

ON THE ERADICABILITY OF INFECTIONS WITH PARTIALLY PROTECTIVE VACCINATION IN MODELS WITH BACKWARD BIFURCATION

MUNTASER SAFAN

Mathematics Department, Faculty of Science, Mansoura University
35516 Mansoura, Egypt

KLAUS DIETZ

Department of Medical Biometry, Faculty of Medicine, University of Tuebingen
Westbahnhofstr. 55, 72070 Tuebingen, Germany

ABSTRACT. The SIS model of Hader and Castillo-Chavez [9] with a constant transfer rate of susceptibles into a partially protected state has been modified to take into account vaccination at birth. The model shows backward bifurcation (existence of multiple endemic stationary states) for certain values of parameters. Parameter values ensuring the existence and nonexistence of endemic equilibria have been discussed. Local and global stability of equilibria have been investigated. The minimum effort required to eradicate the infection has been determined.

1. Introduction. A well known concept in mathematical epidemiology, known as the basic reproduction number and denoted by R_0 , plays a key role in evaluating controlling infectious diseases. For models without backward bifurcation it has the property that for $R_0 < 1$ the infection disappears while for $R_0 > 1$ the infection persists. Recently it was shown, however, that there are many models for which the basic reproduction number can not be used as a threshold value in the infection eradication process (see for example [6], [8], [9], [12], [13], [14], [15], [17], [20], and [21]). This is because of the appearance of multiple positive infected stationary states for $R_0 < 1$. Hence another concept (satisfying the property that if it is less than one then the infection disappears while if it is bigger than one the infection persists) has to be found. Safan et al [18] introduced such a concept (denoted by \mathcal{R}). It is the minimum effort required to eradicate infections. It can also be interpreted as a reproduction number.

In general vaccines do not fully protect an individual against infections. Nevertheless, partially protective effective (imperfect) vaccines may be used to protect both individuals and whole populations [7]. We aim in this work to see, through mathematical modelling, whether a public health strategy based solely on the use of an imperfect vaccine can lead to the effective control of the infection under consideration. In other words, is there a feasible solution for the inequality $\mathcal{R} < 1$

2000 *Mathematics Subject Classification.* Primary: 58F15, 58F17; Secondary: 53C35.

Key words and phrases. epidemic model, vaccination, backward bifurcation, local stability, global stability, eradication effort.

in terms of the vaccination coverage p (the proportion of newborns who get vaccinated immediately after birth). Our analysis is motivated by the model introduced by Haderler and Castillo-Chavez [9]. We consider a model that is a modification of theirs to the case when a proportion p of newborns is vaccinated immediately after birth. If the vaccine gives only partial protection, then the relative susceptibility of vaccinated individuals compared to unvaccinated individuals is lower than one.

The paper is organized as follows. We introduce the model in Section 2. In Section 3 we study the existence and stability of the trivial stationary state (infection free equilibrium). Both the bifurcation equation and the direction of bifurcation are shown in Section 4. In Section 5 we study the conditions on parameters for which positive equilibria exist and we evaluate the minimal/critical contact rate (the supremum of all values of the contact rate for which no feasible infected equilibrium exists). Local stability of the infected stationary states is shown in Section 6 while the global stability of equilibria is shown in Section 7. In Section 8 we estimate the minimum effort required to eradicate the infection and we find the constraints, under which it is possible to eradicate the infection by vaccination only. A summary and conclusion is shown in Section 9.

2. The model. The present model is based on the model by Haderler and Castillo-Chavez [9], if we allow the vaccine to be given to a proportion p of the newborns immediately after birth rather than vaccinating susceptible individuals with rate ψ (according to their notation). The total population is divided into three classes: the first class is that of susceptibles of type one whose proportion in the total population is S_1 ; the second class is that of infected individuals whose proportion in the total population is I ; and the last one is that of susceptibles of type two whose proportion in the total population is S_2 . Infected individuals are those being able to transmit the infection. The transitions between the states of the model are shown in Figure 1. Unvaccinated individuals are assumed to be born as susceptibles of type one with rate μ . All individuals are assumed to die according to the mortality rate μ . A proportion p , $0 \leq p \leq 1$, of the newborns is assumed to get vaccinated immediately after birth. Type one susceptible individuals can either die or get infected with force of infection βI . Infected individuals can either die or recover with rate α . At recovery, individuals may either pass into the class of type two susceptible individuals at rate $g\alpha$, $0 \leq g < 1$, or return to the class of type one susceptible individuals at rate $(1-g)\alpha$. Individuals in the class S_2 can either die or get infected with force of infection, different from the previous one, $r\beta I$ where r is the relative susceptibility of individuals in the compartment S_2 to those in the compartment S_1 . The mathematical representation of the model is

$$\begin{aligned}\dot{S}_1 &= (1-p)\mu - (\beta I + \mu)S_1 + (1-g)\alpha I, \\ \dot{S}_2 &= p\mu - (r\beta I + \mu)S_2 + g\alpha I, \\ \dot{I} &= \beta(S_1 + rS_2)I - (\alpha + \mu)I,\end{aligned}\tag{1}$$

where the dot means the derivative with respect to time, all parameters are non-negative, and $0 \leq r < 1$.

