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# The Effect of Cross-Immunity in a Multi-Strain Epidemic Model

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## ABSTRACT

A multi-strain SIR (susceptible-infected-recovered) epidemiological model was studied and rigorously analyzed. A new parameter called cross-immunity among strains played a key role in the dynamic behavior of the model. The model had a local, asymptotically stable, disease-free equilibrium (DFE) whenever the maximum of the associated reproduction numbers of the two strains (denoted by $R_0$) was less than unity. It was shown that the model could have infinitely many co-existence equilibria if infection with one strain conferred complete cross-immunity against the other strain and the associated reproduction number of each strain exceeded unity. On the other hand, if infection with one strain conferred partial cross-immunity against the other strain, disease elimination, competitive exclusion or co-existence of the two strains could occur.


**Keywords:** multi-strain SIR model, cross-immunity, stability

## INTRODUCTION

Many epidemiological models have been studied to account for the sustained oscillation in the number of infected hosts (for example, Aron and Schwartz, 1984; Schwartz, 1985). However, these models have focused only on the dynamics of single strain epidemics. It is known that individuals who recover from one strain become permanently immune to that strain, and may become partially or temporarily immune (or both) to other strains (WHO, 1986). In other words, individuals who recovered from one strain could enjoy cross-immunity against another strain. In the case of echovirus epidemics, for instance, there are almost 30 serologically defined sub-types (echo1, echo2, etc.), and the major types change year by year. A recent nationwide outbreak occurred in 1991 in Japan with the major type being echo30. In 1992, however, very few echo30 infections were reported, and instead, echo9 caused most of infections (IAS report, 1984–1997).

Several mathematical models have been developed in the literature to gain insights into the transmission mechanism and control of diseases produced by multiple strains or serotypes of the same pathogen. Such diseases include influenza and malaria. The kind of relationship (cross-immunity, co-existence or super-infection) that may exist among different strains or serotypes has been analyzed by several authors (for instance, Andreasen *et al*., 1997; Kamo and Sasaki, 2002; Adams and Boots, 2007). Feng and Velasco-Hernandez (1997) investigated the competitive exclusion principle in a two-strain dengue model. Esteva and Vargas (2003) consider the co-existence and relationship between two serotypes

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of dengue virus by analyzing the factors that allow the invasion and persistence of different serotypes in a human population. Sharomi and Gumel (2008) presented a deterministic HIV treatment model, which incorporates a wild (drug sensitive) and a drug-resistant strain, for gaining insights into the dynamic features of the two strains, and for determining effective ways to control HIV spread in this situation. The current study also considers the transmission dynamics of a multi-strain epidemic model.

In this paper, an SIR (susceptible-infected-recovered) model that incorporates two strains was designed and qualitatively analyzed. The objective was to gain insights into the dynamics of the two strains and to explore scenarios for the effective control of the new parameter, cross-immunity.

## MATERIALS AND METHODS

### Model formulation

The total population at time *t*, denoted by *N(t)*, was sub-divided into nine mutually-exclusive sub-populations of humans: susceptible to both strains *(SS(t))*, infected with strain 1 and susceptible to strain 2 *(IS(t))*, infected with strain 2 and susceptible to strain 1*(SI(t))*, infected with both strains *(II(t))*, recovered from strain 1 but susceptible to strain 2 *(RS(t))*, recovered from strain 2 but susceptible to strain 1 *(SR(t))*, infected with strain 2 but recovered from strain 1 *(RI(t))*, infected with strain 1 and recovered from strain 2 *(IR(t))* and recovered from both strains *(RR(t))*, represented in Equation 1.

$$N(t) = SS(t) + SI(t) + IS(t) + II(t) + RS(t) + SR(t) + RI(t) + IR(t) + RR(t) \quad (1)$$

