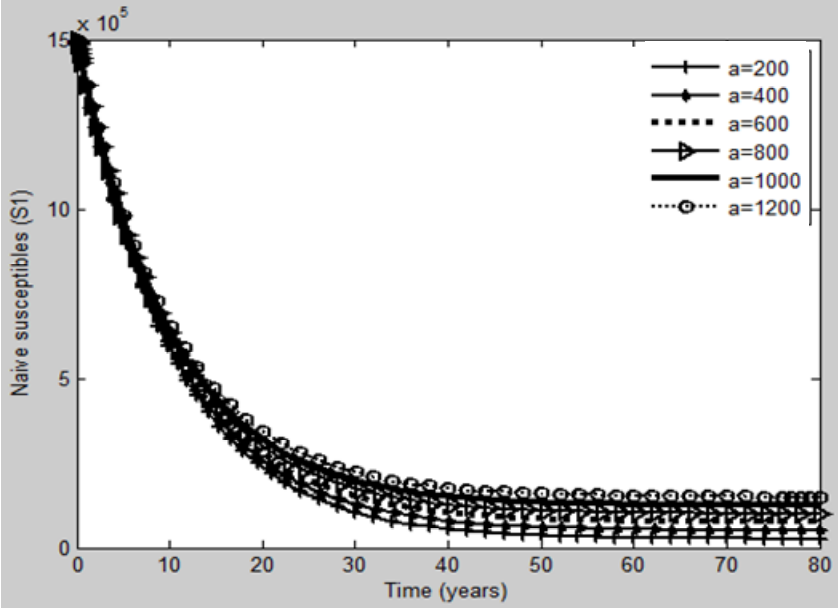


Figure 3. The variation of the susceptible individuals S_1 at different numbers of immigrants.

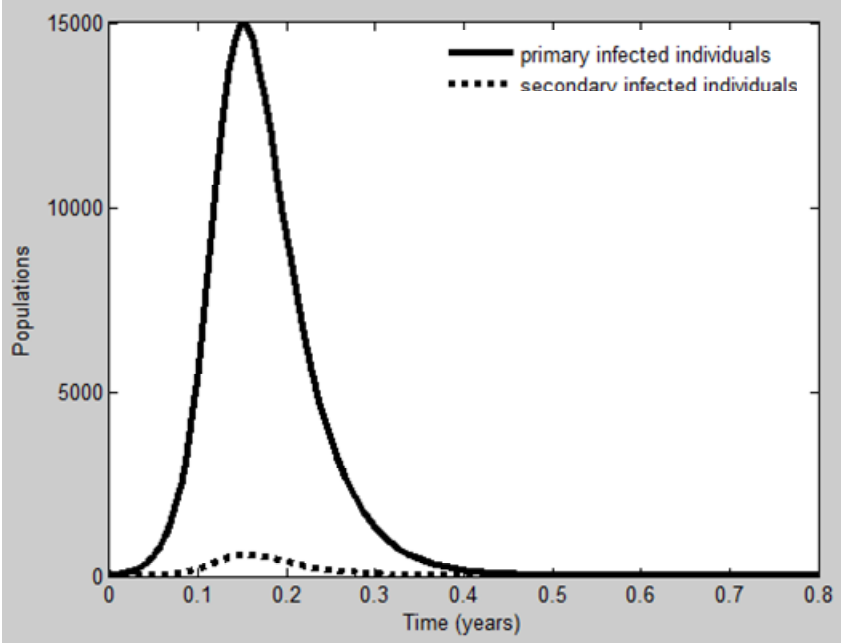


Figure 4. Variation of the primary and secondary infected individuals.

susceptible immigrants A into a population tends to lower the first-dose vaccination. Therefore the disease eradication is not attainable with the first-dose vaccinations.

Figure 3 shows that the increase on the number of susceptible immigrants tends to lower the vaccination coverage, such that the first dose-vaccination cannot eradicate the disease in the community. Under this circumstance, the booster vaccination program must be improved so as to shift these individuals to vaccinated class so that they can be protected against re-infections from infectious diseases.

