Journal of Applied Analysis and Computation
Volume 12, Number 4, August 2022, 1532–1543
Website:http://www.jaac-online.com
DOI:10.11948/20210326

THE DYNAMIC EFFECTS OF DIFFERENT QUARANTINE MEASURES ON THE SPREAD OF COVID-19*

Chuanqing Xu[1], Zonghao Zhang[1], Xiaotong Huang[1], Jing'an Cui[1,†] and Xiaoying Han[1]

Abstract COVID-19 is pandemic worldwide, and different countries have adopted different measures to stop the spread of the epidemic. In order to study the impact of quarantining close contacts on the spread of coronavirus disease 2019 (COVID-19), based on data published by Beijing Municipal Health Commission, World Health Organization (WHO) and Korea Central Disaster Control Headquarters (KCDC), SEIR dynamic models of virus transmission in Beijing and South Korea were set up respectively; the Genetic algorithm was used to fit the important parameters such as transmission rate, recovery rate and quarantine rate; calculated the control reproduction number; we discuss the impact of quarantining close contacts on daily new cases in South Korea, the daily new cases decrease after a week, and drop to 16.93 after 30 days. When close contacts were quarantined, the maximum value of daily new cases $I_{max} = 57.4$ obtained by simulation is only 13% of the actual maximum value actual $I_{max} = 441$; the influences of different quarantine rates and the number of the susceptible on the number of daily new cases are also discussed, the quarantine of close contacts has significant effect on reducing the number of daily new cases compared with less stringent control measures. Vigorous control measures reduce the number of daily new cases to single digits in just 17 days in Beijing, effectively curbing the transmission of COVID-19. It has vital significance for the prevention and control of the epidemic in other countries and regions.

Keywords COVID-19, close contacts, SEIR model, reproduction number.

MSC(2010) 34A34, 92B05.

1. Introduction

On December 31, 2019, the Chinese government alerted the World Health Organization (WHO) to an outbreak of pneumonia of unknown cause in Wuhan, Hubei Province, China. On 21 January 2020, WHO raised the possibility of sustained human-to-human transmission. 2019-nCoV was the temporary name for the virus announced by WHO at the beginning of the outbreak, and WHO now

†The corresponding author. Email: cuijingan@bucea.edu.cn (J. Cui)
[1]School of Science, Beijing University of Civil Engineering and Architecture, Beijing 102699, China
*The authors were supported by NSFC (11871093), Postgraduate Teaching Research and Quality Improvement Project(J2021010) and BUCEA Post Graduate Innovation Project(2021098, 2021099).

named it COVID-19 or SARS-CoV-2 [6]. Coronaviruses are enveloped, single-stranded, positive-sense RNA viruses [5]. The coronavirus was first discovered in 1965, and there are three types of coronaviruses that have been discovered so far, SARS, MERS and Ebola. There have been some large-scale outbreaks in recent decades [12]. In 2003, “SARS” broke out in Mainland China [8], in 2012, ”Middle East Respiratory Syndrome” broke out in Saudi Arabia [14] and in 2015 in South Korea [15], in 2014 Ebola virus broke out in Africa.

Most coronaviruses originate from wild animals. COVID-19 virus is a new virus that spreads from person to person, and its animal origin has not been confirmed. People can get infected through contact with infectious people, and the virus is spread from person to person in droplets emitted from the nose or mouth when a person coughs, sneezes or talks [16]. A joint mission report from China and the World Health Organization says, the symptoms of COVID-19 are nonspecific, ranging from asymptomatic to severe pneumonia and death. Typical symptoms and signs include fever, dry cough, fatigue, expectoration, shortness of breath, sore throat, headache, myalgia or joint pain, chills, nausea or vomiting, nasal congestion, diarrhea, hemoptysis and conjunctival congestion. Patients usually develop mild respiratory symptoms and fever on average 5-6 days after infection, with an average incubation period of 5-6 days and a range of 1-14 days.