The present model is a special case of equation (6) in the paper by Haderler and van den Driessche [10]. Here we set $\psi = \delta = 0$. Their κ is our p and their σ is our g . Their β_1 is our β , while their β_2 is our $r\beta$. They concentrate on the effect of ψ for the existence of backward bifurcation. They do not seem to be aware that even for $\psi = \delta = 0$ there is a possibility of backward bifurcation. Another version of

Hadeler and van den Driessche [10] has been considered by Reluga and Medlock [17] where they focused on the effect of resistance type (behavioral or immunological) for the existence of backward bifurcation. However, we concentrate here on the possibility for eradicating the infection, by vaccination solely, if the model shows backward bifurcation. Moreover, we determine exactly the parameter space where the backward bifurcation occurs and we study the global stability of the solutions.

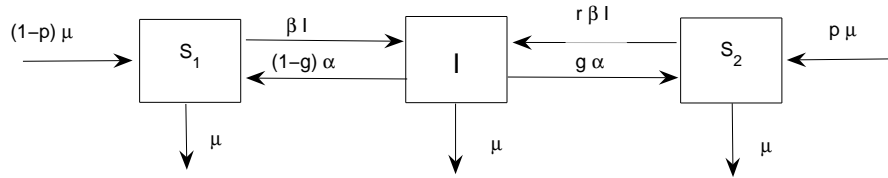


FIGURE 1. Transitions between the states of the model.

3. Existence and local stability of the infection-free equilibrium. We determine the stationary points by setting the derivatives equal to zero which gives the system of equations

$$\begin{aligned}
 0 &= (1 - p)\mu - (\beta\bar{I} + \mu)\bar{S}_1 + (1 - g)\alpha\bar{I}, \\
 0 &= p\mu - (r\beta\bar{I} + \mu)\bar{S}_2 + g\alpha\bar{I}, \\
 0 &= \beta(\bar{S}_1 + r\bar{S}_2)\bar{I} - (\alpha + \mu)\bar{I}, \\
 1 &= \bar{S}_1 + \bar{S}_2 + \bar{I}.
 \end{aligned}
 \tag{2}$$

The stationary state in the absence of the infection (i.e., $\bar{I} = 0$) is unique and reads $E_0 = (1 - p, p, 0)'$ where $'$ represents vector transpose. Since $0 \leq p \leq 1$, then E_0 exists always.

To establish the local stability of the infection-free equilibrium, we evaluate the Jacobian matrix at E_0 and find its characteristic equation

$$\Phi(\lambda) = ((1 - p + rp)\beta - (\alpha + \mu) - \lambda)(\mu + \lambda)^2 = 0.
 \tag{3}$$

The eigenvalues are $\lambda_1 = \lambda_2 = -\mu < 0$ and $\lambda_3 = (1 - p + rp)\beta - (\alpha + \mu) < 0$ if and only if

$$R_v := \frac{\beta}{\alpha + \mu}(1 - p + rp) < 1.$$

The quantity R_v can be interpreted as the vaccine reproduction number. We introduce the following definitions.

Definition 3.1. The basic reproduction number R_0 : It is the expected number of secondary cases produced by an infected case, during the infectious period, when introduced into a totally susceptible population. Mathematically, it is expressed as

$$R_0 = \frac{\beta}{\alpha + \mu}.
 \tag{4}$$

It is the product of the successful contact rate between type one susceptible individuals and infected individuals and the length of the infectious period.

Definition 3.2. The vaccine reproduction number R_v : It is the expected number of secondary cases produced by one case, during the infectious period, when it is introduced into an infection-free population, at equilibrium, in which a proportion p of newborns gets vaccinated immediately after birth. Mathematically, it is

$$R_v = \frac{\beta}{\alpha + \mu} (1 - p + rp) = (1 - p + rp)R_0. \quad (5)$$

It can also be interpreted as the product of the basic reproduction number R_0 and a quantity representing the average susceptibility in the total population. Another way to interpret R_v is to explain it as the average of two reproduction numbers. A third way to interpret it is to say, it is the ratio between the successful contact rate β and the zero successful contact rate, say β_0 , where β_0 means the successful contact rate when the endemic prevalence of infected individuals is reduced to be zero.

Definition 3.3. Zero contact rate β_0 : The zero contact rate β_0 is the value of the contact rate at which the endemic prevalence of infected individuals is zero. This is determined by solving (8) with respect to β when \bar{I} has been cancelled. Therefore,

$$\beta_0 = \frac{(\alpha + \mu)}{(1 - p + rp)}. \quad (6)$$

Definition 3.4. The episode reproduction number R_e [18]: It is the expected number of secondary episodes produced by one episode when the sizes of the sub-populations are given by the fractions (S_1, S_2, I) . It is given by

$$R_e = \frac{\beta}{\alpha + \mu} (S_1 + rS_2). \quad (7)$$

From the third equation in (1) we notice that the episode reproduction number equals one in the steady state. If $R_e > 1$, then I initially increases while if $R_e < 1$ it initially decreases. When the population is completely free from the infection, the vaccine reproduction number coincides with the episode reproduction number.

Proposition 1. *The infection free equilibrium $E_0 = (1 - p, p, 0)'$ is locally asymptotically stable if and only if the vaccine reproduction number R_v is less than one.*

4. Endemic equilibria, bifurcation equation and the direction of bifurcation. We want a simple characterization of the endemic stationary solutions. In (2) we assume $\bar{I} \neq 0$ and we eliminate the variables \bar{S}_1 and \bar{S}_2 . Then we arrive at a scalar equation for the variable \bar{I}

$$0 = F(\beta, \bar{I}) = r\beta^2\bar{I}^2 + ((r + g - rg)\alpha + r\mu + \mu - r\beta)\beta\bar{I} + \mu(\alpha + \mu - (1 - p + rp)\beta), \quad (8)$$

which can be seen as a bifurcation equation. Once a solution $\bar{I} > 0$ of this equation has been obtained, we find positive \bar{S}_2 and \bar{S}_1 from the other equations. Hence we have a one-to-one correspondence between the positive solutions of (8) and the endemic stationary points.

