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Original Article

Effect of evacuation of Japanese residents from Wuhan, China, on preventing transmission of novel coronavirus infection: A modelling study

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ABSTRACT

Introduction: In late January 2020, the Japanese government carried out three evacuations by aircraft from Wuhan, China, to avoid further cases of coronavirus disease 2019 (COVID-19) among Wuhan’s Japanese residents. Evacuation by aircraft may be an effective countermeasure against outbreaks of infectious diseases, but evidence of its effect is scarce. This study estimated how many COVID-19 cases were prevented among the Japanese residents of Wuhan by the evacuation countermeasure.

Methods: We constructed a SETAIR (susceptible-exposed-transitional-asymptomatic-infectious-recovered) model to capture the epidemic growth of COVID-19 cases in Wuhan to estimate the predicted number of COVID-19 cases among Wuhan’s Japanese residents if evacuation had not occurred at the end of January. We used data on the number of COVID-19 cases confirmed in Hubei Province for the period Jan 20-Feb 16, 2020, and on the number of cases of Japanese residents who were evacuated by aircraft on Jan 29, 30, and 31.

Results: Eleven imported COVID-19 cases were reported on Feb 1 from among the total 566 evacuees who returned to Japan. In the case of no evacuations being made, the cumulative number of COVID-19 cases among Wuhan’s Japanese residents if evacuation had not occurred at the end of January was estimated to reach 25 (95% CI [20; 29]) on Feb 8 and 34 (95% CI [28; 40]) on Feb 15. A 1-week delay in the evacuation might be led to 14 additional cases and a 2-week delay to 23 additional cases.

Conclusions: Evacuation by aircraft can contribute substantially to reducing the number of infected cases in the initial stage of the outbreak.

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1. Introduction

Starting at the end of December 2019, Wuhan city in China reported an increasing number of cases of coronavirus disease 2019 (COVID-19) [1,2]. The outbreak appears to have started with zoonotic transmission at a wet market selling game meat in the city [3].

In light of this situation, Japan’s Ministry of Health, Labour and Welfare (MHLW) decided to deploy charter flights to evacuate Japanese residents of Wuhan over 3 consecutive days, on Jan 29, 30, and 31 [4]. Evacuation by aircraft may be an effective countermeasure to reduce the number of infected cases among the Japanese residents during an outbreak, but there is little quantitative evidence of its effect. Thus, the main objective of this study was to elucidate the effect of such intervention quantitatively.

2. Materials and methods

2.1. Data sources

For this modelling study, we used data on the number of COVID-19 cases confirmed in Hubei Province for the period Jan 10–19,
2020 from a report by Wu and colleagues [5] and for the period Jan 20–Feb 16, 2020 from WHO situation reports [1]. The World Health Organization (WHO) situation reports stated the cumulative number of cases in China and its regions from Jan 21, but some data were missing because the reports were not issued daily and did not routinely include regional counts. Therefore, data missing for the daily incidence in Hubei Province for Jan 16–19 [5] and Jan 22–31 [1] were imputed by smoothing with the spline function. We excluded data after Feb 17 due to a change in case definition.

We collected pharyngeal swab specimens to determine the number of COVID-19 cases among the Japanese evacuees who returned on the chartered flights. All 556 evacuees initially went to a quarantine station, and from there 28 with suspected COVID-19 were transported directly to a hospital in Tokyo and all others were excluded data after Feb 17 due to a change in case definition.

We applied the following susceptible-exposed-transitional-asymptomatic-infectious-recovered (SETAIR) model to simulate the dynamics of the target disease under some specified conditions. We simulated the model to the empirical data, we can simulate the dynamics of the target disease under some specified conditions.