The susceptible population is increased by the recruitment of individuals (by birth or immigration and assumed susceptible) into the population at a rate *A*. This population is decreased by infection, which can be acquired by effective contact with the infected population with strain 1 at a rate $\beta_1$ or with strain 2 at a rate $\beta_2$, and by suffering natural death at a rate $\mu$. Thus, the rate of change of the susceptible population is given by Equation 2:

$$\frac{d[SS]}{dt} = A - (\beta_1 y_1 + \beta_2 y_2)\, SS - \mu SS \quad (2)$$

where: $y_1 = IS_{12} + II_{12} + IR_{12}$

$y_2 = SI_{12} + II_{12} + RI_{12}$

The population of infected humans with strain *i* is generated by the infection of susceptible humans with strain $i$ at the rate $\beta_i$. This population decreases due to recovery at a rate $\gamma_i$, super infection with strain *j* (at a reduced rate $\sigma\beta_j$ ; where $j = 1, 2$; $i \neq j$ and $0 \leq \sigma \leq 1$ is the modification parameter associated with the degree of cross-immunity between strains 1 and 2. It should be noted that if $\sigma = 0$ (perfect cross-immunity), then infection with one strain will never be infected by the other strain; if $0 < \sigma < 1$, then primary infection with one strain confers partial immunity against the other strain. Finally, if $\sigma = 1$, then primary infection with one strain does not alter susceptibility to the other strain). These populations are reduced by natural death at the rate $\mu$. This gives Equations 3 and 4.

$$\frac{d[IS]}{dt} = \beta_1 y_1\, SS - \sigma\beta_2 y_2 IS - (\gamma_1 + \mu)IS \quad (3)$$

$$\frac{d[SI]}{dt} = \beta_2 y_2\, SS - \beta_1 \sigma_1 y_1 SI - (\gamma_2 + \mu)SI \quad (4)$$

The population of humans infected with both strains is generated by the super-infection at the rate $\sigma\beta_i$, before recovery. It is reduced by recovery from strain $i$ at the rate $\gamma_i$, and natural death at the rate $\mu$ and is shown in Equation 5.

$$\frac{d[II]}{dt} = \sigma\beta y_1 SI + \sigma\beta y_2 IS - (\gamma_1 + \gamma_2 + \mu)II \quad (5)$$

The population of individuals who have recovered from strain 1 but are susceptible to strain 2 is generated by the recovery individuals infected with strain 1 at the rate $\gamma_1$. This population is reduced by super-infection with strain 2 at the reduced rate $\sigma\beta_2$ and by natural death at the rate

$\mu$. It is assumed that recovered individuals acquire lifelong immunity against re-infection with the same strain, so that individuals in this class do not acquire infection with strain 1 again, and thus produces Equation 6.

$$\frac{d[RS]}{dt} = \gamma_1 IS - \sigma\beta y_2 RS - \mu RS \quad (6)$$

Infected individuals who recovered from infection with strain 2 move into the associated recovered class at the rate $\gamma_2$. This population is reduced by super-infection with strain 1 at the rate $\sigma\beta_1$ and by natural death at the rate $\mu$ (Equation 7).

$$\frac{d[SR]}{dt} = \gamma_2 SI - \sigma\beta_1 y_1 SR - \mu SR \quad (7)$$

The population of individuals who acquire infection with strain $i$ but recovered from strain $j$ (with $i \neq j$) is generated by infection with strain $i$ of individuals who recovered from strain $j$ at the rate $\sigma\beta_i$, and by recovery from strain $j$ of individuals with both strains. This population is reduced by recovery from strain $i$ at the rate $\gamma_i$ and by natural death at the rate $\mu$ (Equations 8 and 9).

$$\frac{d[IR]}{dt} = \sigma\beta_1 y_1 SR + \gamma_2 II - (\gamma_1 + \mu)IR \quad (8)$$

$$\frac{d[RI]}{dt} = \sigma\beta_2 y_2 RS + \gamma_1 II - (\gamma_2 + \mu)RI \quad (9)$$

Infected individuals with strain $i$ who recovered from strain $j$ move into the class of individuals who recovered from both strains at the rate $\gamma_i$. This population of individuals who recovered from both strains is reduced by natural death at the rate $\mu$. It is assumed that individuals who recovered from both strains acquire life long immunity against re-infection. This gives Equation 10.

$$\frac{d[RR]}{dt} = \gamma_1 IR + \gamma_2 RI - \mu RR \quad (10)$$

The model is qualitatively analyzed below.

**Analysis of the model**

The basic dynamic features of the model, defined by Equations 2 to 9 and hereafter called the Model, will be explored in this section. Since the population of individuals who recovered from the two strains (RR) in Equation 10 does not feature in any of the other equations of the Model, then d[RR]/dt is not included in the Model. The following can then be claimed.

