Modeling direct and indirect disease transmission using multi-group model

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A R T I C L E   I N F O

A B S T R A C T

The survival of pathogens outside the host in the environment is an important factor for some diseases transmission. Environment-to-individuals is an indirect mode of transmission, which also plays a role in the dynamics of some disease. In this paper, we proposed a general multi-group epidemic model with nonlinear direct and indirect transmission incidence rates, nonlinear pathogen shedding rates, and common environmental contamination for indirect transmission. Under the certain assumptions, the basic reproduction number of the model is identified. We proved the global stability of the equilibria by using global Lyapunov functions with the specific coefficients and graph-theoretical approach theorem, which are determined by the basic reproduction number. The main result of our model is that we give the specific coefficients of global Lyapunov functions. From the discussion of our model, we conclude that our model contains earlier cholera models, brucellosis models, and other general disease multi-group models as special cases.

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1. Introduction

Infectious disease is a serious public health problem in some areas of the world, such as influenza [18,49], malaria [19], dengue [20], cholera [30], hantavirus [16], brucellosis [4], foot-and-mouth disease virus [38], infectious canine hepatitis virus [46], childhood diseases measles and rubella [7]. Some of these diseases are spread by pathogens outside the host, and the survival of pathogens outside the host is highly important for the epidemiological dynamics of brucellosis [1], cholera [3], hantavirus [17], infectious canine hepatitis virus [46], and influenza [49]. Mathematical modeling suggested that an indirect mode of transmission via

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the natural environment (e.g. respiratory droplets, fomites, fungal spores, waterborne pathogens) was an epidemic pattern for disease transmission [31]. This mechanism is in contrast to direct transmission which postulates that the pathogen is acquired through an infectious contact with an infected individual. For diseases transmitted through indirect pathways with the pathogens to survive outside of its host has also been used to play a vital role in the transmission dynamics process of hantavirus [17,31], cholera [3,8, 27,28,32,39,40] and brucellosis [1,13,14,25,26]. Most of these studies are focused on multiple transmission pathways which involve both direct and indirect modes. Mukandavire et al. [27,28] introduced a dynamic model of cholera in Zimbabwe, the direct transmission (fast transmission pathway) is bilinear incidence and the indirect transmission (slow transmission pathway) is saturating incidence. Eisenberga et al. [8] proposed a cholera model in a patchy environment with water and human movement, Hou et al. [14] represented a brucellosis model for animal diseases, Shuai and van den Driessche [32] studied a cholera model with differential infectivity, the direct and indirect transmission of these three models are nonlinear incidence. Under the reasonable assumption of nonlinear incidence, the global stability of endemic equilibrium is given when basic reproduction number is larger than one.

In reality, due to the heterogeneity in host population, the host population can be divided into multiple groups. Multi-group model is a class of highly heterogenous models with complex interactions among distinct groups corresponding to different infection source targets for specific purpose in studying disease transmission dynamics. Its applications became widely noticed in literature since 1970s [12,21], but large scale utilizations are just recently due to its mathematical breakthrough and surging computing capacity for simulations. In recently years, many multi-group models have been introduced to describe the transmission dynamics of infectious diseases [10,11,24,35,36,48]. The difficulty of global dynamics of multi-group models lies in establishing uniqueness and global stability of endemic equilibrium when basic reproduction number is larger than one. Guo et al. [10,11] firstly proved the global stability of endemic equilibrium of multi-group models with bilinear incidence of cross infection by using global Lyapunov functions and graph-theoretical approach. Li and Shuai [24] further made the proof more integrated to simpler formulas and became a standard procedure. Afterwards, a series of papers involving multi-group models utilized the methods to establish global dynamics as shown in reference [35,36,48]. However, most of the modeling work focused on analyzing the spread of infectious diseases uses a direct transmission mechanism, and there are few studies to analyze the multi-group dynamic model which incorporates both direct and indirect transmission. In paper [25], Li et al. proposed a multi-group brucellosis dynamical model for bilinear direct and indirect transmission incidence with different environmental contamination between cattle and sheep in the public farm, and the global dynamic behavior of the model was also given. In paper [26], Li et al. studied a multi-group sheep brucellosis model with common environmental contamination, but they could not give the global stability of the endemic equilibrium. Hence, taking an example of brucellosis, we want to study the global dynamic behavior of general multi-group *SEI-W* type model for the transmission of brucellosis that involves both nonlinear direct and indirect transmission, and common environmental contamination with indirect bacteria transmission for different groups. For our model, general forms for direct and indirect transmission include mass action, saturating incidence and other incidence. Our model contained earlier cholera models in [3,27, 28,39,40] and brucellosis models in [1,13,25,26] as special cases. We proved the global stability of the equilibria by using global Lyapunov functions and graph-theoretical approach theorem, which are determined by the basic reproduction number. Our conclusions also contained the global stability of endemic equilibrium which was not addressed in previous paper [26]. The proofs of the main results of our paper exploited the method of constructing Lyapunov functions and a graph-theoretical technique in estimating the derivatives of Lyapunov functions, and also improved the related works in [15,42,43]. In this paper we gave the specific coefficients of global Lyapunov functions which are absent from previous papers [10,11,24,32,35,36,45,48].

The organization of this paper is as follows. In Section 2, we construct a multi-group brucellosis model with common environmental contamination of bacteria for different groups, and give some dynamic analysis