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Contents lists available at ScienceDirect

Travel Medicine and Infectious Disease

journal homepage: www.elsevier.com/locate/tmaid

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Changed transmission epidemiology of COVID-19 at early stage: A nationwide population-based piecewise mathematical modelling study

Dear Editor,

COVID-19 has widely transmitted both nationwide and internationally since its outbreak which was firstly reported in December 2019 in Wuhan city, China. As of July 2, 2020, about 85,263 confirmed cases have been reported in China, of which 68,135 cases are from Hubei province [1]. The past six months have witnessed a considerable number of studies regarding the transmission dynamics of COVID-19 in China and in other countries as well. In the first quarter of 2020, most of the studies endeavored to establish compartmental or/and statistical models, compute the basic reproduction number (R_0), and predict the future epidemic of COVID-19 [2,3], while only a few studies focused on the early stage of the epidemic dynamics in Hubei province. The accumulated evidences in the past several months definitely showed a strong heterogeneity of the epidemics among different regions and at different stages, indicating that the transmission dynamics of COVID-19 were coined by exceptionally spatiotemporal characteristics [4]. However, the specific mechanism of transmission and disease control remains largely unclear.

Here, we introduce a model, which actually was established in early February, describing spatiotemporal transmission dynamics of COVID-19 at the early stage in China. Within the model, we divided the transmission dynamics into three epidemic substages defined by population movement during Lunar New Year, implementation of control measures and locations. The continuous-time but piecewise model was based on the Susceptible-Exposed-Infectious-Removed (SEIR) meta-population model with three substages [5]. Substage 1 commenced on December 1, 2019 when the first COVID-19 case was detected, and ended on January 9, 2020, prior to the mass Lunar New Year population movement. Substage 2 of the epidemic from January 10 to 22, 2020 covered the period of mass migration of people returning to their hometown for the Lunar New Year. Finally, substage 3 commenced from January 23, 2020 when a lockdown was in effect in Wuhan. During substages 1 and 2, we focused on the epidemic dynamics in Wuhan while in substage 3 the transmission process was investigated nationwide. In substage 3, considering that the tightened control policies reduced the contact frequencies of residents within each province, an attenuation effect was added to the infection risk from exposed individuals in their incubation period and an enhancement term was added to the case recovery rate

due to the fact that the medical resources in Wuhan were exhausted first but improved later on with aid from other regions of the country. To further describe the infectivity of COVID-19, we applied the controlled reproduction number (R_c) instead of R_0 in substage 3. This multi-stage SEIR model was sketchily illustrated in Fig. 1(a) and the details of the model were provided in Ref. 5.

The key parameters of the established SEIR model was estimated using the epidemiological data collected from the National, Hubei Provincial and Wuhan Municipal Health and Family Planning Commissions and the population movement data estimated by Baidu Huiyan (<http://huiyan.baidu.com>), an APP based on big-data technology which covers more than 1.1 billion mobile devices and more than 150 million points of information (POIs). For Wuhan, the estimated R_0 's for substages 1 and 2 and R_c for substage 3 were 4.90, 3.00, and 4.75, respectively. The estimated R_c 's for the other cities in Hubei province except Wuhan was 2.07. The key parameters for the other regions in mainland China were estimated in Ref. [5] and depicted in Fig. 1(b).

To address the concern of under-reported cases at the early stage of the epidemic, we designed a source tracing strategy implemented through transportation in substage 2. In the source tracing algorithm, we considered a simplified SE model to describe the transmission during the population flow via public transportations. Here, we used parameters estimated in substage 2 for Wuhan and the numbers of exposed individuals in the other provinces at the beginning of substage 3 to infer the number of exposed individuals on January 10 in Wuhan, i.e., retrospective-estimation in time. Considering the compact space in the vehicles, a correction factor, k , was introduced to describe the infectivity when the contacts were much closer in the vehicles than in the general society. With the estimated parameters, the estimated number of exposed individuals on January 10, 2020 in Wuhan was regarded as a function of k and I_0 , the number of infected individuals on January 10, 2020. As is shown in Fig. 1(c), the number of initial exposed individuals decreases significantly as k increases, and decreases in a linear mode as I_0 increases. Additionally, the estimated number of exposed individuals was much greater than the number of the reported infectious individuals on January 17, 2020 (7 days or an incubation period after January 10, 2020) in Wuhan.

Our numerical results implied that, at the early stage of the outbreak, a number of under-reported individuals were likely to be existent in an

<https://doi.org/10.1016/j.tmaid.2020.101918>

Received 24 April 2020; Received in revised form 5 July 2020; Accepted 9 November 2020