With the rapid spread of COVID-19 around the world, the epidemic has become the biggest challenge affecting countries around the world. Different countries have adopted different prevention and control strategies. China has taken more stringent prevention and control measures and has achieved remarkable results. Data from the Beijing Municipal Health Commission [2] showed that on June 11, 2020, an epidemic occurred in Beijing, where there were no new confirmed cases in the past two months. In just 17 days, Beijing’s strict prevention and control measures have reduced the number of new cases per day to single digits, and contained the epidemic; The data from the Korea Central Disaster Control Headquarters (KCDC) [9] shows that since the first case was reported on 24 January 2020, the number of daily new confirmed COVID-19 cases in South Korea also dropped to single digits on 28 April, but subsequently the data of confirmed cases fluctuated greatly.

On August 7, 2020, the daily new cases of new coronary pneumonia in South Korea have maintained double digits for many consecutive days as shown in Figure 1. We want to use mathematical modeling to assess the impact of measures to isolate close contacts on the spread of the epidemic.

Mathematical models can provide possible analysis results for the study of infectious diseases, and provide possible control strategies, and evaluate the effectiveness of these strategies. Try to use simplified mathematical models to describe the dynamic complexity of infectious diseases, so as to obtain some insight on the spreading of diseases and to test control strategies [1]. Since the outbreak of COVID-19, there have been many results based on actual data and the dynamics of the virus transmission mechanism. Lin et al. [10] proposed a conceptual model of covid-19 that considered individual behavioral responses and government actions based on the Wuhan epidemic, estimated the impact of individual responses and government actions on the Wuhan epidemic, and gave the case report ratio. Based on individual epidemiology and intervention measures, Tang [12] and other researchers designed a deterministic compartmental model, and concluded that the basic reproduction number of the new crown epidemic may be as high as 6.47 (95% CI 5.71-7.23). And through the sensitivity analysis, the intervention measures can effectively re-

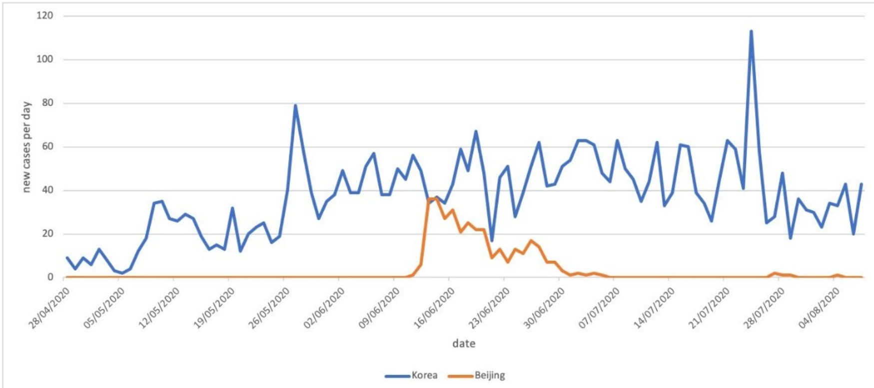

Figure 1. Curve of daily new confirmed COVID-19 cases in Beijing and Korea.

duce the risk of controlling the number of reproduction and the spread of the virus. Neil M Ferguson [7] and his colleges present the results of epidemiological modelling which has informed policymaking in the UK and other countries and they got that the effectiveness of any one intervention in isolation is likely to be limited, requiring multiple interventions to be combined to have a substantial impact on. Wang et al. [17] used the improved SEIR model of infectious disease dynamics to correct the basic reproduction number of COVID-19 and predicted the development trend of the epidemic situation in Hubei Province, China and South Korea. Tang and Xiao [13] established a COVID-19 dynamic model including China's national defense control strategy, calculated the basic regeneration number and effective regeneration number, and assessed the development trend of the epidemic and the final size of infection.

In this study, according to the data released by the Beijing Municipal Health Commission, and the South Korean Central Epidemic Prevention Countermeasures Headquarters we build a compartmental SEIR dynamic model based on the epidemic data and the transmission mechanism of the virus to explore the impact of quarantining close contacts on the spread of COVID-19.

2. Methods

2.1. Data

The COVID-19 data we used comes from the World Health Organization [16], Beijing Municipal Health Commission [2] and Korea Central Disaster Control Headquarters (KCDC) [9], including the daily number of newly confirmed cases, cumulative number of confirmed cases, daily number of new deaths, cumulative number of deaths, and cumulative number of cured cases in Beijing and South Korea from April 28 to September 15, 2020.