2.2. Model structure

Traditionally, dynamics of infectious disease epidemiology has been described by a system of four differential equations (susceptible-exposed-infectious-recovered, SEIR) model [7].

\[
\frac{dS}{dt} = -\beta S(t) I(t),
\]

\[
\frac{dE}{dt} = \beta S(t) I(t) - \sigma E(t),
\]

\[
\frac{dI}{dt} = \sigma E(t) - \gamma I(t),
\]

\[
\frac{dR}{dt} = \gamma I(t).
\]

Here, the compartment S means the number of people who are "susceptible" to the disease. The compartment E (exposed) means the number of people who are already infected but have not presented symptoms and infectiousness. The compartment I means the number of infected people who can transmit the disease to "susceptible" population, and the compartment R means the number of people who have already recovered from the disease and never move to other compartments. In the equations above, \( \beta \) is the rate at which "susceptible" individuals are infected by contacting "infectious" individuals, (also known as the 'force of infection'), \( \sigma \) is the rate at which pre-infectious individuals become infectious, and \( \gamma \) is the rate at which infectious individuals become immune. By fitting the model to the empirical data, we can simulate the dynamics of the target disease under some specific conditions.

We applied the following susceptible-exposed-transitional-asymptomatic-infectious-recovered (SETAIR) model to simulate the epidemic in Hubei Province, by modifying SEIR model:

\[
\frac{dS}{dt} = -p \beta_0 S(t) (T(t) + A(t)) - \beta_0 S(t) I(t),
\]

\[
\frac{dE}{dt} = p \beta_0 S(t) (T(t) + A(t)) + \beta_0 S(t) I(t) - \sigma E(t),
\]

\[
\frac{dT}{dt} = \sigma E(t) - \epsilon T(t),
\]

\[
\frac{dA}{dt} = (1 - \delta) \epsilon T(t) - \gamma A(t),
\]

\[
\frac{dI}{dt} = \delta \epsilon T(t) - \gamma I(t),
\]

\[
\frac{dR}{dt} = \gamma A(t) + \gamma I(t).
\]

We created the model based on the assumptions that a substantial proportion of patients are asymptomatic or pauci-symptomatic (as suggested by the clinical characteristics of COVID-19) [8–10] and that transmission may be possible in mild cases (which include asymptomatic and pauci-symptomatic ones) as well as moderate cases [8,11,12], but only some cases become critically ill. Hence we additionally introduced "transitional" compartment T and "asymptomatic" compartment A into the standard SEIR model [7,13] to create the abovementioned SETAIR structure. In our model, total duration of infectious period is assumed to be the sum of \( \sigma \), \( \epsilon \), and \( \gamma \), where \( \sigma \) is the duration of the "exposed" phase (E), \( \epsilon \) is the duration of "transitional" phase (T), and \( \gamma \) is the duration of the "asymptomatic" phase (A) and "infectious" phase (I) (we assume that A and I have similar durations and largely overlap). Furthermore, we assume that only a fraction of individuals (\( \delta \)) move from T to I and that the remaining fraction of individuals (1 - \( \delta \)) move to A before moving to R. Assuming that infectiousness is the same for "transitional" and "asymptomatic" but less than that of "infectious", we introduce a coefficient \( p \) to describe the infectiousness of "transitional" and "asymptomatic" as \( p \beta_0 \). The model structure is shown in Fig. 1.

In the early phase of an outbreak when it is not yet recognised as such, the diagnosis rate is considered to be small and not all cases are detectable [5,14–16]. The diagnosis rate will increase over the course of a pandemic, so we introduce time-dependent function \( a(t) \) to represent each day's ascertainment rate, which reflects people's awareness of COVID-19. Here we assume that \( a(t) \) is a logarithmic growth curve and that the number of reported cases \( C(t) \) is given by

\[
C(t) = a(t) \times \text{number of cases in China and its regions from Jan 21, but some data were missing because the reports were not issued daily and did not routinely include regional counts. Therefore, data missing for the daily incidence in Hubei Province for Jan 16–19 [5] and Jan 22–31 [1] were imputed by smoothing with the spline function. We excluded data after Feb 17 due to a change in case definition. We collected pharyngeal swab specimens to determine the number of COVID-19 cases among the Japanese evacuees who returned on the chartered flights. All 556 evacuees initially went to a quarantine station, and from there 28 with suspected COVID-19 were transported directly to a hospital in Tokyo and all others were excluded data after Feb 17 due to a change in case definition. We applied the following susceptible-exposed-transitional-asymptomatic-infectious-recovered (SETAIR) model to simulate the dynamics of the target disease under some specified conditions. We simulated the model to the empirical data, we can simulate the dynamics of the target disease under some specific conditions. We applied the following susceptible-exposed-transitional-asymptomatic-infectious-recovered (SETAIR) model to simulate the epidemic in Hubei Province, by modifying SEIR model:

\[
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\]

\[
\frac{dE}{dt} = p \beta_0 S(t) (T(t) + A(t)) + \beta_0 S(t) I(t) - \sigma E(t),
\]

\[
\frac{dT}{dt} = \sigma E(t) - \epsilon T(t),
\]

\[
\frac{dA}{dt} = (1 - \delta) \epsilon T(t) - \gamma A(t),
\]

\[
\frac{dI}{dt} = \delta \epsilon T(t) - \gamma I(t),
\]

\[
\frac{dR}{dt} = \gamma A(t) + \gamma I(t).
\]