**Basic properties of the Model**

First, note that the region of biological interest

$\Gamma = \{(SS, IS, SI, II, RS, SR, IR, RI) \in R_+^8 : SS + IS + SI + II + RS + SR + IR + RI \leq A / \mu\}$

is positively-invariant and attracting for the Model, since the vector field on the boundary of $\Gamma$ does not point to the exterior of $\Gamma$.

Hence, it is sufficient to consider the dynamics of the flow generated by Equations 2 to 9 in $\Gamma$. In this region, the model can be considered as it has been epidemiologically and mathematically well posed (Sharomi and Gumel, 2008).

**Disease-free equilibria (DFE)**

The DFE of the Model

is given by Equation 11:

$$E^0 = (A / \mu, 0, 0, 0, 0, 0, 0, 0, ) \quad (11)$$

The linear stability of the Model can be established using the next generation operator method. Using the notation in Van den Driessche and Watmough (2002), it follows that the *basic reproduction number*, denoted by $R_0$, is given by Equation 12:

$$R_0 = \max\{R_1, R_2\} \quad (12)$$

where: $R_1$ and $R_2$ are the associated reproduction numbers for strain 1 and strain 2, respectively, given by $R_1 = \frac{\beta_1 A}{\mu(\gamma_1 + \mu)}$ and $R_2 = \frac{\beta_2 A}{\mu(\gamma_2 + \mu)}$.

Hence, using Theorem 2 of Van den Driessche and Watmough (2002), the following result is established.

**Lemma 1** The DFE, $E^0$, of the Model is locally asymptotically stable (LAS) in $\Gamma$ if $R_0 < 1$, and unstable if $R_0 > 1$.

The threshold quantity, $R_0$, is the basic reproduction number of the disease (Anderson and May, 1991) and represents the average number of secondary cases that one infected case can generate if introduced into a completely susceptible population.

**Existence and local stability of boundary equilibria**

The non-trivial equilibria of the Model, where at least one of the infected variables is nonzero, cannot be clearly expressed in closed form. The approach in Velasco-Hernandez (1994) was used to explore the possibility of the existence and stability of non-trivial equilibria. By inspection, the possible equilibria of the Model are:

1) Strain 1-only boundary equilibrium ($E_1^*$),
$E_1^* = (SS_1^*, IS_1^*, 0, 0, RS_1^*, 0, 0, 0)$.

2) Strain 2-only boundary equilibrium ($E_2^*$),
$E_2^* = (SS_2^*, 0, SI_2^*, 0, 0, SR_2^*, 0, 0)$.

3) Co-existence equilibrium or equilibria (the two strains coexist) ($E_{12}^*$),
$(SS_{12}^*, IS_{12}^*, SI_{12}^*, II_{12}^*, RS_{12}^*, SR_{12}^*, IR_{12}^*, RI_{12}^*)$.

Solving the Model at steady state gives Equation 13 .

$$SS_{12}^* = \frac{A}{\beta_1 y_1^* + \beta_2 y_2^* + \mu},\ IS_{12}^* = \frac{\beta_1 y_1^*}{\sigma\beta_2 y_2^* + (\gamma_1 + \mu)} SS_{12}^*,$$

$$RS_{12}^* = \frac{\gamma_1}{\sigma\beta_2 y_2^* + \mu} IS_{12}^*,\ SI_{12}^* = \frac{\beta_2 y_2}{\sigma\beta_1 y_1 + \gamma_2 + \mu} SS_{12}^*,$$

$$II_{12}^* = \frac{\sigma\left(\beta_1 y_1^* SI_{12}^* + \beta_2 y_2^* SI_{12}^*\right)}{\gamma_1 + \gamma_2 + \mu},\ RI_{12}^* = \frac{\sigma\beta_2 y_2^* RS_{12}^* + \gamma_1 II_{12}^*}{\gamma_2 + \mu},$$

$$RI_{12}^* = \frac{\sigma\beta_2 y_2^* RS_{12}^* + \gamma_1 II_{12}^*}{\gamma_2 + \mu},\ SR_{12}^* = \frac{\gamma_2}{\sigma\beta_1 y_1^* + \mu} SI_{12}^*,$$

$$IR_{12}^* = \frac{\sigma\beta_1 y_1^* SR_{12}^* + \gamma_2 II_{12}^*}{\gamma_1 + \mu}. \quad (13)$$