Figure 4 shows that the number of the primary infected individuals from susceptible individuals S_1 is greater than

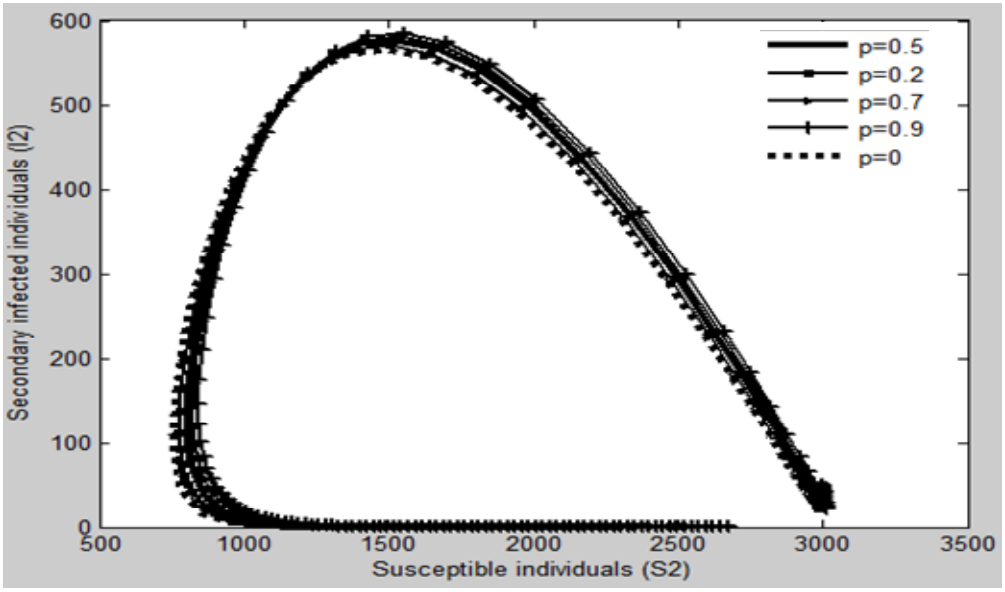


Figure 5. Variation of S_2 against I_2.

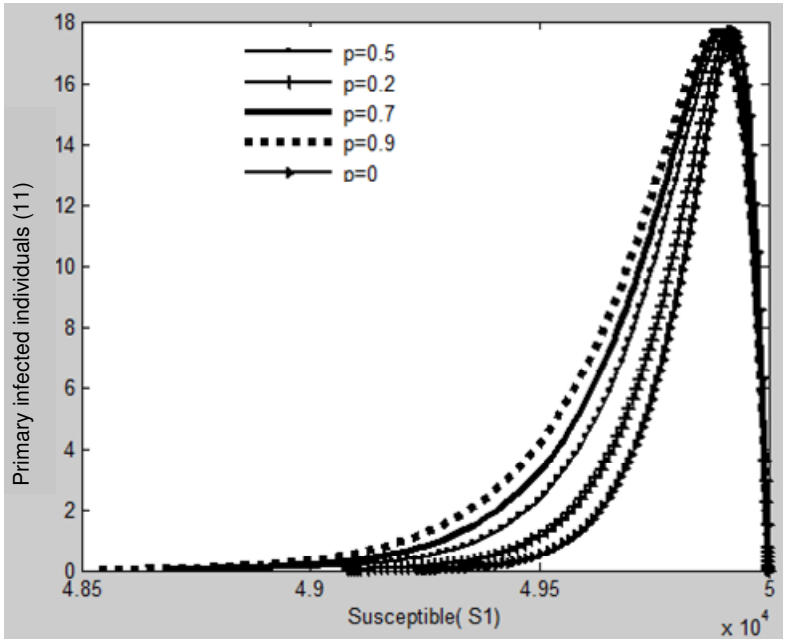


Figure 6. Variation of S_1 against I_1.

the number of the secondary infected individuals. The reason is that, most of the individuals in S_1 have no immunological memory against foreign pathogens. Therefore they can easily respond to infectious diseases. On the other hand, because the individuals in S_2 have been exposed to the diseases and some of them have been given vaccinations, they then have immunological memories which fight the foreign pathogens and they slowly responds to infectious diseases. This is the evidence of the reason of infants been given the first-dose vaccination after seven days to prevent them against infectious diseases.

Figure 5 illustrates how the susceptible individuals S_2 undergo re-infections under the presence of immigrants.