2.2. The Model

Based on the epidemiology of COVID-19 and the prevention and control measures taken by the government, we established the SEIR model. We divided the populations as susceptible (S), exposed (E), infectious (I) and recovered (R) compartments. China has adopted strict prevention and control measures, namely, quarantining close contacts of confirmed cases. Therefore, further divide the population who have close contacts with the cases as quarantined susceptible (S_q) and isolated exposed (E_q) compartments. Assuming that the close contacts with the q ratio are quarantined. The quarantined individuals will be moved to the compartment E_q if they are effectively infected, or they will be moved to the compartment S_q. And the other proportion, $(1-q)$ of individuals exposed to the virus who are missed from the contact tracing once effectively infected will move to the compartment E or stay in the compartment S. β is the probability of susceptible individuals infected by infectious people; σ is the conversion rate from the exposed to the infected compartment; λ is the conversion rate from the quarantined susceptible to the susceptible compartment; γ_I is the removal rate from the infectious to the recovered compartment; δ_I is the conversion rate from the infectious compartment to hospital; δ_q is the conversion rate from the isolated exposed compartment to hospital; γ_H is the removal rate from hospital to the recovered compartment; α is the disease-induced death rate. Diagram of the model is shown in Figure 2.

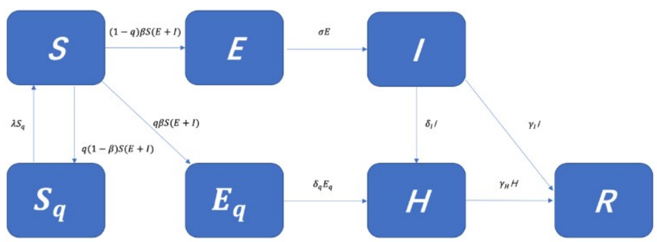

Figure 2. Diagram of the model adopted in this study for simulating the COVID-19 in Beijing. Interventions including intensive contact tracing followed by quarantine and isolation are indicated.

The transmission dynamics are governed by the following system of equations:

$$\begin{cases} \dfrac{dS}{dt} = -(\beta + q(1-\beta))S(E+I) + \lambda S_q, \\ \dfrac{dE}{dt} = (1-q)\beta S(E+I) - \sigma E, \\ \dfrac{dI}{dt} = \sigma E - (\delta_I + \gamma_I)I, \\ \dfrac{dS_q}{dt} = q(1-\beta)S(E+I) - \lambda S_q, \\ \dfrac{dE_q}{dt} = q\beta S(E+I) - \delta_q E_q, \\ \dfrac{dH}{dt} = \delta_q E_q + \delta_I I - (\gamma_H + \alpha)H, \\ \dfrac{dR}{dt} = \gamma_I I + \gamma_H H. \end{cases} \tag{2.1}$$

South Korea has adopted a more relaxed epidemic prevention and control strategy to isolate the infected. The large gathering of church members has led to the spread of the COVID-19 epidemic in South Korea in the domestic community, and it has become more difficult to trace and quarantine close contacts [11].

We established the SEIR model according to actual condition. We stratified the populations as susceptible (S), exposed (E), infectious (I), hospital (H) and recovered (R) compartments. Here β is the probability of susceptible individuals infected by contact with the source of infection; σ is the conversion rate from the exposed to the infected compartment; γ_I is the removal rate from the infectious to the recovered compartment; δ_I is the conversion rate from the infectious compartment to hospital; γ_H is the removal rate from hospital to the recovered compartment; α is the disease-induced death rate. Diagram of the model is shown in Figure 3.

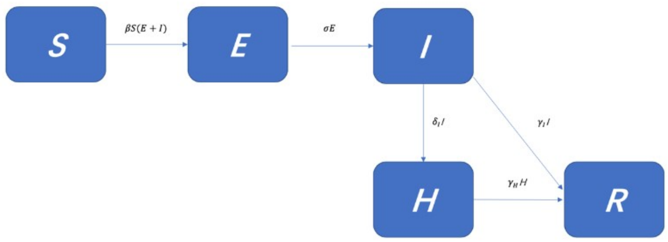

Figure 3. Diagram of the model adopted in this study for simulating the COVID-19 infection in south Korea. The tracking and quarantine of close contacts are not considered.

