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Impact of visitors and hospital staff on nosocomial transmission and spread to community



Ying-Hen Hsieh^{a,b,*}, Junli Liu^c, Yun-Huei Tzeng^{a,d}, Jianhong Wu^e

^a Department of Public Health, China Medical University, Taichung 40402, Taiwan

^b Center for Infectious Disease Education and Research, China Medical University, Taichung 40402, Taiwan

^c School of Science, Xian Polytechnic University, Xian 710048, China

^d Center for General Education, China Medical University, Taichung 40402, Taiwan

^e Department of Mathematics and Statistics and Centre for Disease Modelling, York University, Toronto, Ontario, Canada M3J 1P3

HIGHLIGHTS

• Metapopulation model to qualify disease transmission in a community and its healthcare facility.

• Focus on the roles of healthcare workers at and visitors to the healthcare facility.

• Quantify disease transmission within the facility and to the community during a disease outbreak.

• Infections by infective residents and visitors in healthcare facility are most important factors.

• Preventing infections of healthcare staff is of the highest priority in disease prevention.

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ABSTRACT

We develop a deterministic meta-population model to qualitatively capture some key features of disease transmission between a community and its healthcare facility. We consider the disease transmission dynamics within a healthcare facility and between the healthcare facility and its community. The focus of this study is to quantify the roles of the healthcare workers at and visitors to this healthcare facility in shaping the transmission dynamics during a disease outbreak. We stratify the total population into the general population in the community and the healthcare workers and visitors in the healthcare facility, to account for nosocomial transmission in the case when an individual in the community may be exposed to an infection due to a visit to the healthcare facility. Equilibrium stability analysis is carried out to inform long-term outcomes of disease dynamics in the coupled community-health care facility system. The basic reproduction number is calculated and its dependence on the waiting time and various disease transmission rates is analyzed. Numerical simulations are performed with pertussis as the disease in question. The results show that waiting time only affects the peak number of infections in the waiting reception area. The results also indicate that transmission rate of infective residents in the community and the transmission rate of the infective visitors at the healthcare facility have decisive impact on disease eradication/persistence of the coupled system; while other modes of transmissions are less important, affecting the peak number of infections at best.

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1. Introduction

In recent years, impact of travel on the spread of diseases has become an important topic of interest for public health policy formation and implementation, qualification of which has imposed a formidable challenge to modelers. Rvachev and Longini (1985)

E-mail address: hsieh@mail.cmu.edu.tw (Y.-H. Hsieh).

considered the airline network and used discrete time difference equations to study the global spread of influenza. Sattenspiel and Dietz (1995) proposed a model with travel between populations to describe the transmission dynamics of measles in the Caribbean island of Dominica. More recently, Arino and van den Driessche (2003a) formulated an SIS model with patches for residents of multiple cities (or discrete geographical regions) who may travel between them, and gave an explicit expression for the basic reproduction number for the model, which is a threshold between extinction and invasion of the disease, with simulations to illustrate that travel can both stabilize and destabilize the disease-free equilibrium. An SEIRS model was later

^{*} Corresponding author at: Department of Public Health, China Medical University, Taichung 40402, Taiwan.

considered by Arino and van den Driessche (2003b), with analytical results similar to those of Arino and van den Driessche (2003a). In these studies, travel was assumed to be independent of disease states. Relevant studies also include Wang and Mulone (2003) and Wang and Zhao (2004, 2005). Salmani and van den Driessche (2006) considered an SEIRS epidemic model for a population with travel between multiple patches, and established the global asymptotical stability of the disease-free equilibrium when the basic reproduction number is less than unity. They also presented a detailed study of the disease transmission dynamics for a disease with very short exposed and immune periods in an environment with two patches. Hsieh et al. (2007a) formulated an SEIRP model including partially immune individuals, and established relations, expressed by inequalities, between the basic reproduction number of the full model and the basic reproduction number of each patch in isolation. Their numerical simulations indicated that banning the border does not necessarily always have a positive impact on the overall spread of disease. Similar results were also obtained in Gojovic et al. (2009) using the USA and Canada as two separated patches connected primarily by border crossing. All these studies demonstrate that travel between patches can influence disease spread in a very complicated way.

The concepts of patch and travel can be considered in a very general setting, depending on how a heterogeneous population is partitioned into non-overlapping sub-populations with flows among them. In this study, by considering one of the patches as a major health care facility such as a hospital, we use a patch model to address nonsocomial infections and infections spread between the facility and its community. Nosocomial infections of many communicable diseases are widespread, they result in substantial morbidity, prolong hospital stay and lead to increase in direct patient care costs and mortality. Nosocomial transmission can occur between patients, hospital personnel or, less often, visitors, from people who may be infectious, in the incubation period (with mild or no symptoms), or even from chronic carriers. The US Centers for Disease Control and Prevention (USCDC) reports that nearly two million patients each year were infected while in a US hospital, with about 90,000 of them died from the infection. Deaths due to nosocomial infections is the fourth leading cause of death in US after heart disease, cancer, and strokes. The USCDC also estimated an additional cost of 5 billion dollars to US healthcare in 2000 due to nosocomial infections.