It should be noted that the expressions for $y_1$ and $y_2$ in the endemic steady state, denoted by $y_1^*$ and $y_2^*$, are given by Equations 14 and 15.

$$y_1^* = IS_{12}^* + II_{12}^* + IR_{12}^*, \quad (14)$$

$$y_2^* = SI_{12}^* + II_{12}^* + RI_{12}^*. \quad (15)$$

Substituting the expressions in Equation 13 into Equations 14 and 15 gives Equation 16.

$$y_1^* = \phi_1(y_1^*, y_2^*) = \frac{\left(\mu + \beta_1\sigma y_1^* + \beta_2\sigma y_2^*\right)\beta_1 A y_1^*}{U_1\left(\beta_1\sigma y_1^* + \mu\right)\left(\beta_1 y_1^* + \beta_2 y_2^* + \mu\right)},$$

$$y_2^* = \phi_2(y_1^*, y_2^*) = \frac{\left(\mu + \beta_1\sigma y_1^* + \beta_2\sigma y_2^*\right)\beta_2 A y_2^*}{U_2\left(\beta_2\sigma y_2^* + \mu\right)\left(\beta_1 y_1^* + \beta_2 y_2^* + \mu\right)}, \quad (16)$$

where: $U_1 = \gamma_1 + \mu$, $U_2 = \gamma_2 + \mu$.

The equilibria of the Model can then be obtained by finding the fixed points of the system (Equation 17):

$$x = \Phi(x) = \begin{pmatrix} \phi_1(y_1^*, y_2^*) \\ \phi_2(y_1^*, y_2^*) \end{pmatrix}, \quad (17)$$

where $x = \begin{pmatrix} y_1^* \\ y_2^* \end{pmatrix}$, as follows.

**Existence and stability of strain 1-only boundary equilibrium ($E_1^*$)**

Setting in Equation 16 gives the following general form of the strain 1-only boundary equilibrium (denoted by) in Equation 18:

$$E_1^* = \left(SS_1^*, IS_1^*, 0, 0, RS_1^*, 0, 0, 0\right), \quad (18)$$

where: $SS_1^* = \frac{A}{\beta_1 y_1^* + \mu},\ IS_1^* = \frac{\beta_1 A y_1^*}{U_1\left(\beta_1 y_1^* + \mu\right)},$

$$RS_1^* = \frac{\gamma_1\beta_1 A y_1^*}{\mu U_1\left(\beta_1 y_1^* + \mu\right)}.$$

The following theorem can be claimed.

**Theorem 1.** The Model has a unique strain 1-only boundary equilibrium, $E_1^*$, whenever $R_2 < 1 < R_1$.

**Proof.** Let $R_2 < 1$. It is easy to show that for $R_2 < 1$, $(IS_1^*, RS_1^*) \to (0, 0)$ as $t \to \infty$. Further, it is clear from Equation 16 that $\phi_2 = (y_1^*, 0) = 0$ Thus, a fixed point of $\phi_1 = (y_1^*, y_2^*)$, = is obtained by solving Equation 19

$$\phi_1 = (y_1^*, 0) = y_1^* \quad (19)$$

It follows that $y_1^*$ is the root of Equation 20

$$y_1^* (U_1\beta_1 y_1^* + (U_1\mu - \beta_1 A)) = 0 \quad (20)$$

It is clear that $y_1^* = 0$ and $y_1^* = -\frac{\mu}{\beta_1}(1-R_1)$ are the roots of Equation (20). Clearly, $y_1^* = -\frac{\mu}{\beta_1}(1-R_1)$ is positive (negative) if $R_1$ is greater than (less than) unity, respectively. Further, it should be stated that for $E_1^*$ to exist, it is necessary that strain 2 does not (that is, $R_2 < 1$). Thus, a unique strain 1-only boundary equilibrium exists whenever $R_2 < 1 < R_1$.