We keep the parameters μ, α, r, g and p fixed and discuss the equation in terms of β and \bar{I} . Eventually we are interested in the solutions \bar{I} for a given value of β and in the global dependence of \bar{I} depending on β .

The function F is a polynomial of order four in two variables β and \bar{I} . Now we describe qualitative features of the null set. For fixed β , the polynomial is quadratic in \bar{I} and hence there are at most two solutions \bar{I} . For fixed \bar{I} , the polynomial is quadratic in β and hence there are at most two solutions β . For $\beta = 0$ there are no solutions. For large β , i.e., $|\beta| \rightarrow \infty$, the asymptotes are $\bar{I} \sim 0$ and $\bar{I} \sim 1$. For $\bar{I} = 0$, the only solution is positive, $\beta = \beta_0$.

Hence the curve described by $F(\beta, \bar{I}) = 0$ has at least two branches, one in $\beta > 0$ and one in $\beta < 0$. There are only two branches because otherwise there would be more than two solutions for some given \bar{I} . The negative branch looks like a hairpin in $0 < \bar{I} < 1$ with asymptotes 0 and 1, the positive branch is another hairpin which is asymptotic to 1 from below and also asymptotic to 0 from below. It crosses the β axis at $\bar{I} = 0$, $\beta = \beta_0$ where β_0 is the zero contact rate. Of course only the positive branch is of interest with respect to the epidemiological problem.

At $\beta = \beta_0$, $\bar{I} = 0$ we compute the direction of bifurcation:

$$\frac{d\bar{I}}{d\beta} = -\frac{F_\beta}{F_{\bar{I}}}$$

whereby

$$\begin{aligned} F_\beta|_{(\beta_0,0)} &= -\mu(1-p+rp) < 0, \\ F_{\bar{I}}|_{(\beta_0,0)} &= \beta_0[(r+g-rg)\alpha+r\mu+\mu-r\beta_0]. \end{aligned}$$

Using the definition of β_0 , we thus find

$$\frac{d\bar{I}}{d\beta} = \frac{\mu(1-p+rp)^2}{\beta_0[(1-p+rp)(\mu+(1-r)g\alpha)-r(1-r)(\mu+\alpha)p]}.$$

Hence we have a forward bifurcation if

$$(1-p+rp)(\mu+(1-r)g\alpha)-r(1-r)(\mu+\alpha)p > 0 \tag{9}$$

and a backward bifurcation if

$$(1-p+rp)(\mu+(1-r)g\alpha)-r(1-r)(\mu+\alpha)p < 0. \tag{10}$$

We show the following proposition.

Proposition 2. *The condition (10) for backward bifurcation is equivalent with the following set of inequalities:*

$$0 < r < r_1 := \frac{(1-g)\alpha}{\mu+(1-g)\alpha}, \tag{11}$$

$$p > p := 1/\left(1 + \frac{r((1-g)\alpha + \mu)}{(1-r)g\alpha + \mu} \left(\frac{(1-g)\alpha}{(1-g)\alpha + \mu} - r\right)\right). \tag{12}$$

The inequality (11) ensure that $0 < p < 1$. Figure (2) shows the areas in the plane (r,p) in which the direction of bifurcation is backward as well as that in which it is forward.

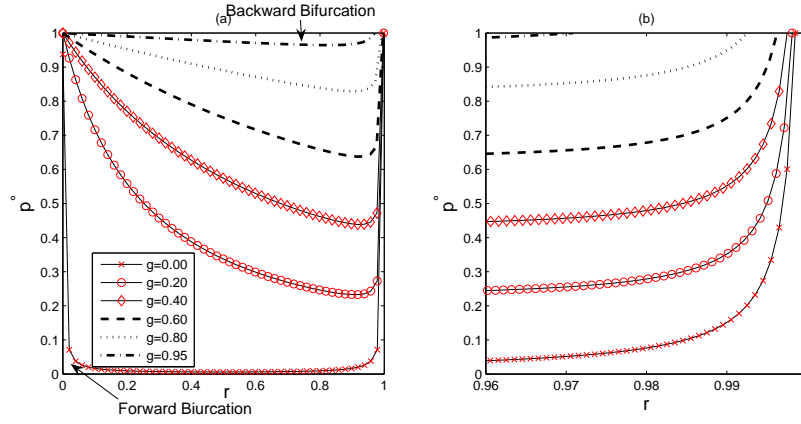


FIGURE 2. The (r, p) plane is divided according to the direction of bifurcation. The curves have been drawn with parameter values $\alpha = 10$ per year, $\mu = 0.015$ per year, and g varying from 0 to 0.95 as explained in the legend on the left. Above any curve the bifurcation is backward while below it the bifurcation is forward (part (a)). Part (b) is a zoom in for the right narrow corner of part (a).

