



Regional transport and its association with tuberculosis in the Shandong province of China, 2009–2011



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ABSTRACT

Human mobility has played a major role in the spread of infectious diseases such as tuberculosis (TB) through transportation; however, its pattern and mechanism have remained unclear. This study used transport networks as a proxy for human mobility to generate the spatial process of TB incidence. It examined the association between TB incidence and four types of transport networks at the provincial level: provincial roads, national roads, highways, and railways. Geographical information systems and geospatial analysis were used to examine the spatial distribution of 2217 smear-positive TB cases reported between 2009 and 2011 in the Shandong province. The study involved factors such as population density and elevation difference in conjunction with the types of transport networks to predict the disease occurrence in space. It identified spatial clusters of TB incidence linked not only with transport networks of the regions but also differentiated by elevation. Our research findings provide evidence of targeting populous regions with well-connected transport networks for effective surveillance and control of TB transmission in Shandong.

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1. Introduction

There is compelling evidence that much of disease spread today is related to global movement of people, animals, and goods. It has also been observed that the most recent outbreak of Ebola and its intense transmission in West Africa are being monitored and tracked closely because there is real risk of new countries being affected (Gomes et al., 2014; Wesolowski et al., 2014). While migratory birds have contributed to the spread of avian influenza, it has been said that modern modes of transportation, especially air travel, are responsible for the unprecedented volume and speed of cross-border and cross-continental transmission of diseases in the 21st century.

Hagerstrand's theory of diffusion (Ellegård and Svedin, 2012) is the basis for the formulation of many epidemic models. His time-geographic concepts link individuals in one or more places through movement in space and time. Diffusion of disease is examined by

tracking where an infected individual has been and with whom the infected has been in contact. The outbreak of SARS in 2003 highlighted the importance of tracking a highly infectious index patient in Hong Kong that resulted in an acute outbreak almost went out of control. The 2009 Swine flu also painted a bleak picture of disease transmission and diffusion. But the tracking of individuals' space–time movement is a daunting task (Kwan, 2000; Chen et al., 2011). Even with today's technological advances in following people's small-scale movements and activity space, scientists are baffled by the immense detail and volume of data and how to make sense of the placing and patterning of human activities.

1.1. The notion of distance decay

Disease diffusion concerns the spread of a disease from its source to new locations and the pattern of diffusion is affected by barriers such as time, distance, physical, and cultural factors

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(Bossak and Welford, 2015). It is well documented that the farther away from the source of a disease, the more time it takes to feel the impact. This friction of distance is what geographers refer to as the distance decay effect. The likelihood of disease spread can be explained by the mechanisms of expansion and relocation (deBlij and Murphy, 2003). Expansion diffusion is said to occur when the number of infected individuals in an area grows continuously larger in space and time. Expansion can occur through an established structure, also known as hierarchical diffusion, or through a group of people or an area, also known as contagious diffusion (Cliff et al., 1981; Meade et al., 2000). Relocation is a sequential diffusion process whereby an infection is transmitted through movement of its carrier agents or a migrating population (Cliff and Haggett, 2004; Martens and Hall, 2000; Stoddard et al., 2009). The distance decay function in geographic profiling (the circle hypothesis and the distance decay theory) of disease investigation is highly influenced by human activities and environmental attributes. As the impact of human activities spread more widely through global transportation networks, disease can be transported via many different processes and pathways. However, the processes generally result in some degree of distance decay.

The fact that disease emergence decays with distance from population centers has been reported time and time again (Fotheringham and Rogerson, 1993; Xia et al., 2004). With new evidence highlighting that disease spread tended to occur faster along established transportation routes (such as major roads, waterways, and coastlines) (Kausrud et al., 2010; Wen et al., 2012), it is more certain that both environmental factors and population movements play important roles in disease transmission. Although the modeling of complex spatial interaction of disease phenomena is far from being perfect, understanding the role of disease spread along these networks and the travel patterns would allow for better identification of distance jumps or rate of disease infection. For example, Balcan et al. (2009) found that the effect of short-range commuting flows was larger than that of long-range airline flows and that the epidemic behavior would be different due to multi-scale mobility processes in the disease dynamics. The ability to estimate how fast or broad an infection would spread under different conditions could help public health officials refine disease control or intervention measures.