Although our understanding of the epidemiology of nosocomial transmission has increased dramatically over the last two decades, the incidence of nosocomial transmission continues to affect the hospitalized patients. This is particularly so for the 2003 SARS outbreak when nosocomial transmission occurred in all the affected regions. This first major infectious disease outbreak in the 21st century has been modeled and investigated intensively (e.g., Lipsitch et al., 2003; Riley et al., 2003; Chowell et al., 2003, 2004; Wang and Ruan, 2004; Gumel et al., 2004; Hsieh et al., 2004a, 2005, 2007b; Webb et al., 2004; Zeng et al., 2007), where model-based analysis clearly revealed the profound impact of nosocomial transmissions. In Taiwan, 301 (77.3%) of the 390 cases with a confirmed source of infection had been infected within a hospital, of which 67 (22.3%) had died. In particular, of 232 SARS patients who had been admitted to the National Taiwan University Hospital (NTUH) from March 14 to June 19, 31 (13.4%) did not have a history of travel, exposure to SARS patients, or a hospital visit within 10 days before illness. Hence the only contact history for these patients was at the NTUH Emergency Room (ER) (Chen et al., 2004). These 31 cases were almost evenly divided among 3 groups: ER patients, people who accompanied or visited the patients, and hospital staff. This ER outbreak finally led to a temporary shutdown of emergency service at NTUH on May 12 (Hsieh et al., 2004b). A major reason for this outbreak at NTUH was the closing of two nearby hospitals on April 24 and 26 due to nosocomial SARS outbreaks, which forced many individuals living in the neighborhood community who had been visiting these two hospitals regularly prior to shutdowns (including some individuals who had already been infected) to seek medical care at NTUH instead. This directly contributed to a more congested ER at NTUH, longer waiting time, and increased likelihood of contacting SARS infectives during this period before its shutdown. Since some of those infected in NTUH during this period later infected others in the community, their clinical visit and waiting time had a direct impact on their likelihood of being infected nosocomially and on the subsequent spread of SARS in the community.

Another more current example is the nosocomial transmission of Bordetella pertussis, also commonly called whooping cough. classically recognized as a disease of infants and children. Reported incidence in adolescents and adults has increased globally at a significant rate over the past decade or so (Edwards and Talbot, 2006). The incubation period for pertussis is typically seven to ten days with range of four to 21 days, after which there are usually some cold-like symptoms such as mild coughing, sneezing, or runny nose. After one to two weeks, the coughing classically develops into uncontrollable fits of severe coughing, mostly in children that could continue for weeks. One of the reasons for this increase is nosocomial infection of healthcare workers (HCWs) (Wright et al., 1999; De et al., 2000) by unsuspected (asymptomatic/subclinical) pertussis patients. Infected HCWs then serve as vectors of infection to other susceptible contacts, including their patients, other employees, and even their own children at home, resulting in substantial costs to the healthcare system. Prevention by vaccination is of primary importance given the seriousness of the disease in children. Although treatment is of little direct benefit to the person infected, antibiotics are recommended because they shorten the duration of infectiousness (Heininger, 2010).

In this work, we propose a deterministic compartmental model that focuses on waiting and clinical visit and their roles in disease transmission within a healthcare facility and in a community. We assume that individuals waiting at a hospital (or an emergency room) reception and waiting area can get infected during the waiting process due to the nosocomial transmission from others waiting there. We also assume that individuals can get infected during clinical visits due to the nosocomial transmission from other visiting individuals as well as infected hospital personnel. Those infected within the healthcare facility then serve as vectors of infection for community spread. Incorporating these assumptions into a patch model involving two patches, i.e., the community and the healthcare facility, leads naturally to a system of differential equations.

The paper is organized as follows. We formulate the model in Section 2. In Section 3, we obtain the basic reproduction number of the model explicitly in terms of model parameters and we describe the stability of the disease-free equilibrium when the basic reproduction number is below unity, and persistence of the disease and the existence of the positive equilibrium when the basic reproduction number is larger than unity. Numerical simulations, with pertussis as the disease being modeled, are given in Section 4, to demonstrate the impact of various model parameters, such as within-patch and between patch disease transmission, waiting/visiting, and others, that might affect the disease spread. Finally, we give our conclusions in Section 5.

2. Model formulation

We consider an SIR type of disease transmission, where the population is divided into three classes: susceptible individuals, infectious individuals, and recovered individuals. Susceptible Download English Version:

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