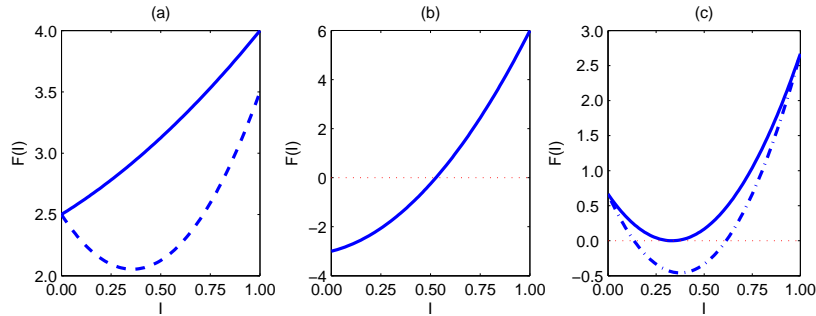


FIGURE 3. The polynomial $F(I) = AI^2 + BI + C = 0$ for different values of the parameters. All curves have been done with parameter values: $\alpha = 10$ per year, $\mu = 0.015$ per year, $g = 0.2$, $r = 0.499$, $p = 0.8$, and β as it would be stated in each part. Part (a) shows that $F(I) = 0$ has no root in the interval $(0, 1]$ where the curves have been drawn with β values 8 per year for the solid line and 12.56 per year for the broken line. However, part (b) shows that it has a unique root in the mentioned interval where the curve has been drawn with $\beta = 17$ per year, and part (c) shows that it can have two different solutions (the dashed-dotted line corresponding to $\beta = 12.7$ per year) which can decline to coincide and show two equal roots (the solid curve corresponding to $\beta = \beta^* = 12.5977$ per year).

5. **Existence of the endemic equilibria and the critical contact rate.** Equation (8) can be considered as a polynomial of the second degree in the proportion \bar{I} , if we consider the model parameters to be fixed. Therefore,

$$0 = F(\bar{I}) = r\beta^2\bar{I}^2 + ((r + g - rg)\alpha + r\mu + \mu - r\beta)\beta\bar{I} + \mu(\alpha + \mu - (1 - p + rp)\beta). \tag{13}$$

We notice that

$$\begin{aligned} F(1) &= \mu(\alpha + \mu) + ((g + (1 - g)r)\alpha + (p + (1 - p)r)\mu)\beta, \\ F(0) &= (\alpha + \mu - (1 - p + rp)\beta)\mu. \end{aligned} \tag{14}$$

It is clear that $F(1) > 0$ for all parameter values, but $F(0)$ can be positive or negative according to the values of the parameters. Since F is a polynomial of degree two in $\bar{I} \in [0, 1]$ and $F(1) > 0$, hence the number of roots of (13) depends on the sign of $F(0)$. Therefore, we have the following proposition:

Proposition 3. *In the presence of backward bifurcation, the following cases hold:*

- i) If $F(0) \leq 0$, then there is a unique endemic equilibrium in addition to the infection free equilibrium (see Figure 3(b)).*
- ii) If $F(0) > 0$, $\frac{dF}{dI}(0) < 0$ and $F(I^*) \leq 0$ where $\frac{dF(I^*)}{dI} = 0$, then there are two endemic equilibria in addition to the infection-free equilibrium (see Figure 3(c), the dashed-dotted line). These two endemic equilibria coincide when $F(I^*) = 0$ (see Figure 3(c), the solid line). The point, in the plane (β, I) , corresponding to this coincidence is called the turning point [19].*
- iii) Otherwise, the infection free equilibrium is unique and no endemic state exists (see Figure 3(a)).*

The first item of proposition 3 implies that $\beta \geq \beta_0 := (\alpha + \mu)/(1 - p + rp)$, i.e.,

$$R_v := \frac{\beta}{\alpha + \mu}(1 - p + rp) \geq 1. \tag{15}$$

On the other hand, we notice that $F(0) < 0$ iff $\beta < \beta_0$, while $\frac{dF}{dI}(0) < 0$ iff $\beta > (\mu + r\mu + (r + g - rg)\alpha)/r$. However, $F(I^*) \leq 0$ iff

$$r^2\beta^2 - 2((1 - (1 - r)(1 - g))\alpha - (1 - r)(1 - 2p)\mu)r\beta + (\mu + r\mu + (r + g - rg)\alpha)^2 - 4r\mu(\alpha + \mu) \geq 0.$$

Collecting these three conditions together implies that $\beta_1^* \leq \beta < \beta_0$ where

$$\begin{aligned} \beta_1^* &= \frac{1}{r}\{r\alpha + (1 - r)(g\alpha + (2p - 1)\mu) \\ &+ 2\sqrt{(1 - r)\mu((1 - p)\mu + (1 - g)\alpha)pr - (1 - p)(p\mu + g\alpha)}\}. \end{aligned} \tag{16}$$

Thus for $\beta \in [\beta_1^*, \beta_0)$, there are two positive solutions for (13) which are given by

$$\bar{I}_1 = \frac{-B - \sqrt{B^2 - 4AC}}{2A}, \tag{17}$$

$$\bar{I}_2 = \frac{-B + \sqrt{B^2 - 4AC}}{2A}, \tag{18}$$

$$\begin{aligned} A &= r\beta^2, \\ B &= (\mu + r\mu - r\beta + (r + (1 - r)g)\alpha)\beta, \\ C &= (\alpha + \mu - (1 - p + rp)\beta)\mu. \end{aligned} \tag{19}$$

The equality in (15) corresponds to the case when \bar{I}_1 declines to zero, while the equality in (16) corresponds to the turning point at which both \bar{I}_1 and \bar{I}_2 coalesce

and coincide with $I^* = -B/(2A)$.

