CHAPTER 1 INTRODUCTION

1.1 Introduction

The spread of infectious diseases between discrete geographic regions (or cities) is a phenomenon that involves many different compartments. To control the spread of an infectious disease, one has to understand how the growth and spread of the disease affect its outbreak. There are many factors that lead to the dynamics of an infectious disease of humans. They include such human behaviors as population dislocations, living styles, sexual practices and rising international travel. In addition, climate change enables diseases and vectors to expand their range. Generally speaking, for some kind of infectious diseases such as foot-and-mouth disease and SARS, travel and commerce are important factors affecting their spread between discrete geographic regions (or cities). Epidemiology is the study of the spread of disease in space and time, aiming at tracing factors that give rise to their occurrence.

Since Kermack and Mckendrick [1] constructed a system of ODE to study epidemiology in 1927, the concept of compartment modeling is used until now. From then on, many epidemic models are proposed and investigated [2–4], and most of the research literature assumes that population lives in the fixed place, without travel. In reality, people usually travel among different places, thus models involving dispersal are necessary. The population dispersal, as a common phenomenon in human society, may cause many diseases such as influenza and SARS, which can be easily transmitted from one region to other regions. Since the first AIDS cases were reported in the United States in June 1981, the number of cases and deaths among persons with AIDS increased rapidly during the 1980s followed by substantial declines in new cases and deaths in the late 1990s. In 2003, SARS began in Guangdong province of China; however, it broke out at last in almost all parts of China and some other cities in the world due to dispersal [5]. Recently, some epidemic models have been proposed to understand the spread dynamics of infectious disease. In mathematical epidemiology a few models which incorporate discrete geographical regions have been studied to gain insights into the transmission dynamics of the disease in a community (see, for instance, [5–12]). Discrete time difference equations in a continuous state space were used by Longini [6]. Rvachev and Longini [5] to study the global spread of influenza, taking into account the airline network. Sattenspiel and Dietz [7] introduced a model with travel between populations. They identified parameters in the case of the transmission of measles in the Caribbean island of Dominica, and numerically studied the dynamics of the model. Sattenspiel and Herring [13] considered the same type of the model but applied it to travel between populations in the Canadian subarctic, which can be thought of as a closed population where travel is easily quantified. In 2003, Sattenspiel and Herring [14] formulated a model that includes quarantine and applied it to data of the 1918-1919 influenza epidemics in the center of Canada. Fulford et al. [8] formulated a meta-population model with age-structure. Wang and Mulone [11] and Wang and Zhao [15, 16] proposed epidemic models to describe the dynamics of disease spread between two patches and n patches. Arino and van den Driessche [9] developed a multi-city epidemic model to analyze the spatial spread of infectious diseases. All these investigations ignored the possibility for the individuals to become infective during travel. Recently, Cui et al. [17] have proposed a SIS epidemic model to understand the effect of transport related infection on disease spread. Considering entry screening and exit screening to detect infected individuals, Liu and Takeuchi [18] proposed an $SIQS$ model to study the effect of transport-related infection and entry screening. Mathematically, Cui, Takeuchi and Saito mainly studied local asymptotical stability of model introduced by Cui et al. [17] and the endemic equilibrium was proven to be asymptotically stable with an additional condition besides the condition for its existence. Subsequently, Takeuchi et al. [19] studied further the global dynamics of model in [17]. They proved the global stabilities of equilibria disease-free and endemic equilibriums, still required additional condition besides the condition for their existence. Obviously, the models in [17–19] assumed that a susceptible individual becomes infectious immediately after infected. However, for many diseases, a host stays in a latent period before becoming infectious after infected. Wan and Cui [10] formulated an $SEIS$ epidemic model to describe the transmission of infectious diseases related by transports. When the individuals have immunity to the disease after recover, model that are more general than the SEI or $SEIS$ types need to be studied to investigate the role of incubation in disease transmission. Using a compartmental model based on the assumption that a susceptible individual first goes through a latent period (and is said to become exposed or in the class E) after infection before becoming infectious and the individuals have immunity to the disease after recover, the resulting model are of $SEIR$ or $SEIRS$ type, respectively, depending on whether the acquired immunity is permanent or otherwise.

The purposes of this thesis is to modify the model presented in [10] based on $SEIRS$ model in order to describe the transmission of infectious disease related by transports, to analyze the dynamics of models at some significant cases, and to discuss the effect of transport–related infection on its outbreak and final size of all individuals for the populations. The thesis is organized as follows.

In Chapter 2, epidemic models with transport–related infection are reviewed, and background mathematics used in later chapters are given.

Chapter 3 deals with formulating an $SEIRS$ (susceptible – exposed – infected – recovered) epidemic model with transport-related infection. The basic reproduction number of the formulated model is derived. The local stability is analyzed to verify that the equilibria of the formulated model are locally asymptotically stable under the condition of the basic reproduction number.

Chapter 4 discusses the numerical solutions of the models to describe the effect of transport–related infection on its outbreak and the final size of all individuals for the populations. The $SEIRS$ model and $SEIRS$ model with transport–related infection are applied to predict the SARS outbreak within a city and two cities, respectively.

Finally, discussion and conclusions of this thesis are given in Chapter 5.