The transmission dynamics are governed by the following system of equations:

$$\begin{cases} \dfrac{dS}{dt} = -\beta S(E+I), \\ \dfrac{dE}{dt} = \beta S(E+I) - \sigma E, \\ \dfrac{dI}{dt} = \sigma E - (\delta_I + \gamma_I)I, \\ \dfrac{dH}{dt} = \delta_I I - (\gamma_H + \alpha)H, \\ \dfrac{dR}{dt} = \gamma_I I + \gamma_H H. \end{cases} \tag{2.2}$$

According to model (2.1), we used the next generation matrix to derive a formula for the control reproduction number when control measures are in force in Beijing, as follows: $R_{c1} = ((1-q)\beta/\sigma + (1-q)\beta/(\delta_I + \gamma_I))S_{(0)}$, Where $S_{(0)}$ represents the initial value of the susceptible, here it is the value of the total population of Beijing $S_{(0)} = 40176000$; similarly, we derive the control reproduction number when control measures are in force in south Korea, as follows: $R_{c2} = (\beta/\sigma + \beta/(\delta_I + \gamma_I))S_{(0)}$, Where $S_{(0)}$ represents the initial value of the susceptible, here it is the value of the total population of Seoul $S_{(0)} = 10040000$.

Interpretation of the biological significance of the control reproduction number:

The control reproduction number is the basic reproduction number under the control measures, which can represent the number of individuals infected by a patient into the susceptible population during the average infectious period of the disease. In model (2.1),$R_{c1} = ((1-q)\beta/\sigma + (1-q)\beta/(\delta_I + \gamma_I))S_{(0)}$, One of the patients has $(1-q)\beta(\delta_I + \gamma_I)S_{(0)}$ contact with the susceptible, the average duration is $1/(\sigma(\delta_I + \gamma_I))$; in model (2.2), $R_{c2} = (\beta/\sigma + \beta/(\delta_I + \gamma_I))S_{(0)}$. One of the patients has $\beta(\delta_I+\gamma_I+\sigma)S_{(0)}$ contact with the susceptible, the average duration is $1/(\sigma(\delta_I+\gamma_I))$.

2.3. Model analysis

Model (2.1) can be transformed into a system of equations:

$$\begin{cases} -(\beta+q(1-\beta))S(E+I)+\lambda S_q=0, \\ (1-q)\beta S(E+I)-\sigma E=0, \\ \sigma E-(\delta_I+\gamma_I)I=0, \\ q(1-\beta)S(E+I)-\lambda S_q=0, \\ q\beta S(E+I)-\delta_q E_q=0, \\ \delta_q E_q+\delta_I I-(\gamma_H+\alpha)H=0, \\ \gamma_I I+\gamma_H H=0. \end{cases} \tag{2.3}$$

When $I=0$, calculated that $H=0, E=0, R=0, E_q=0, S_q=0, S=N$. We can obtained that the disease-free equilibrium of the model (2.1) is $(N,0,0,0,0,0,0)$, where N is the total number of people; similarly, we can obtained that the disease-free equilibrium of the model (2.2) is $(N,0,0,0,0)$, where N is the total number of people. For model (2.1),$I\neq 0$, the endemic equilibrium of model (2.1) has one endemic equilibrium$(S^*,E^*,I^*,S_q^*,E_q^*)$ and satisfies the following conditions: $S^*=S_{(0)}/R_{c1}, E^*=((\delta_I+\gamma_I)/\sigma)I^*, S_q^*=((q(1-\beta)(\delta_I+\gamma_I))/\lambda\beta(1-q))I^*, E_q^*=(q(\delta_I+\gamma_I)/\delta_q(1-q))I^*$, here $S_{(0)}$ is the value of the total population of Beijing $S_{(0)}=40176000$. Similarly, when $I\neq 0$, the model (2.2) has one endemic equilibrium and satisfies the following conditions $S^*=S_{(0)}/R_{c2}, E^*=((\delta_I+\gamma_I)/\sigma)I^*, H^*=(\delta_I/(\gamma_H+\alpha))I^*$, I^* is the number of infected people in a day.