**Theorem 2.** The strain1-only boundary equilibrium, $E_1^*$, of the Model is LAS in Γ whenever $R_2 < 1 < R_1$.

**Existence and stability of strain 2-only boundary equilibrium ($E_2^*$)**

Similarly, setting $y_1^* = 0$ in Equation 16 gives the following general form of the strain 2-only boundary equilibrium (denoted by $E_2^*$) in Equation 21:

$$E_2^* = \left(SS_2^*, 0, SI_2^*, 0, 0, SR_2^*, 0, 0\right) \quad (21)$$

where $SS_2^* = \frac{A}{\beta_2 y_2^* + \mu}$,

$$SI_2^* = \frac{\beta_2 A y_2^*}{\left(\beta_2 y_2^* + \mu\right)},$$

$$SR_2^* = \frac{\gamma_2 \beta_2 A y_2^*}{\mu U_2 \left(\beta_2 y_2^* + \mu\right)}.$$

Thus, the following theorems can be claimed.

**Theorem 3.** The Model has a unique strain 2-only boundary equilibrium, $E_2^*$, whenever $R_2 < 1 < R_1$.

**Proof.** It is clear from Equation 16 that $\phi_1 = (0, y_2^*) = 0$ Thus, a fixed point of $\phi_2 = (y_1^*, y_2^*)$ is obtained by solving Equation 22

$$\phi_2 = (0, y_2^*) = y_2^* \quad (22)$$

It follows that $y_2^*$ is the root of Equation 23.

$$y_2^*(U_2\beta_2 y_2^* + (U_2\mu - \beta_2 A)) = 0 \quad (23)$$

It is clear that $y_2^* = 0$ and $y_2^* = -\frac{\mu}{\beta_2}(1-R_2)$ are the roots of Equation 23. Clearly, $y_2^* = -\frac{\mu}{\beta_2}(1-R_2)$ is positive (negative) if $R_2$ is greater than (less than) unity. For $E_2^*$ to exist, it is necessary that the strain 1 does not (that is, $R_1 < 1$). It follows that a unique strain 2-only boundary equilibrium exists whenever $R_1 < 1 < R_2$.

**Theorem 4.** The strain 2-only boundary equilibrium, $E_2^*$, of the Model is LAS in Γ whenever $R_1 < 1 < R_2$.

**Existence and local stability of co-existence equilibria**

Here, the interest is in the solutions of the Model for which the two strains co-exist. The following special cases is studied based on various combinations of the cross-immunity parameters (σ).

Consider the case when infection with one strain produces complete immunity against the other strain, so that σ = 0. Then, the expressions in Equation 16 can be re-written as Equation 24:

$$y_1^* = \frac{\mu R_1 y_1^*}{\left(\beta_1 y_1^* + \beta_2 y_2^* + \mu\right)} \text{ and } y_2^* = \frac{\mu R_2 y_2^*}{\left(\beta_1 y_1^* + \beta_2 y_2^* + \mu\right)}. \quad (24)$$

It follows from Equation 24 that

$$\begin{aligned} \beta_1 y_1^* + \beta_2 y_2^* &= \mu(R_2 - 1) \\ \beta_1 y_1^* + \beta_2 y_2^* &= \mu(R_1 - 1) \end{aligned} \quad (25)$$

Since the left-hand sides of the system (Equation 25) are always positive, it is necessary that $R_2 > 1$ and $R_1 > 1$. If $R_1 \neq R_2$, then the system (Equation 25) is inconsistent, and there is no positive co-existence equilibrium in this case. Hence, for the system (Equation 25) to be consistent, it is necessary that $R_1 = R_2 > 1$ It is worth mentioning that in this case, a continuum (infinitely many) of endemic equilibria will arise (this phenomenon was also observed in a study of TB dynamics by Castillo-Chavez *et al*. (1999). That is, setting $R_1 = R_2 = R > 1$ implies that $\beta_1 y_1^* + \beta_2 y_2^* = \mu(R-1)$, so that $0 < y_1^* < \frac{\mu(R_1-1)}{\beta_1}$ and $0 < y_2^* < \frac{\mu(R_2-1)}{\beta_2}$. This result is summarized below.

**Theorem 5.** The Model has a continuum of positive co-existence endemic equilibria, denoted by $E_{12}^n$ ($n \in Z_+$), whenever the following conditions hold

(i) $R_1 = R_2 = R_0 > 1$, (ii) $0 < y_1^* < \frac{\mu(R_1 - 1)}{\beta_1}$,

(iii) $0 < y_2^* < \frac{\mu(R_2 - 1)}{\beta_2}$, (iv) $y_1^* < \frac{\mu(R_0 - 1 - \beta_2 y_2^*)}{\beta_1}$,

and there are no co-existence equilibria otherwise. Note that conditions (ii)–(iv) are needed to preserve the non-negativity (positivity) of $y_1^*$ and $y_2^*$ in Equations (16). The next theorem verifies stability of the positive co-existence endemic equilibrium of the model.

