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The Characteristics of Middle Eastern Respiratory Syndrome Coronavirus Transmission Dynamics in South Korea

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Abstract

Objectives: The outbreak of Middle Eastern respiratory syndrome coronavirus (MERS-CoV) was one of the major events in South Korea in 2015. In particular, this study pays attention to formulating a mathematical model for MERS transmission dynamics and estimating transmission rates.

Methods: Incidence data of MERS-CoV from the government authority was analyzed for the first aim and a mathematical model was built and analyzed for the second aim of the study. A mathematical model for MERS-CoV transmission dynamics is used to estimate the transmission rates in two periods due to the implementation of intensive interventions.

Results: Using the estimates of the transmission rates, the basic reproduction number was estimated in two periods. Due to the superspreader, the basic reproduction number was very large in the first period; however, the basic reproduction number of the second period has reduced significantly after intensive interventions.

Conclusion: It turned out to be the intensive isolation and quarantine interventions that were the most critical factors that prevented the spread of the MERS outbreak. The results are expected to be useful to devise more efficient intervention strategies in the future.

1. Introduction

One of the most significant events in South Korea in 2015 was the introduction and diffusion of Middle Eastern respiratory syndrome coronavirus (MERS-CoV). It is a novel coronavirus which was first identified in Saudi Arabia in September 2012 [1]. After that,

MERS-CoV exhibited outbreaks in several regions and the last one was in South Korea (at the time of writing). It is known as having a high fatality rate and having a resemblance in clinical features with severe acute respiratory syndrome coronavirus (SARS-CoV) [2], thus, it has drawn much concern both from the public health authority and the general public when the first index

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case was identified in May 2015, for the first time in Korea.

In the case of the outbreak in South Korea, it is characteristic in that a single importation of the pathogen sparked a large cluster of infected cases, while sporadic importations did not lead to local outbreaks in other regions [3]. It was surprising because South Korea has been said to have one of the most advanced medical and public health systems in the world [4], and it raises fears that the situation would be much worse in countries with less developed public health systems. Thus, the investigation of this study about the South Korean incidence is expected to give an invaluable lesson both to public health authorities around the world and the community of epidemiology researchers. Moreover, it might be able to provide a quantified result with mathematical modeling and statistical analysis, which is beneficial given that the studies about the South Korean case are largely comprised of epidemiological descriptions [4,5].

It is not only in the South Korean case but also in MERS-CoV studies in general that case studies and epidemiological descriptions are the main approach. Assiri et al [6] provided a detailed description of cases in the Middle East, Drosten et al [7] and Guery et al [8] analyzed the clinical features of infected cases, and Memish et al [9] and Al-Tawfiq et al [1] described the epidemiological data with respect to family clusters and hospitalized patient respectively. The most thorough description of the South Korean case is presented by Korea Centers for Disease Control and Prevention [5], while it was briefly mentioned by Chowell et al [3] and Cho and Chu [4].

Other than these descriptive studies, a small number of literature tried to assess the transmissibility of MERS-CoV in a more quantified fashion. Cachemez et al [10] estimated the incubation period and generation time from publicly available data and calculated the reproduction numbers both in animal-to-human and human-to-human transmission cases. Breban et al [11] compared the possibility of MERS-CoV being pandemic by comparing the basic reproduction number (Appendix) with that of SARS. Using MERS-CoV outbreak data, Chowell et al [12] delved further and calculated two reproduction numbers based on different epidemiological scenarios: one is when all reported zoonotic cases are severe and the other is not. Chowell et al [3] took a different approach that compared the reproduction numbers in SARS and MERS-CoV in large hospital clusters.

Since South Korea is where the largest number of cases was reported outside the Middle East, we need to pay more attention to the South Korean case. While a few researches have dealt with the South Korean case, as briefly mentioned above, research gaps still exist that need to be filled. First of all, whether some demographic characteristics, such as age or sex, and locations have influence on the possibility of being infected needs to be explored. Also,

the transmissibility needs to be investigated with more detail. As done in some literature, transmissibility in hospitals and in general need to be calculated separately and it needs to be taken into consideration whether the transmissibility might change in time. Here, the SIR-type mathematical modeling is of great use, while there are very few in MERS-CoV studies. Its usefulness might be boosted if combined with real-world data, which will be done in the present study.

The purpose of this study is to uncover the characteristics of MERS-CoV transmission in South Korea in 2015. To this aim, a mathematical model will be built and analyzed. In particular, it will be observed whether there were any periods with different transmissibility and, if so, they will be estimated in general and hospital circumstances. Before this, some statistical analysis will be conducted in order to identify which group was more susceptible to MERS-CoV based on South Korean data.

2. Materials and methods

A mathematical model of MERS-CoV transmission in South Korea is suggested based on the model in Chowell et al [12]. It categorizes each individual into one of six epidemiological classes; susceptible (S), exposed (or high-risk latent) (E), symptomatic and infectious (I), infection but asymptomatic class (A), hospitalized (H), and recovery class (R). It is assumed that only infectious and hospitalized individuals can infect others and asymptomatic individuals cannot. In Chowell et al [12], the actual data of the zoonotic case were gathered so they were able to take secondary cases as well as index cases into account. By contrast, there was no zoonotic transmission except the primary case in South Korea, thus we do not consider the zoonotic case of MERS-CoV model in the present study. The model takes the following form:

$$\frac{dS}{dt} = -S\frac{\beta(I + lH)}{N}$$

$$\frac{dE}{dt} = S\frac{\beta(I + lH)}{N} - \kappa E$$

$$\frac{dI}{dt} = \kappa\rho E - (\gamma_a + \gamma_I)I$$

$$\frac{dA}{dt} = \kappa(1 - \rho)E \qquad (1)$$

$$\frac{dH}{dt} = \gamma_a I - \gamma_r H$$

$$\frac{dR}{dt} = \gamma_I I + \gamma_r H$$

where β is the human-to-human transmission rate per unit time (day) and l quantifies the relative transmissibility of hospitalized patients; κ is the rate at which