3. Model simulation

3.1. Determine the parameters in the model

In this study, the COVID-19 data comes from the WHO [16], Beijing Municipal Health Commission [2] and KCDC [9]. According to official data, the permanent population of Beijing in 2018 was 21.542 million, of which the urban population was 18.634 million; the permanent population of Seoul in 2018 was 10.04 million. Taking into account the travel restrictions during the epidemic control period in China and the fact that most cases in South Korea are concentrated in the capital area, namely near Seoul, the initial value of the susceptible in Beijing and South Korea is selected as 15 million in the simulation.

In order to control the epidemic, Beijing has implemented strict tracking and quarantine measures, and close contacts of the cases will be quarantined and observed for 14 days ($\lambda=1/14$). According to official data, the initial value is selected as $[15000000, 290, 2, 1940, 46, 1]$. The genetic algorithm is used to fit the actual case data and the model, the fitted image is shown in Figure 4, and the fitted parameter values and the specific values of the parameters in model (2.1) are given: $\beta=6.3210^{-8}[fit]; \sigma=0.1429$ [3]; $\delta_I=0.8[fit]; \delta_q=0.01[fit]; \gamma_I=0.09[fit]; \gamma_H=0.12[fit]; \alpha=0.00027$ [3]; $q=0.01[fit]; \lambda=1/14$ [3].

Taking into account practical factors such as close contacts not cooperating with tracking and quarantine, it is assumed that South Korea's epidemic prevention policy only isolates infected people for treatment. According to official data, the initial value is selected as $[15000000, 720, 28, 28]$, the genetic algorithm is also used to fit the actual case data and the model, the fitted image is shown in Figure 5, and the fitted parameter values and the specific values of the parameters in model (2.2) are: $\beta = 2.3210^{-8}[fit]; \sigma = 0.19[fit]; \alpha = 0.0039$ [17]; $\delta_I = 0.1648$ [4]; $\gamma_I = 0.125$ [4]; $\gamma_H = 0.18[fit]$.

The Genetic algorithm was used to fit the important parameters and the fitting effect is fine.

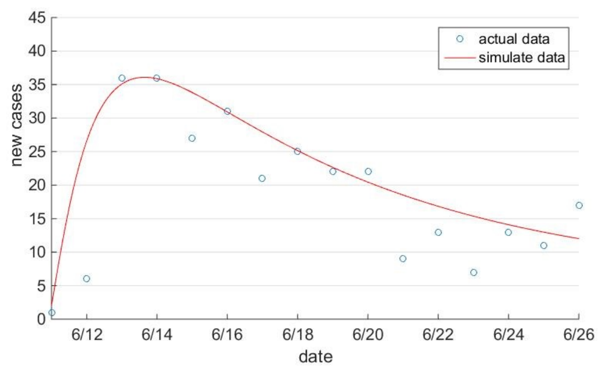

Figure 4. Actual data and fitting images (Beijing).

Figure 5. Actual date and fitting images (Korea).

3.2. The impact of the tracking and quarantine measures

On June 11, 2020, in Beijing, where there were no new local COVID-19 cases after more than two months, a new local confirmed case appeared. As of July 5, a total of 335 confirmed cases have been reported in Beijing. Strict control measures of the government have reduced the number of new cases per day to single digits in about two weeks. Beijing's successful experience in epidemic control gives a good example.

On August 9, 2020, the COVID-19 epidemic in South Korea continued to spread, and the number of daily new cases continued to increase from 28 to 246 on August 17, and it maintained a triple-digit growth for five days. As of 0:00 on August 18, South Korea has a total of 15,761 confirmed cases, including 306 deaths. For the severe epidemic in South Korea, it is necessary to consider implementing more stringent control measures. Therefore, in the simulation of the model (2.2), the same control measures as Beijing have been added, namely the tracking and quarantine of close contacts of confirmed cases.

