Contents lists available at ScienceDirect



Journal of Mathematical Analysis and Applications

www.elsevier.com/locate/jmaa



Coinfection dynamics of two diseases in a single host population



Daozhou Gao^{a,b}, Travis C. Porco^{b,c,d,*}, Shigui Ruan^e

^a Mathematics and Science College, Shanghai Normal University, Shanghai, China

^b Francis I. Proctor Foundation, University of California, San Francisco, CA, USA

^c Department of Ophthalmology, University of California, San Francisco, CA, USA

^d Department of Epidemiology & Biostatistics, University of California, San Francisco, CA, USA

^e Department of Mathematics, University of Miami, Coral Gables, FL, USA

ARTICLE INFO

Article history: Received 24 February 2015 Available online 19 April 2016 Submitted by J. Shi

Keywords: Coinfection Invasion reproduction number Backward bifurcation Bistability Hopf bifurcation Uniform persistence

ABSTRACT

A susceptible-infectious-susceptible (SIS) epidemic model that describes the coinfection and cotransmission of two infectious diseases spreading through a single population is studied. The host population consists of two subclasses: susceptible and infectious, and the infectious individuals are further divided into three subgroups: those infected by the first agent/pathogen, the second agent/pathogen, and both. The basic reproduction numbers for all cases are derived which completely determine the global stability of the system if the presence of one agent/pathogen does not affect the transmission of the other. When the constraint on the transmissibility of the dually infected hosts is removed, we introduce the invasion reproduction number, compare it with two other types of reproduction number and show the uniform persistence of both diseases under certain conditions. Numerical simulations suggest that the system can display much richer dynamics such as backward bifurcation, bistability and Hopf bifurcation.

 $\ensuremath{\mathbb O}$ 2016 Elsevier Inc. All rights reserved.

1. Introduction

Different infectious agents may infect or colonize a host at the same time [21]. Many examples can be found, these involving HIV [30,37] (for example, HIV and TB [19], HIV and Hepatitis B [12,26], HIV and Hepatitis C [23], and HIV and malaria [2]), as well as some not involving HIV (for example, Hepatitis B and C coinfection [11], gonorrhea and Chlamydia [13], and herpes simplex viruses 1 and 2 [41,59]). Moreover, simultaneous infection may occur with multiple strains or serotypes of the same organism, as is the case for influenza [20,49], human papilloma virus [9], and HIV [55,63,22], for just three of many examples. However, simultaneous colonization or infection may occur even when there appears to be little or no interaction between the two agents, as in the case of infection by ocular strains of chlamydia and nasopharyngeal colo-

http://dx.doi.org/10.1016/j.jmaa.2016.04.039 0022-247X/© 2016 Elsevier Inc. All rights reserved.

^{*} Corresponding author. Correspondence to Francis I. Proctor Foundation, UCSF, San Francisco, CA 94143-0412, USA. *E-mail address:* travis.porco@ucsf.edu (T.C. Porco).

nization by pneumococcus [24]. The dynamics of coinfection is important in this case, because antimicrobials used to treat one infection may affect the other (e.g., [51,24]).

A variety of mathematical models for coinfections with multiple specific diseases, such as HIV/TB [43, 48,6,47], HIV/gonorrhea [40], HIV/malaria [1,39], malaria and meningitis [29], general diseases [5,7,35,28], and microparasites (viruses, bacteria, protozoa, fungi) [54,10,3,4,61], have been developed and analyzed in the past few years. Ferguson et al. [16] and Kawaguchi et al. [27] presented models to describe the coinfection of two serotypes of dengue virus in a human community. With respect to the interaction between nonspecific agents or pathogens, Blyuss and Kyrychko [7] studied a two-disease SIS model with equal transmission efficiency for both susceptible and singly infected individuals; Allen et al. [5] studied an SI model for a single host population with two viral infections, in which one is vertically transmitted and the other is horizontally transmitted; Zhang et al. [60] proposed an ODEs coinfection model with two strains of parasites and two host types to study the influence of heterogeneities in parasite virulence and host life history on the persistence and spread of parasite strains; Martcheva and Pilyugin [35] considered an epidemic model of two diseases: a primary disease and a secondary disease, structured by time since infection structure (for the primary disease); in the monograph of Keeling and Rohani [28], the interaction of two pathogens spreading through a host population was discussed in four cases: complete cross-immunity, no cross-immunity, enhanced susceptibility and partial cross-immunity. Among these models either the uninfected hosts cannot become infected with both diseases/strains directly [38,35,28,10], or there is no recovery and an infection is lifelong [54,5,4], or both [60,3].

In this paper, we develop and analyze a simple model of multiple infections; this model includes the possibility that the two agents are simultaneously transmitted, thereby inaugurating a dual infection. It exhibits aspects of *Chlamydia trachomatis* and pneumococcus, though we do not restrict the analysis to this setting (see [31,46] for examples of cotransmission in vector-borne disease ecology and human case reports, respectively). Our model will also include the possibility that an individual who is currently infected with one agent will become dually infected as a result of an exposure to the second agent. In this paper, the condition of being simultaneously infected by multiple agents will be referred to simply as *coinfection*. Our model is similar to the model of Blyuss and Kyrychko [7] where the disease induced mortality is included, the doubly infected hosts recover from both diseases simultaneously and strong restrictions on transmission parameters are required, and to the models for coinfection by different species in Tanaka and Feldman [54] and Alizon [4] where disease-induced mortality may occur, but no recovery is possible (and the forces of infection follow a different rule).

We will assess a two-disease SIS model with no immunity or cross-immunity. For simplicity, we will refer to the first and second disease, recognizing that the model applies equally well to colonization or to subclinical infections. In Section 3, we carry out a complete global stability analysis of the model for the case where the force of infection of one disease is not affected by the presence of the other (i.e., no interaction between two infections). In Section 4, when the two infections interact with each other, we calculate the invasion reproduction numbers and obtain their epidemiologically meaningful lower and upper bounds, and show that the interaction outcome could be extinction of one or both diseases or persistence of both diseases. In Section 5, four numerical examples are provided to support the existence of competitive exclusion, backward bifurcation, bistability and Hopf bifurcation, respectively.

2. The model

We propose a simple SIS epidemic model with two infectious agents (or strains of the same agent) spreading through one host species. Let S(t), $I_1(t)$, $I_2(t)$ and $I_{12}(t)$ be the fractions of the population infected with no infectious agent, the first agent, the second agent and both agents at time t, respectively. A susceptible individual who contacts coinfected persons can be infected with either one or both disease agents as a result of a single contact. Using ocular strains of *Chlamydia trachomatis* and nasopharyngeal

Download English Version:

https://daneshyari.com/en/article/4613960

Download Persian Version:

https://daneshyari.com/article/4613960

Daneshyari.com