The third item of the proposition corresponds to the case $\beta < \beta_1^*$. Hence we show the following proposition.

Proposition 4. *In the presence of backward bifurcation, the following cases hold:*
i) If $\beta \geq \beta_0$, then there is a unique endemic equilibrium in addition to the infection-free equilibrium.

ii) If $\beta_1^ \leq \beta < \beta_0$ and $(0 < r < r_1 \& p > p_1$ or $r > r_2 \& p < p_2)$, then there are two endemic equilibria in addition to the infection-free equilibrium. These two endemic equilibria coincide when $F(I^*) = 0$. The point, in the plane (β, I) , corresponding to this coincidence is called the turning point [19].*

iii) If $0 < \beta < \beta_1^$, then the infection-free equilibrium is unique and no endemic state exists.*

Let us now consider the case when the direction of bifurcation is forward (i.e., when (11) and (12) do not hold. In this case the value \bar{I} at the turning point is negative and hence $\beta^* > \beta_0$ has no biological meaning. However, in the case of backward bifurcation we have $\beta^* < \beta_0$ and the corresponding value I^* is positive. In this case β^* is the critical (minimal) contact rate for which there are infected stationary solutions. Now it makes sense to define the critical contact rate comprising both cases of backward and forward bifurcation.

Definition 5.1. The critical contact rate β^* : It is the value of the minimum contact rate at which the endemic prevalence of infected individuals is positive, i.e., it is the contact rate separating between nonexistence and existence of endemic states. Therefore

$$\beta^* = \begin{cases} \beta_1^* & \text{if the bifurcation is backward,} \\ \beta_0 & \text{if the bifurcation is forward.} \end{cases} \quad (20)$$

6. Local stability of the endemic equilibria. To establish the stability of the endemic solutions, we reduce model (1) to get a two-dimensional one. Assume that the size of the population is equal to the equilibrium value 1, then we can use $S_2 = 1 - S_1 - I$ in the last equation of (1) to get the reduced model

$$\begin{aligned} \dot{S}_1 &= \mu(1-p) - (\mu + \beta I)S_1 + \alpha(1-g)I, \\ \dot{I} &= \beta(r + (1-r)S_1 - rI)I - (\alpha + \mu)I. \end{aligned} \quad (21)$$

This model has the trivial stationary state $\bar{E}_0 = (1-p, 0)'$ which corresponds to the infection-free equilibrium E_0 of the original model (1). The endemic equilibria of (21) satisfy (13) and are given by $\bar{E}_1 = (S_{11}, I_1)'$, and $\bar{E}_2 = (S_{12}, I_2)'$ where

$$S_{11,12} = \frac{(\alpha + \mu - r\beta) + r\beta I_{1,2}}{(1-r)\beta}. \quad (22)$$

Now for a general equilibrium $(\bar{S}_1, \bar{I})'$, assume that we make a small perturbation $(x(t), y(t))'$. Therefore, the linearized system of (21) reads

$$\begin{aligned} \dot{x}(t) &= -(\mu + \beta\bar{I})x(t) + ((1-g)\alpha - \beta\bar{S}_1)y(t), \\ \dot{y}(t) &= (1-r)\beta\bar{I}x(t) + ((1-r)\beta\bar{S}_1 + r\beta(1-2\bar{I}) - (\alpha + \mu))y(t). \end{aligned}$$

It can be written in matrix form as

$$\frac{d}{dt} \begin{pmatrix} x \\ y \end{pmatrix} = \begin{pmatrix} -(\mu + \beta\bar{I}) & (1-g)\alpha - \beta\bar{S}_1 \\ (1-r)\beta\bar{I} & (1-r)\beta\bar{S}_1 + r\beta(1-2\bar{I}) - (\alpha + \mu) \end{pmatrix} \begin{pmatrix} x \\ y \end{pmatrix}. \quad (23)$$

We denote the coefficient matrix by J . Hence the characteristic equation of J is

$$\lambda^2 - \text{tr}(J)\lambda + \det(J) = 0, \quad (24)$$

where, using (22)

$$\text{tr}(J) = -(\mu + (1+r)\beta\bar{I}) < 0, \quad (25)$$

and

$$\begin{aligned} \det(J) &= \bar{I}(2r\beta^2\bar{I} + \beta(\mu + r\mu - r\beta + (r+g-rg)\alpha)) \\ &= \bar{I}(2A\bar{I} + B) \\ &= \mp\bar{I}\sqrt{B^2 - 4AC} \\ &= \begin{cases} < 0 & \text{if } \bar{I} = I_1, \\ > 0 & \text{if } \bar{I} = I_2. \end{cases} \end{aligned}$$

Therefore, we get the following proposition:

Proposition 5. *The endemic equilibrium $\bar{E}_1 = (S_{11}, I_1)'$ is unstable whenever it exists, while the other one $\bar{E}_2 = (S_{12}, I_2)'$ is locally asymptotically stable whenever it exists.*

7. Global stability of the equilibria. Let us consider the reduced model (21). It is easy to check that the stable manifold of \bar{E}_0 is on the S_1 -axis. If $S_1 = 0$, then $\dot{S}_1 = \mu(1-p) + \alpha(1-g)I > 0$ for $I > 0$. Therefore, the first quadrant and consequently the set $\Omega := (S_1, I) : S_1 \geq 0, I \geq 0, S_1 + I \leq 1$ are positively invariant regions for the system (21), for any solution of (21) starting in the interior of Ω . Hence the ω -limit set of its trajectory must be contained in Ω . Assume that

$$\begin{aligned} X(S_1, I) &= \mu(1-p) - (\mu + \beta I)S_1 + \alpha(1-g)I, \\ Y(S_1, I) &= \beta(r + (1-r)S_1 - rI)I - (\alpha + \mu)I, \end{aligned}$$

and consider the Dulac function $D = \frac{1}{I}$, where $I > 0$. Hence

$$\frac{\partial(DX)}{\partial S_1} + \frac{\partial(DY)}{\partial I} = -\left(r\beta + \frac{\mu + \beta I}{I}\right) < 0.$$

Therefore, using Dulacs criterion [16], the reduced model (21) has no limit cycle in the first quadrant.