According to official data, the initial value is selected as [15000000,720,28,8000, 2000,28], other parameters remain the same as before. Simulate the daily new cases after adding the tracking and quarantine measures of close contacts to Model (2.2), as shown in Figure 6.

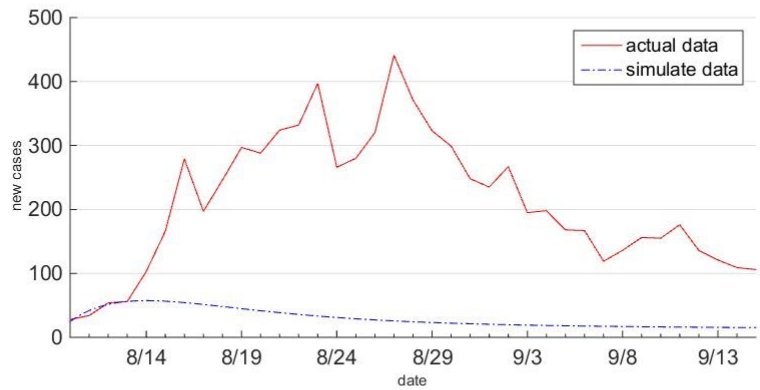

Figure 6. Tracking and quarantine measures are added to Model (2.2).

From the figure 6, it can be observed that the actual number of daily new cases in South Korea remains high under the current control measures. In the simulation, according to the prevention and control intensity of Beijing, close contacts are strictly tracked and quarantined in South Korea. On the one hand, the number of daily new cases showed a downward trend within a week, and it could drop to 16.93 after 30 days. On the other hand, the maximum number of daily new cases is much lower than the actual maximum number of daily new cases. The simulation shows that the maximum number of daily new cases is $I_{max} = 57.40$. In fact, the actual value of South Korea reached 441 cases, which was 7.70 times the maximum value obtained by simulation.

3.3. The impact of the quarantine ratio q

At the same time, considering the impact of the quarantine ratio q on the daily new cases in South Korea. We simulated the situation of daily new cases when the isolation ratio q was 0.01, 0.001, and 0.0001. It can be seen from the Figure 7 that the higher the quarantine ratio, the lower the number of newly confirmed cases; when the quarantine ratio is from 0.0001 to 0.01, the control effect is significant: at this time, the maximum number of daily new cases in South Korea obtained by simulation is 181.31, 72.52 and 57.40 respectively, while the actual maximum is 2.43 times, 6.08 times and 7.70 times respectively.

We also discussed the impact of the quarantine ratio q on the control reproduction number. As shown in Figure 8, the relationship between the quarantine ratio q of close contacts in South Korea and the control reproduction number is simulated. When the quarantine ratio q is greater than 0.65, the control reproduction number can be reduced to less than 1.

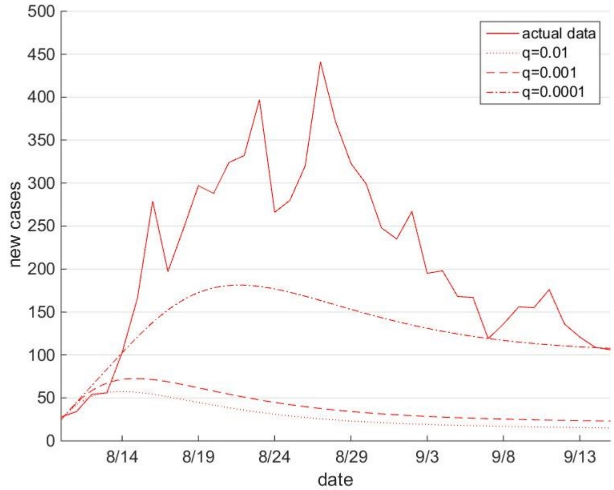

Figure 7. Simulate the impact of different quarantine ratios on new daily cases.