**Theorem 6.** The positive co-existence endemic equilibrium of the Model, given by $E_{12}^n$, is LAS whenever $R > 1$ where $R = \max\{R_1, R_2\}$.

## RESULTS AND DISCUSSION

Simulations were used to illustrate some of the theoretical results obtained in this paper. A set of parameter values, $A = 10000$, $\mu = 1/67$, $\gamma_1 = \gamma_2 = 0.1428$, $\sigma = 0.15$ and varying $\beta_1, \beta_2$, were chosen for this purpose. The simulations were carried out as follows. Figures 1(A) and 1(B) depict simulations for the case where $R_2 < 1 < R_0$, showing the persistence of strain 1, while strain 2 dies out. Numerical simulations for the case $R_1 < 1 < R_2$ are depicted in Figures 2(A) and 2(B), where strain 1 dies out and strain 2 establishes itself at steady state. In summary, the model undergoes competitive exclusion, with strain $i$ driving out strain $j$ if $R_i > 1 > R_j$ The aforementioned results for the boundary equilibria were consistent with those reported in Esteva and Vargas (2003). Figure 3 illustrates the existence of such a continuum of co-existence equilibria when the two reproduction numbers ($R_1$ and $R_2$) are equal and greater than unity. The phenomenon of having infinitely many co-existing equilibria has been observed in other epidemiological settings, such as in the study of the dynamics of multiple strains of TB (Castillo-Chavez *et al.*, 1999) and HIV (Sharomi and Gumel, 2008).

Further simulations of the Model were carried out to illustrate the effect of cross-immunity on transmission dynamics by varying the value of the cross-immunity parameter ($\sigma$). The results showed that the number of people infected with strain 1 ($IS + II + IR$) and strain 2 ($SI + II + RI$) increased with increasing values of $\sigma$, compared with the case $\sigma = 0$ (Figures 4(A) and 4(B)). Note that the peak of the number of cases was recorded for the largest value of $\sigma$ used in the simulation ($\sigma = 0.8$). Thus, these simulations showed that both strains co-exist, with the system converging to the endemic steady state $E_{12}^n$.

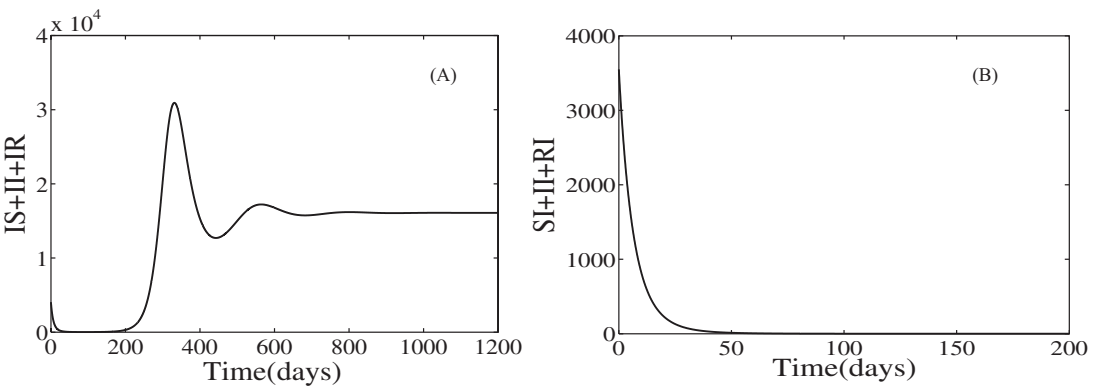


**Figure 1** Time series plots for the Model with $\beta_1 = 3.1545 \times 10^{-7}$, $\beta_2 = 2.2884 \times 10^{-7}$ (so that $R_2 = 0.9721 < 1 < R_1 = 1.3400$). (A) Population of individuals infected with strain 1 ($IS + II + IR$); (B) Population of individuals infected with strain2 ($SI + II + RI$).