Available online 13 November 2020

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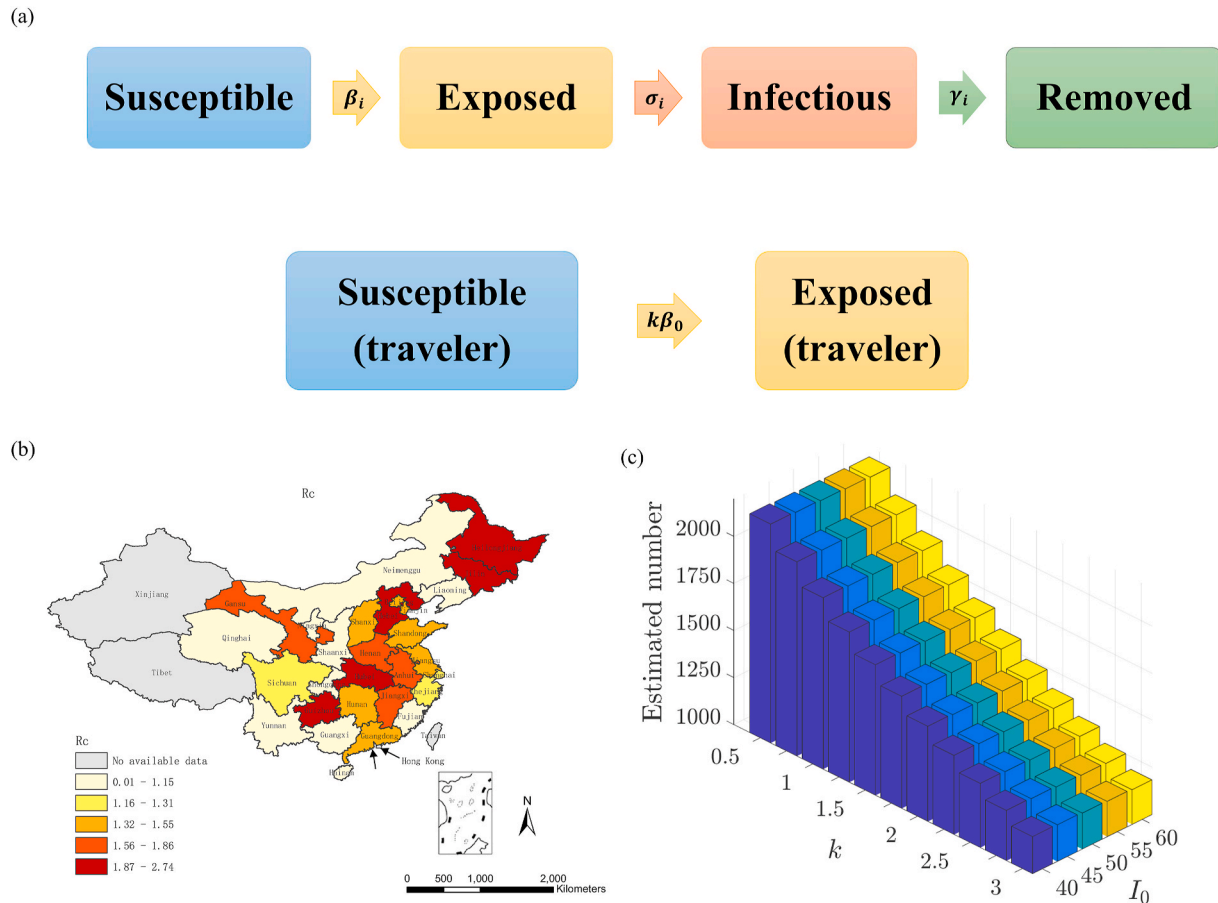


Fig. 1. A sketch for the computational model and its simulation results. (a) A schematic description of the transmission processes with normal social contact (upper panel) and via public transportations (lower panel). (b) Estimated controlled reproduction numbers (R_c) in different regions of mainland China. Here, the cities of Tibet and Xinjiang are excluded due to a lack of available data. (c) Estimated exposed numbers in Wuhan on January 10, 2020 change with different pairs of values for variables k and I_0 .

out-of-hospital manner, which was somewhat in agreement with the results in Ref. [6]. These hardly-undetected, exposed individuals probably became a major source of intra- or/and inter-provincial infection. Under-reporting these exposed individuals naturally resulted in an underestimation of infectious individuals in substages 1 and 2, and also led to the abnormally rapid increase of the infectious number in substage 3 in Wuhan. Finally, it is concluded that of practical significance is using piecewise models for retrospective estimations, accurate predictions, precise evaluations of this COVID-19 pandemic and its control measures.

Funding

This work was supported by the National Natural Science Foundation of China from ZJZ (81673239, 81973102), WL (11925103 & 61773125), the National Major Infectious Disease Project of the Ministry of Science and Technology of China (2017ZX10305501002), the National Key R&D Program of China (Grant no. 2018YFC0116600), and the STCSM (Grant no. 18DZ1201000).

Disclaimer

The funder of the study had no role in study design, data collection, data interpretation, or writing of the report. The corresponding authors had final responsibility for the decision to submit for publication.

Declaration of competing interest

The authors declare no conflict of interest.

References

- [1] July 2: daily briefing on novel coronavirus cases in China. National Health Commission of the People's Republic of China. http://en.nhc.gov.cn/2020-07/02/c_80968.htm.
- [2] Ai L. Modelling the epidemic trend of the 2019-nCoV outbreak in Hubei Province, China. medRxiv 2020;2020. 01.30.20019828.
- [3] Li Q, et al. Early transmission dynamics in wuhan, China, of novel coronavirus-infected pneumonia. N Engl J Med 2020;382:1199–207. <https://doi.org/10.1056/NEJMoa2001316>.
- [4] Zheng RZ, Xu Y, Wang WQ, Ning G, Bi YF. Spatial transmission of COVID-19 via public and private transportation in China. Trav Med Infect Dis 2020;34:101626. <https://doi.org/10.1016/j.tmaid.2020.101626>.
- [5] Hou JW, et al. Changing transmission dynamics of COVID-19 in China: a nationwide population-based piecewise mathematical modelling study. medRxiv 2020:2020.03.27.20045757.
- [6] Read JM, Bridgen JR, Cummings DA, Ho A, Jewell CP. Novel coronavirus 2019-nCoV: early estimation of epidemiological parameters and epidemic predictions. medRxiv 2020:2020. 01.23.20018549.

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