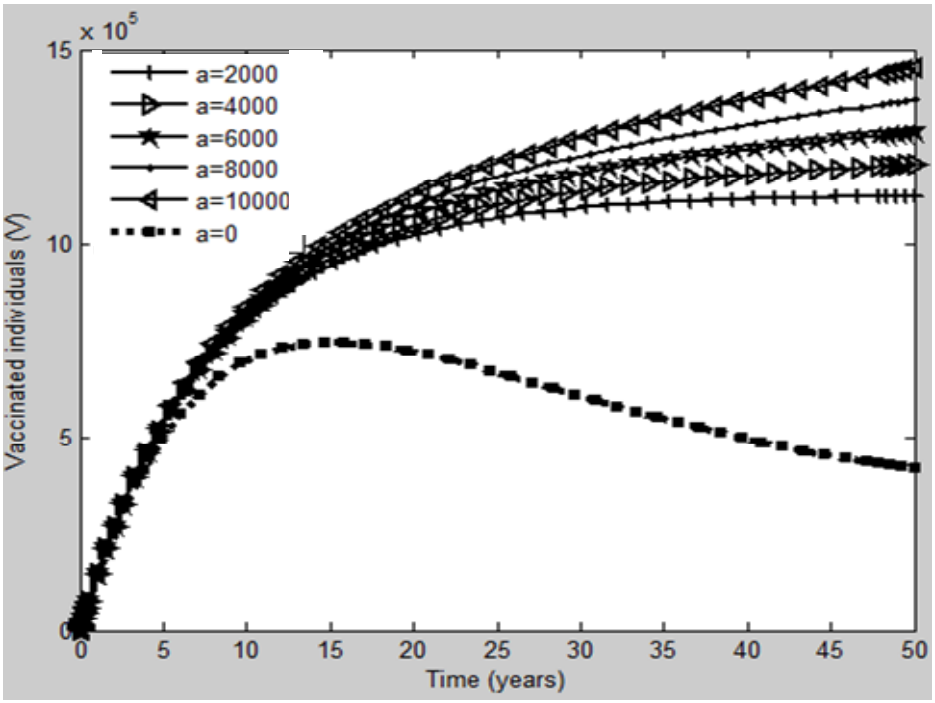


Figure 7. Variation of the vaccinated individuals with time.

The graph shows that, when the individuals become infected, they do not recover permanently. This means that the infected individuals recover temporarily and after some time they lose their immunity and go back to susceptible class S_1 which is different from the naive susceptible individuals S_1'. Under this circumstance, the booster vaccination must be administered to prevent the individuals to undergo re-infections.

Figure 6 assess the impact of immigrants in a vaccinated and temporary protected population. The graph shows that as the number of immigrants increase in the population the disease become endemic in the population. Consequently, the immigrants tend to lower the vaccination coverage in a population and the disease cannot be eradicated.

Figure 7 shows that the constant flow of the naive susceptible immigrants into a population increase the probability of the outbreak of infectious diseases. Therefore the governments have to seek the strategies for increasing the vaccination rate such that most of the individuals become vaccinated in a population so as to prevent them against infectious diseases.

Figure 8 illustrates the variation of the recovered individuals with time in a population which is temporary protected. The individuals recover from both the primary and secondary infected classes in which the number of recovered individuals from secondary infected class is greater than the number of recovered individuals from the primary infected class. Since the individuals have not recover permanently, after certain time the individuals start to lose their immunities and join the susceptible class in which they may undergo re-infection again.

CONCLUSIONS AND DISCUSSION

In this paper, a six-dimensional deterministic model for the transmission dynamics of infectious diseases by susceptible immigrants in a vaccinated and temporary immune protected population was qualitatively and quantitatively studied. The model incorporates the assumption that immigrants enter in the respective population with an immunity received from either vaccination or recover from the disease.