Now, since for $\beta > \beta_0$ the system (21) has a unique endemic state $\bar{E}_2 = (S_{12}, I_2)'$ (which is locally asymptotically stable) in addition to the unstable infection-free equilibrium $\bar{E}_0 = (1-p, 0)'$, then (taking into account the previous properties) the local asymptotic stability implies the global stability of \bar{E}_2 for $\beta \geq \beta_0$. Similarly, since the infection-free equilibrium $\bar{E}_0 = (1-p, 0)'$ is unique and locally asymptotically stable for $\beta < \beta^*$, then it is globally asymptotically stable provided that $\beta < \beta^*$. Therefore, we summarize our results in the following proposition:

Proposition 6. *For the reduced model (21) and therefore the original model (1) the following items hold:*

- i) If $\beta < \beta^*$, then the infection-free equilibrium is unique and globally asymptotically stable.*
- ii) For $\beta^* \leq \beta < \beta_0$, there are two positive stationary states in addition to the infection free equilibrium which is locally asymptotically stable as well as the higher positive infected stationary solution, while the lower positive infected solution (lying in between) is unstable.*

iii) For $\beta_0 < \beta$, there is a unique and globally asymptotically stable positive infected stationary state in addition to the unstable infection-free equilibrium.

8. The minimum eradication effort. Safan et al [18] introduced a method to evaluate the minimum effort required to eradicate infections for a model with backward bifurcation. The method depends on determining the episode reproduction number at the turning point, i.e., the point in the plane (β, I) separating between nonexistence and existence of endemic states $E^* = (S_1^*, I^*, S_2^*)$ where

$$I^* = \begin{cases} = 0 & \text{if } \beta^* = \beta_0, \\ = \frac{r\beta^* - \mu - r\mu - (g+(1-g)r)\alpha}{2r\beta^*} & \text{if } \beta^* = \beta_1^* < \beta_0, \end{cases} \quad (26)$$

$$S_1^* = \frac{\alpha + \mu - r\beta^*(1 - I^*)}{(1 - r)\beta^*}, \quad (27)$$

$$S_2^* = 1 - S_1^* - I^*. \quad (28)$$

Hence

$$\begin{aligned} R_e(\beta, S_1^*, S_2^*) &= \frac{\beta}{\alpha + \mu}(S_1^* + rS_2^*) \\ &= \frac{\beta}{\alpha + \mu}((1 - r)S_1^* + r(1 - I^*)) \\ &= \frac{\beta}{\alpha + \mu} \left(\frac{\alpha + \mu}{\beta^*} - r(1 - I^*) + r(1 - I^*) \right) \\ &= \frac{\beta}{\beta^*}. \end{aligned}$$

Therefore we show the following proposition:

Proposition 7. *The minimum effort required to eradicate the infection is given by*

$$\mathcal{R} = \frac{\beta}{\beta^*}. \quad (29)$$

$$= \begin{cases} \frac{\beta}{\beta_0} = R_v & \text{if the bifurcation direction is forward,} \\ \frac{\beta}{\beta_1^*} & \text{if the bifurcation direction is backward.} \end{cases} \quad (30)$$

Hence the ratio β/β^* can be interpreted as a reproduction number and eradicating the infection requires a reduction of \mathcal{R} to a value slightly less than one. However, the question now is how to reduce \mathcal{R} to below one. Can we do it by vaccination only or do we need additional efforts? This can be clarified if we solve the inequality $\mathcal{R} < 1$ with respect to $p \in [0, 1]$. We have three cases:

Case I: $r = 0$

In this case the bifurcation is always forward and therefore, $\mathcal{R} = \frac{\beta}{\beta_0} = \frac{(1-p)\beta}{\alpha + \mu} < 1$ iff $1 - p < \frac{1}{R_0}$. Therefore, the infection can be eradicated from the population if we vaccinate a proportion (of the newborns) slightly higher than $1 - \frac{1}{R_0}$.