We created the model based on the assumptions that a substantial proportion of patients are asymptomatic or pauci-symptomatic (as suggested by the clinical characteristics of COVID-19) [8–10] and that transmission may be possible in mild cases (which include asymptomatic and pauci-symptomatic ones) as well as moderate cases [8,11,12], but only some cases become critically ill. Hence we additionally introduced "transitional" compartment T and "asymptomatic" compartment A into the standard SEIR model [7,13] to create the abovementioned SETAIR structure. In our model, total duration of infectious period is assumed to be the sum of \( \sigma \), \( \epsilon \), and \( \gamma \), where \( \sigma \) is the duration of the "exposed" phase (E), \( \epsilon \) is the duration of "transitional" phase (T), and \( \gamma \) is the duration of the "asymptomatic" phase (A) and "infectious" phase (I) (we assume that A and I have similar durations and largely overlap). Furthermore, we assume that only a fraction of individuals (\( \delta \)) move from T to I and that the remaining fraction of individuals (1 - \( \delta \)) move to A before moving to R. Assuming that infectiousness is the same for "transitional" and "asymptomatic" but less than that of "infectious", we introduce a coefficient \( p \) to describe the infectiousness of "transitional" and "asymptomatic" as \( p \beta_0 \). The model structure is shown in Fig. 1.

In the early phase of an outbreak when it is not yet recognised as such, the diagnosis rate is considered to be small and not all cases are detectable [5,14–16]. The diagnosis rate will increase over the course of a pandemic, so we introduce time-dependent function \( a(t) \) to represent each day's ascertainment rate, which reflects people's awareness of COVID-19. Here we assume that \( a(t) \) is a logarithmic growth curve and that the number of reported cases \( C(t) \) is given by.
The left panel shows the actual number of reported cases (grey bars) and the estimated number of reported cases by the spline method (purple dots) and the SETAIR model (blue triangles) in Hubei Province. The right panel shows the number of patients estimated by the SETAIR model as transitional cases (green dots), asymptomatic cases (yellow dots), infectious cases (red dots), and the number of total cases, including unreported cases (brown dots).

Table 1
Values of the fixed parameters used in our SETAIR model.

| Parameter                        | Value  | Reference |
|----------------------------------|--------|-----------|
| Duration of incubation period \( r \) | 5.2 days | Li et al. |
| Duration of mild illness \( e \)   | 4.6 days | Li et al. |
| Total duration of illness \( e + \gamma \) | 9.1 days | Li et al. |

\[
C(t) = a(t) I(t) = \frac{1}{1 + \exp\left(-k(t - t_0 - D)\right)} I(t).
\]

In addition to the change in diagnosis rate over time, people pay more attention to prevention and start wearing masks and washing their hands more frequently as public awareness increases. It is reported that such behavioural changes lower transmission rate \( \beta_0 \) and this effect is captured by

\[
\beta(t) = \beta_0 r (1 - a(t)) = \beta^* (1 - a(t)),
\]

where \( r \) is a proportionality constant and \( \beta^* = \beta_0 r \).

Details of the fixed parameters used are shown in Table 1.

To compute the number of COVID-19 patients among the Japanese evacuees from Wuhan based on the estimated total number of COVID-19 cases in Hubei Province, we assume two scenarios with respect to the study population and then estimate parameter values. 1) Most of the patients reported in Hubei Province are residents of Wuhan, so the Wuhan population (\( \approx 1.1 \times 10^7 \)) is taken to be representative of the Wuhan population. 2) Patients occur across all of Hubei Province, so the Wuhan population is considered to be representative of the Hubei population (\( \approx 5.9 \times 10^7 \)). We calculate the incidence rates for the Wuhan and Hubei populations as the number of total estimated COVID-19 patients and apply these rates to the number of Japanese evacuees. The rate for Wuhan leads to overestimation because the city is more strongly affected and conversely the rate for Hubei leads to underestimation, so we also calculated the number of COVID-19 patients among Japanese evacuees based on the actual incidence rate determined in Japan on Feb 1 (11/564).