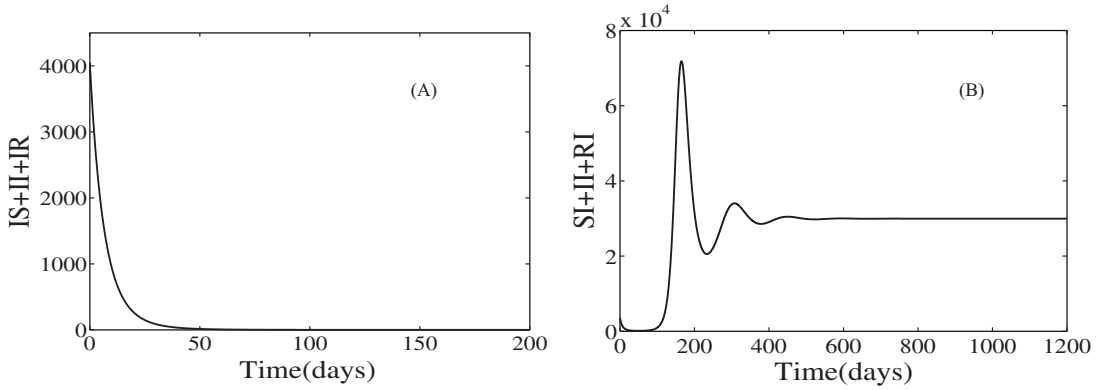


**Figure 2** Time series plots for the Model with $\beta_1 = 2.2418 \times 10^{-7}$, $\beta_2 = 4.4610 \times 10^{-7}$ (so that $R_1 = 0.9523 < 1 < R_2 = 1.8950$): (A) Population of individuals infected with strain 1 ($IS + II + IR$); (B) Population of individuals infected with strain2 ($SI + II + RI$).

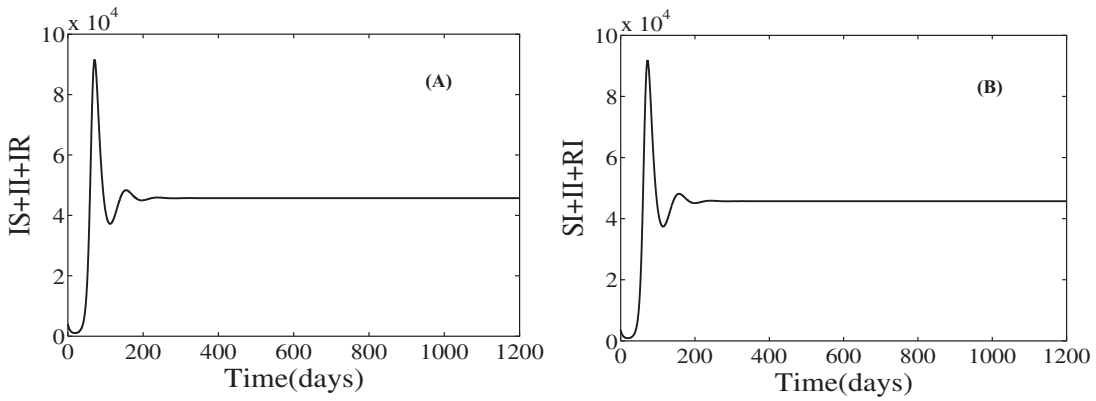


**Figure 3** Model simulations showing the continuum of positive co-existence equilibria with $\beta_1 = \beta_2 = 9.3041 \times 10^{-7}$ (so that, $R_1 = R_2 = 3.9523$): (A) strain 1 ($IS + II + IR$); and (B) strain 2 ($SI + II + RI$).