Case II: $0 < r < r_1 := \frac{(1-g)\alpha}{\mu + (1-g)\alpha} < 1$

In this case the model shows backward bifurcation. To eradicate the infection we simply seek strategies to reduce the reproduction number

$$\mathcal{R} = \begin{cases} \frac{\beta}{\beta_0} = R_v & \text{if the bifurcation direction is forward,} \\ \frac{\beta}{\beta_1^*} & \text{if the bifurcation direction is backward} \end{cases}$$

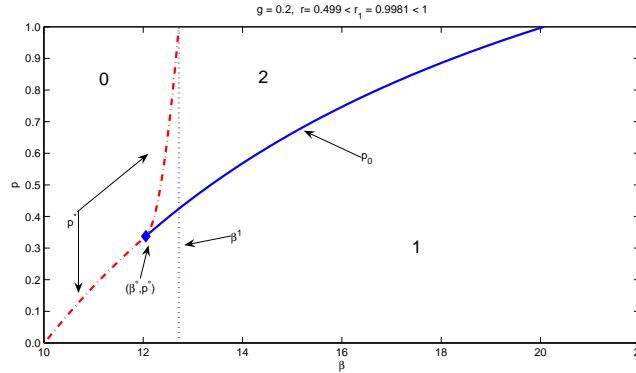


FIGURE 4. Bifurcation diagram in the (β, p) plane. The solid line represents p_0 as a function of β , while the dashed-dotted line represents p^* as a function of β . The parameter values being chosen are $\alpha = 10$ per year, $\mu = 0.015$ per year, $g = 0.2$, and $r = 0.499 < 0.9981 = r_2$. The numbers 0, 1, and 2 denote respectively to the number of persistent solutions in the corresponding areas.

to a value slightly less than one. To do so, we consider p as a function of the successful contact rate β . Therefore, we solve equations (6) and (16) to, respectively, get

$$p_0 = \frac{1}{1-r} \left(1 - \frac{\alpha + \mu}{\beta} \right) = \frac{1}{1-r} \left(1 - \frac{1}{R_0} \right) \tag{31}$$

and

$$p_1^* = \frac{(\mu + r\mu - r\beta + (r + g - rg)\alpha)^2 - 4r\mu(\alpha + \mu - \beta)}{4r(1-r)\mu\beta} \tag{32}$$

which is well defined if and only if

$$\beta < \frac{g\alpha + (\sqrt{(1-r)\mu} + \sqrt{(1-g)r\alpha})^2}{r} := \beta^1. \tag{33}$$

Hence the correspondence of (20) is

$$p^* = \begin{cases} p_1^* & \text{if } \beta < \beta < \beta^1, \\ p_0 & \text{if } \alpha + \mu < \beta < \beta. \end{cases} \tag{34}$$

The inequality $\mathcal{R} < 1$ corresponds to $p > p^*$; see figure (4) for more explanation. Hence if $\beta < \beta^1$, then vaccinating a proportion p slightly higher than p^* of the newborns immediately after birth is sufficient to eradicate the infection. However if $\beta > \beta^1$, then there is no feasible p sufficient to reduce \mathcal{R} below 1. Therefore, vaccination solely can not be used to eradicate the infection, but we have apply additional control measures which reduce the transmission rate β below β^1 and then vaccinate a proportion p of the newborns slightly above p^* in order to eradicate the infection.

Case III: $r_1 := \frac{(1-g)\alpha}{\mu+(1-g)\alpha} \leq r < 1$

In this case the model shows only forward bifurcation, and the critical contact rate separating between nonexistence and existence of positive endemic solutions is $\beta_0 = (\alpha + \mu)/(1 - p + rp)$. Hence

$$\mathcal{R} = R_v = (1 - p + rp) \frac{\beta}{\alpha + \mu}.$$

However $\mathcal{R} < 1$ if and only if $p > \frac{1}{1-r}(1 - \frac{1}{R_0}) := p_c$. We notice that $\beta_0 = \alpha + \mu$ when $p = 0$, while $\beta_0 = \beta_2 := (\alpha + \mu)/r \neq \infty$ when $p = 1$. Therefore, a feasible proportion $p \in [0, 1]$ does not exist if $\beta \geq \beta_2$ so that the infection gets eradicated. Hence, control measures (other than vaccination) aiming to reduce the successful contact rate β to below β_2 should be applied before vaccinating a proportion $p > p_c$ of the newborns immediately after birth.

We summarize the above results in the following proposition:

Proposition 8. (1) *For $r = 0$, the model shows only forward bifurcation and the infection can be eradicated from the population by vaccinating a proportion of the newborns, immediately after birth, slightly higher than $1 - \frac{1}{R_0}$.*

(2) *For $0 < r < r_1 := \frac{(1-g)\alpha}{\mu+(1-g)\alpha} < 1$, the model shows backward bifurcation for certain parameter values and vaccination solely is not sufficient to eradicate the infection. However, it can be eradicated from the population in two steps. We first apply control measures aiming to reduce the contact rate β to below some level β^1 (as defined in (33)), and then we vaccinate a proportion, of the newborns immediately after birth, slightly higher than p_1^* (as defined in (32)).*

(3) *For $r_1 := \frac{(1-g)\alpha}{\mu+(1-g)\alpha} < r < 1$, the model shows only forward bifurcation and the infection can be eradicated in two steps. We first reduce β to a value slightly less than $\frac{\alpha+\mu}{r}$ (i.e., to reduce R_0 to a value slightly less than $\frac{1}{r}$) and then we vaccinate a proportion p , of the newborns immediately after birth, slightly higher than*