Table 1. Maximum number of daily new cases under different quarantine ratios.

q	0.001	0.01	0.1
I_{max}	181.31	72.52	57.40
$(Actual - I_{max})/I_{max}$	2.43	6.08	7.70

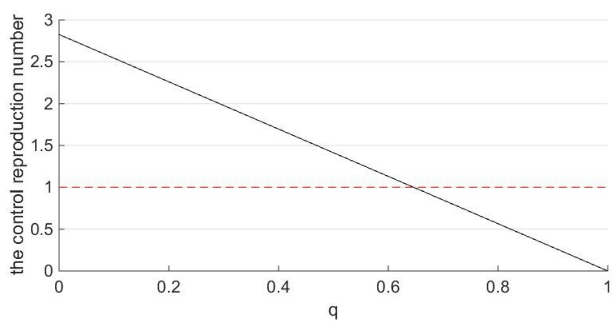

Figure 8. The impact of the quarantine ratio q on the control reproduction number.

The number of the susceptible also has impacts on the control reproduction number. In order to control the epidemic, China has implemented measures of "lockdown" and "travel restrictions " to reduce the number of the susceptible, which has a very obvious effect. Therefore, we have considered taking further control measures for the susceptible in South Korea. For example, travel restrictions can effectively reduce the number of the susceptible. As shown in Figure 9, we have simulated the influence of the number of the susceptible on the control reproduction

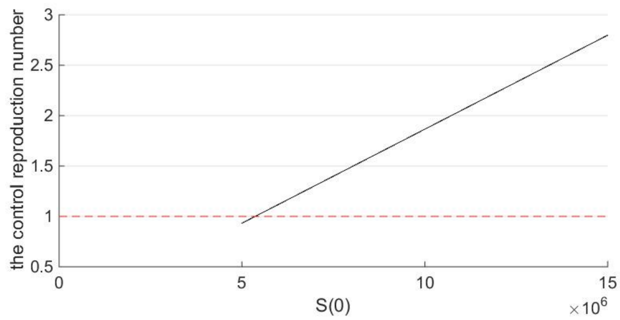

Figure 9. The impact of the susceptible on the control reproduction number.

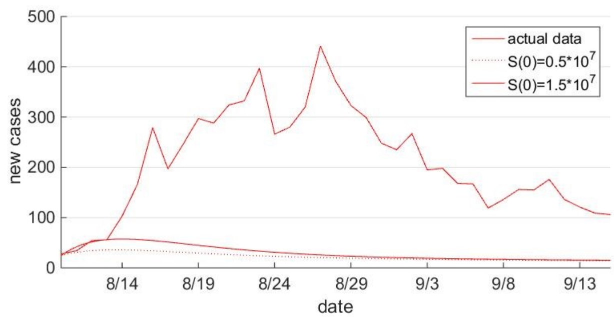

Figure 10. The impact of the number of the susceptible on the number of daily new cases.

number. When the number of the susceptible is less than 5.37 million, the control reproduction number can be reduced to less than 1. And controlling the number of the susceptible can effectively reduce the maximum number of daily new cases. When the number of the susceptible is 5 million, the simulation shows that the maximum number of daily new cases is only 62.47% of the maximum number of daily new cases when the number of the susceptible is 15 million, as shown in Figure 10.

4. Conclusion

According to data from the World Health Organization, it took less than 6 months for the COVID-19 to erupt from the initial outbreak in Wuhan to the worldwide outbreak. There are many reasons for this. On the one hand, the virus is cunning. It has a long incubation period, there are asymptomatic infections, and asymptomatic infections are contagious, and the characteristics of the virus itself are extremely difficult to prevent and control. Countries all over the world are working hard, and vaccines have been available since December 8, 2020. However, it cannot stop the spread of the COVID-19. Especially the sudden appearance of the mutant virus and the failure of immunity will cause the epidemic to worsen and break out again. According to data released by the World Health Organization, As of July 6, 2021, the global cumulative number of confirmed cases of new crown has reached 172,630,637, and the cumulative number of deaths is 3,718,683. The number of newly confirmed cases on that day is 386,217, and the number of deaths is 9,272. The COVID-19 epidemic has become a major public health challenge that all countries in the world need to face. Numerical simulations of the disease model suggest that it is urgent for us to implement strict and effective prevention and control measures. Many countries still adopt measures only for confirmed cases. The isolation and treatment measures for cases failed to prevent the spread of potentially infected persons among close contacts, which is one of the reasons why the epidemic has persisted. China's strict medical tracking and isolation measures for confirmed cases and their close contacts have successfully contained the epidemic. This has a non-ignorable reference value for the formulation of prevention and control policies in other countries and regions in the world.