It was shown that there exists a feasible region where the model is well posed and for which a unique disease free equilibrium point exists. It was also shown that the control reproduction number R_{vac} is linearly asymptotically stable when it is less that one and unstable when it is greater than one. When there is no vaccination, $R_{vac} = R_0$. From the analysis of the model, the vaccination rate v_1^c was determined and found that the disease can be eradicated in the community when $v_1 > v_1^c(v_2)$, otherwise the disease stays in the

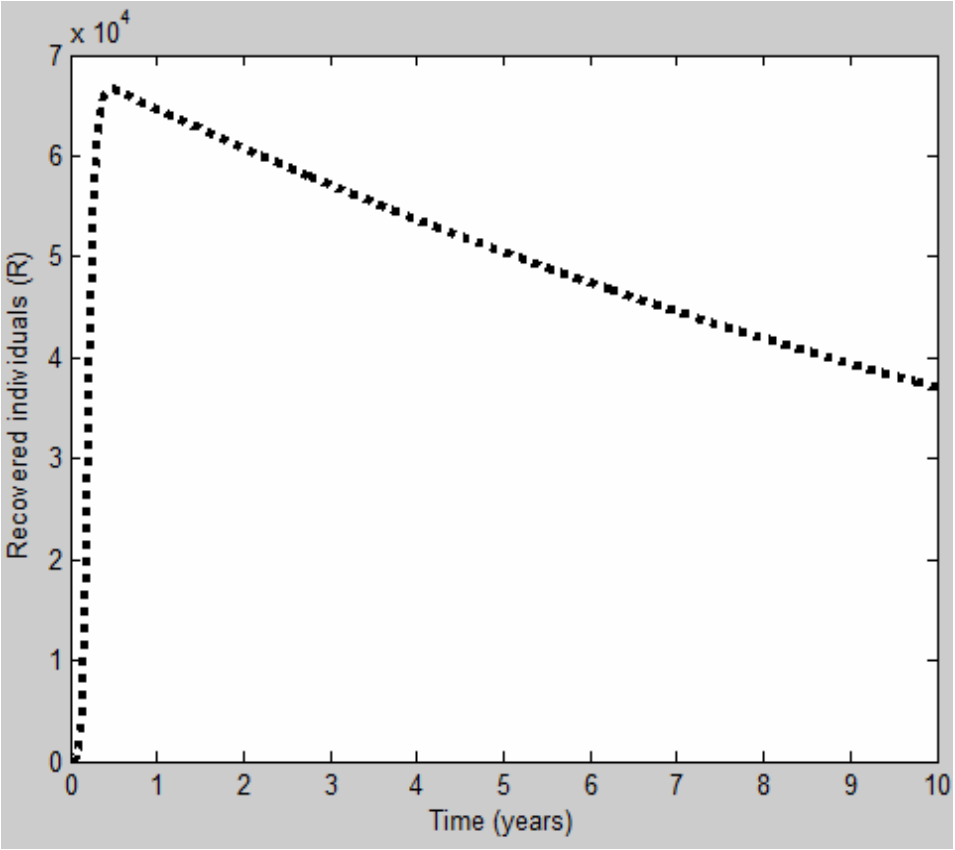


Figure 8. Variation of recovered individuals with time.

community. However if the vaccine induces lifelong immunity the disease eradication is attainable only with the single-dose vaccination only. The possibility of backward bifurcation for the model was investigated, and it was shown that under certain conditions, the model may exhibit backward bifurcation.

The impact of susceptible illegal immigrants into a population was assessed and found that if the number of susceptible immigrants increases into a population which is temporary protected is a major obstacle to the eradication of infectious diseases as the immigrants tends to lower the first-dose vaccination coverage. An epidemiological consequence of this result is that, for relatively low coverage of v_1, a booster vaccination program (two-dose) may fail to control the disease. The impact of immigration can have a dramatic consequence on national public health programs, and the influx of illegal susceptible immigrants who may lack access to medical care creates additional challenges. To assess the potential impact of susceptible immigrants and minimize the out breaks of such infectious diseases, public health programs should find out the ways to monitor the flow of immigrants into populations and collaborate with the global control policies. In addition, the possibility of providing access of health care for populations of illegal susceptible immigrants should be seriously assessed. For instance, the improved community planning, management mechanisms and improved access to and use of low-cost quality services in health, nutrition, education, water and environmental sanitation will contribute to poverty eluviations and help to reduce the worst effects of the immigrant influx in a population.

It may be observed from the Figures 2 to 8 that the increase of the number of immigrants in a population tends to lower the vaccination coverage. It was shown that under the absence of immigrants, the vaccination coverage is attainable with a single-dose vaccination only and hence the disease can be eradicated in a population with single-dose vaccination only.

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