$$\frac{1}{1-r} \left(1 - \frac{1}{R_0}\right).$$

9. Summary and conclusion. The importance of vaccinating individuals in a population is to protect them from an infection. However, for many infections vaccines are not perfect. In other words, individuals lose their immunity being acquired by vaccination. We try here to show the possibility of eradicating the infection by vaccination only. In this respect, we have modified the SIS model of Haderler and Castillo-Chavez (1995), with a constant transfer rate of susceptibles into a partially protected state, to take into account vaccination at birth. The key parameter is the relative susceptibility of susceptible individuals of type two with respect to those of type one. If $r = 0$, then individuals in the S_2 -state are totally protected and the infection can be eradicated by vaccination alone. However, if r increases from zero to some level $r_1 = (1 - g)\alpha/(\mu + (1 - g)\alpha) < 1$, then the model shows backward bifurcation for certain parameter values and eradicating the infection requires a reduction of the successful contact rate β to below some level β^1 and then we vaccinate a proportion of the newborns slightly higher than some level p_1^* . Hence, vaccination solely can not be used to eradicate the infection. If r increases further from r_1 to 1, then the model shows only forward bifurcation, but vaccination solely is not sufficient to eradicate the infection. We have to apply control measures, other than vaccination, aiming to reduce the successful contact rate to below some level $(\alpha + \mu)/r$ before vaccinating a proportion (of the newborns) slightly above some level $(1 - 1/R_0)/(1 - r)$ where $R_0 = \beta/(\alpha + \mu)$ is the basic

reproduction number.

Acknowledgments. We would like to thank the referees as well as the editor very much for their valuable comments and suggestions. This work is dedicated to Prof.Dr. KP Haderler.

REFERENCES

- [1] J. Arino, K. L. Cooke, P. van den Driessche and J. Velasco-Hernández, *An epidemiology model that includes a leaky vaccine with a general waning function*, Discrete and Continuous Dynamical Systems-Series B (DCDS-B), **4** (2004), 479–495.
- [2] C. Castillo-Chavez and B. Song, *Dynamical models of tuberculosis and their applications*, Mathematical Biosciences and Engineering, **1** (2004), 361–404.
- [3] O. Diekmann and J. A. P. Heesterbeek, “Mathematical Epidemiology of Infectious Diseases: Model Building, Analysis and Interpretation,” John Wiley & Sons, Chichester, 2000.
- [4] O. Diekmann, J. A. P. Heesterbeek and J. A. J. Metz, *On the definition and the computation of the basic reproduction ratio R_0 in models for infectious diseases in heterogeneous populations*, J. Math. Biol., **28** (1990), 365–382.
- [5] J. Dushoff, W. Huang and C. Castillo-Chavez, *Backwards bifurcations and catastrophe in simple models of fatal diseases*, J. Math. Biol., **36** (1998), 227–248.
- [6] Z. Feng, C. Castillo-Chavez and A. F. Capurro, *A model for tuberculosis with exogenous reinfection*, Theor. Pop. Biol., **57** (2000), 235–247.
- [7] S. Gandon, M. J. Mackinnon, S. Nee and A. F. Read, *Imperfect vaccines and the evolution of pathogen virulence*, Nature, **414** (2001), 751–756.
- [8] D. Greenhalgh, O. Diekmann and M. C. M. de Jong, *Subcritical endemic steady states in mathematical models for animal infections with incomplete immunity*, Math. Biosci., **165** (2000), 1–25.
- [9] K. P. Haderler and C. Castillo-Chavez, *A core group model for disease transmission*, Math. Biosci., **128** (1995), 41–55.
- [10] K. P. Haderler and P. van den Driessche, *Backward bifurcation in epidemic control*, Math. Biosci., **146** (1997), 15–35.
- [11] C. M. Kribs-Zaleta, *Center manifold and normal forms in epidemic models*, in “Mathematical Approaches for Emerging and Reemerging Infectious Diseases: Models, Methods and Theory” (eds. C. Castillo-Chavez et al.), IMA 125, Springer-Verlag, New York, (2002), 269–286.
- [12] C. M. Kribs-Zaleta and M. Martcheva, *Vaccination strategies and backward bifurcation in an age-since-infection structured model*, Math. Biosci., **177 and 178** (2002), 317–332.
- [13] C. M. Kribs-Zaleta and J. X. Velasco-Hernandez, *A simple vaccination model with multiple endemic states*, Math. Biosci., **164** (2000), 183–201.
- [14] S. M. Moghadas, *Analysis of an epidemic model with bistable equilibria using the Poincaré index*, Applied Mathematics and Computation, **149** (2004), 689–702.
- [15] S. M. Moghadas, *Modeling the effect of imperfect vaccines on disease epidemiology*, Discrete and Continuous Dynamical Systems-Series B, **4** (2004), 999–1012.
- [16] L. Perko, “Differential Equations and Dynamical Systems,” Springer-Verlag, New York, 1991.
- [17] T. C. Reluga and J. Medlock, *Resistance mechanisms matter in SIR models*, Mathematical Biosciences and Engineering, **4** (2007), 553–563.
- [18] M. Safan, H. Heesterbeek and K. Dietz, *The minimum effort required to eradicate infections in models with backward bifurcation*, J. Math. Biol., **53** (2006), 703–718.
- [19] R. Seydel, “From Equilibrium to Chaos: Practical Bifurcation and Stability Analysis,” Elsevier, New York, Amsterdam, London, 1988.
- [20] M. van Boven, F. R. Mooi, J. F. P. Schellekens, H. E. de Melker and M. Kretzschmar, *Pathogen adaptation under imperfect vaccination: Implications for pertussis*, Proc. R. Soc. Lond. B, **272** (2005), 1617–1624.
- [21] P. van den Driessche and J. Watmough, *A simple SIS epidemic model with a backward bifurcation*, J. Math. Biol., **40** (2000), 525–540.

Received May 15, 2008. Accepted July 29, 2008.

E-mail address: msafan@mans.edu.eg or muntaser_safan@yahoo.com

E-mail address: klaus.dietz@uni-tuebingen.de