Acknowledgements

This study was funded by Natural Science Foundation of China (No. 11871093), Postgraduate Teaching Research and Quality Improvement Project of BUCEA (No. J2021010), BUCEA Post Graduate Innovation Project (Nos. 2021098, 2021099).We thank all the individuals who generously shared their time and materials for this study.

References

[1] F. Brauer and C. C. Chavez, *Mathematical Models in Population Biology and Epidemiology*, Springer, New York, 2012.

[2] Beijing Municipal Health Commission, News center [EB/OL], 2020, http://wjw.beijing.gov.cn/xwzx_20031/wnxw/.

[3] S. Cao, P. Peng and P. Shi, *Study on the epidemic development of COVID-19 in Hubei province by a modified SEIR model*, Journal of Zhejiang University (Medical Sciences), 2020, 49(02), 178–184.

[4] J. Cui, J. Lv, S. Guo and T. Chen. *Dynamical Model of Emerging Infectious Diseases applied to COVID-19 Transmission*, Acta Mathematicae Applicatae Sinica, 2020, 43(02), 147–155.

[5] Y. Chen, Q. Liu and D. Guo, *Emerging coronaviruses: Genome structure, replication, and pathogenesis*, Journal of Medical Virology, 2020, 92(10), 2249–2249.

[6] China-World Health Organization Joint Investigation Team for COVID-19, *Report*, China Social Security, 2020(04), 11.

[7] N. M. Ferguson, D. Laydon and et al, *Impact of non-pharmaceutical interventions (NPIs) to reduce COVID-19 mortality and healthcare demand*, Imperial College COVID-19 Response Team, 2020. DOI: 10.25561/77482.

[8] D. S. C. Hui and A. Zumla, *Severe Acute Respiratory Syndrome: Historical, Epidemiologic, and Clinical Features*, Infectious disease clinics of North America, 2019, 33(4), 869–889.

[9] Korea Central Disaster Control Headquarters, COVID-19 [EB/OL], 2020, http://ncov.mohw.go.kr/cn/.

[10] Q. Lin, S. Zhao and et al, *A conceptual model for the coronavirus disease 2019 (COVID-19) outbreak in Wuhan, China with individual reaction and governmental action*, International Journal of Infectious Diseases, 2020, 93, 211–216.

[11] E. Shim, A. Tariq, W. Choi, Y. Lee and G. Chowell, *Transmission potential and severity of COVID-19 in South Korea*, Int. J. Infect. Dis., 2020, Apr, 93, 339–344.

[12] B. Tang, X. Wang, Q. Li, N. L. Bragazzi, S. Tang, Y. Xiao and J. Wu, *Estimation of the Transmission Risk of the 2019-nCoV and Its Implication for Public Health Interventions*, Journal of Clinical Medicine, 2020, 9(2), 462.

[13] S. Tang, Y. Xiao, Z. Peng and H. Shen, *Prediction modeling with data fusion and prevention strategy analysis for the COVID-19 outbreak*, Chinese Journal of Epidemiology, 2020, 41(04), 480–484.

[14] E. Wit, N. Doremalen, D. Falzarano and V. J. Munster, *SARS and MERS: recent insights into emerging coronaviruses*, Nature Reviews Microbiology, 2016, 14(Suppl. 1), 523–534.

[15] M. Willman, D. Kobasa and J. Kindrachuk. *A Comparative Analysis of Factors Influencing Two Outbreaks of Middle Eastern Respiratory Syndrome (MERS) in Saudi Arabia and South Korea*, Viruses, 2019, 11(12), 1119.

[16] World Health Organization, Health Topics [EB/OL], 2020, https://covid19.who.int.

[17] S. Wang, H. Tan and D. Li, *Coronavirus disease 2019 epidemic trend prediction based on improved infectious disease dynamics susceptible-exposed-infected-recovered (SEIR) model*, Academic Journal of Second Military Medical University, 2020, 41(06), 637–641.