2. Tuberculosis

Mycobacterium tuberculosis (TB) is a highly contagious bacterium that spreads from person to person via aerosols (Dye, 2006; Jones-López et al., 2013). The worldwide spread of TB has been a continuous threat to public health globally with almost one third of the world's population infected (Dye, 2006). The World Health Organization (WHO, 2012) estimated that the world had over 8.7 million new TB infection and 1 million TB-related deaths in 2012.

The transmission of TB is highly complex and dynamic, and varying spatially (Bryant et al., 2013; Tessema et al., 2013). It has been asserted that traveling by public transports has a role in the emergence and spread of infectious diseases such as TB (Wilson, 1995; Barnett and Walker, 2008). The importance of TB contact locations such as community drop-in centers, bars, and parks, and social networks have been explored to great effect (Cook et al., 2007; Carter et al., 2009). Indeed, the movements of people in space and migrants, in particular, have contributed to the spread of TB in both developing (Long et al., 2008; Wei et al., 2009; Pace-Asciak et al., 2013) and developed countries (Haase et al., 2007; McPherson et al., 2008; Franzetti et al., 2010; Edelson and Phipers, 2011). An earlier study by Jia et al. (2008) reported a higher rate of TB prevalence in migrants than the local residents

of Beijing. Long et al. (2008) also found factors such as long working hours, poor living and working environment, as well as insufficient healthcare support and medical insurance to be probable causes of higher TB prevalence among the migrants. However, findings from these analyses that are confined to sufficiently small population groups and geographic areas might not be appropriate for larger regions with more complex and dynamic patterns of human mobility. For example, China has a large number of labor workers traversing long distances regularly between urban cities and rural areas known to have a high prevalence of TB (CTCC, 2004). These migrant workers not only have increased the likelihood of TB spreading across wide geographic scales but also promulgated the disease to further propagate by local movements through public transports (Edelson and Phipers, 2011).

Wu et al. (2006) defined human mobility as a network of interacting communities where the connection and corresponding intensity represent the flow of people among them. But tracking massive population movement among infected localities is impractical, if not impossible. In a recent study, Balcan and colleagues (Balcan et al., 2009) applied long-range intercontinental airlines and short-range commuting flows to simulate the global process of human mobility and its impact on the spread of influenza-like diseases over multiple geographic scales. The authors acknowledged that the spread of infectious diseases is caused by a strong heterogeneity of transport networks.

Altitude (or elevation) has been applied as a significant predictor in a number of studies of infectious diseases, including TB (Saito et al., 2006) and avian influenza (Gilbert et al., 2008; Ge et al., 2012). In particular, altitude has a protective effect against TB in Peru in which lower disease prevalence and increased household clustering of TB was found in high altitude villages compared to those at sea level (Saito et al., 2006). In this study, we included altitude to capture spatial variation in topography as well as to serve as a surrogate indicator of other unmeasured variables related to TB infection.

This paper makes use of transport networks to explore the association between human mobility and TB occurrences across multiple geographic scales. The primary objective is to study the association modeled on transport networks to address the following issues: (1) spatial patterns of TB incidents and disease clusters or hot spots, (2) degrees of spatial association between TB clusters and transport networks, and (3) types of spatial association differentiated by two elevation groups of high versus low altitude.

3. Data and methods

This was a retrospective study to test the null hypothesis of no association between TB clusters and transport networks differentiated into two separate regions of low and high elevation. We postulated that TB cases are spatially related to transport networks whereby well-connected roads facilitate peoples' movements. We also postulated that provincial roads in zones of low altitude had a higher association with people movement because of their greater accessibility to travelers.

3.1. Study area

The study area was the Shandong province (eastern China) (Fig. 1), the second most populous province of China in 2010. It has a population of 95 million with 45.6 million living in urban areas (SPSB, 2010). The province is a prosperous and relatively rich region with a strong agricultural and industrial foundation, although an imbalanced urban and rural economic development remains a problem. Around 7 million migrants lived in the

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