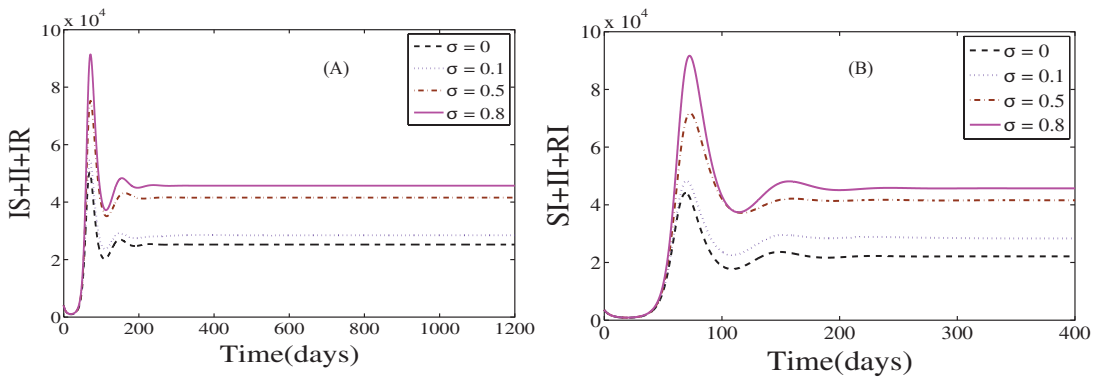


**Figure 4** Model simulations showing effect of cross-immunity on the dynamics of the two strains with $\beta_1 = \beta_2 = 9.3041 \times 10^{-7}$ (so that, $R_1 = R_2 = 3.9523$): (A) strain1 ($IS + II + IR$); and (B) strain 2 ($SI + II + RI$).

## CONCLUSION

A deterministic model for the transmission dynamics of a two-strain disease was designed and analyzed. Some of the main theoretical and epidemiological findings of the study included:

(i) The Model (defined by Equations 2 to 9 above) had a locally-stable disease-free equilibrium whenever the associated reproduction number was less than unity.

(ii) When infection with one strain confers incomplete immunity against the other, the Model exhibited the phenomenon of competitive exclusion, where strain $i$ drives out strain $j$ whenever the associated reproduction number $R_i > 1 > R_j$, where ($i, j = 1, 2, i \neq j$). The two strains will co-exist, when $R_i > R_j > 1$.

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## LITERATURE CITED

Adams, B. and M. Boots. 2007. The influence of immune cross-reaction on phase structure in resonant solutions of a multi-strain seasonal SIR model. **J. Theo. Biol.** 248: 202–211.

Andreasen, V., J. Lin and S.A. Levin. 1997. The dynamics of cocirculating influenza strains conferring partial cross-immunity. **J. Math. Biol.** 35: 825–842.

Anderson, R.M. and R.M. May. 1991. **Infectious Diseases of Humans: Dynamics and Control.** 2nd ed. Oxford University Press, 761 pp.

Aron, J.L. and I.B. Schwartz. 1984. Seasonality and period-doubling bifurcations in an epidemic model. **J. Theo. Biol.** 110: 665–679.

Castillo-Chavez, C., H. Wenzhang and L. Jia. 1999. Competitive exclusion and co-existence of multiple strains in an SIS STD model. **SIAM J. App. Maths.** 5: 1790–1811.

Esteva, L. and C. Vargas. 2003. Coexistence of different serotypes of dengue virus. **J. Math. Biol.** 46(1): 31–47.

Feng, Z. and X.J. Velasco-Hernandez. 1997. Competitive exclusion in a vector host model for the dengue fever. **J. Math. Biol.** 35: 523–544.

IAS report (Infectious Agents Surveillance Report) IAS report. 1984–1997. **J. Med. Sci. Biol.** Suppl. 37–50.

Kamo, M. and A. Sasaki. 2002. The effect of cross-immunity and seasonal forcing in a multi-strain epidemic model. **Physica D** 165: 228–241.

Schwartz, I.B. 1985. Multiple stable recurrent outbreaks and predictability in seasonality forced nonlinear epidemics models. **J. Math. Biol.** 21: 347–361.

Sharomi, O. and A.B. Gumel. 2008. Dynamical analysis of a multi-strain model of HIV in the presence of anti-retroviral drugs. **J. Bio. Dynamics** 2(3): 323–345.

Van den Driessche, P. and J. Watmough. 2002. Reproduction numbers and subthreshold endemic equilibria for compartmental models of disease transmission. **Math. Biosci.** 180: 29–48.

Velasco-Hernandez, J.X. 1994. A model for chagas disease involving transmission by vectors and blood transfusion. **Theo. Popul. Biol.** 46: 1–31.

WHO (World Health Organization) WHO. 1986. Dengue haemorrhagic fever: Diagnosis, treatment and control. Ginebra, [cited: 5 November 2007].[Available from: http://www.who.int/topics/dengue/en/].