2.3. Sensitivity analysis

Parameter estimation was carried out under the assumptions that the parameters \( r, e \), and \( \gamma \) are known. However, because this assumption is not always true, we conducted sensitivity analyses for these fixed parameters to reflect uncertainty, and we compared the number of COVID-19 patients among the evacuees for each parameter pair.

Role of the funding source

No funder supported the present study.

3. Results

Before smoothing with the spline method, we obtained the data shown in Supplementary file. Based on the obtained data, we fitted the SETAIR model with the estimated parameter values. The estimated parameter values with 95% confidence intervals (CIs) based
The actual number of cases among Japanese evacuees as of Feb 1 were 31 and 46, respectively, and the estimated numbers of cases [95% CI] among Japanese evacuees was 0.25; 5.3: 4.6: 30, which lies between these estimates. The incidence rate to the Wuhan and Hubei population-based estimations, cumulative number of COVID-19 patients agreed well between them.

Incidence rates in the Wuhan and Hubei populations were estimated as 612.475/1.1 × 10³ and 590.873/5.9 × 10³, respectively, and the estimated numbers of cases [95% CI] among Japanese evacuees was 31/20.42 and 6/5.7, respectively, which give bounds for over- and underestimation of Japanese evacuee cases. The actual number of cases among Japanese evacuees was 11, which lies between these estimates. The incidence rate among Japanese evacuees was 0.0195 = 11/564. By applying this rate to the Wuhan and Hubei population-based estimations, cumulative numbers of COVID-19 cases among Wuhan’s Japanese residents of were estimated as 25/16.33 and 25/20.29 on Feb 8 and as 34/22.46 and 34/28.40 on Feb 15, respectively, if the evacuation had not been carried out. As of Feb 1, there were 11 diagnosed cases among the evacuees, so a 1-week delay in the evacuation is estimated to lead to 14 additional cases and a 2-week delay to 23 additional cases. The details of estimated number of cases among Wuhan’s Japanese residents are shown in Fig. 4.

3.1. Sensitivity analysis

The parameter values in the base-case scenario were fixed to \( \sigma = 1/5.2, \epsilon = 1/4.6, \) and \( \gamma = 1/(9.1 - 4.6) \) as listed in Table 1. To examine the reliability of our results, we performed sensitivity analyses employing different parameter sets with \( \sigma = 0.1, 0.2, 0.3, 0.4, \epsilon = 0.2, 0.25, 0.3, 0.35, \) and \( \gamma = 0.1, 0.2, 0.3, 0.4. \) Monte Carlo simulations were performed 10,000 times for each combination of parameter values and the number of cases among Wuhan’s Japanese residents on February 15 and the 95% CI were estimated. The results are shown in Fig. 5.

The 95% CIs became wider for several sets of parameter values, although the mean values always stayed within 30–40 cases. Even though the parameters \( \sigma, \epsilon, \) and \( \gamma \) were carefully chosen from previous studies, different values might be necessary for different...
populations or different phases of an outbreak. Overall, our result of 34 cases stays in the same range and we confirmed that the result is robust to a wide range of parameter values.

4. Discussion

To our knowledge, this is the first study to investigate the effect of evacuation by aircraft as a countermeasure against an emerging infectious disease outbreak. Our results showed that evacuation by aircraft can contribute substantially in the short term to reducing the total cumulative number of patients.

One of the strengths of this study is that we could also use all test results from the evacuees, including actual prevalence because we took pharyngeal swabs regardless of presence of symptoms upon their return. It is noteworthy that six of 11 PCR-positive cases were asymptomatic. Furthermore, most of these 11 cases had no obvious contact history with patients with COVID-19 or influenza-like illness. These characteristics are compatible with the long duration of comparatively mild illnesses and a large number of unreported cases [8,10,11,16–21]. Given this information, we modified the existing SEIR model to a SETAIR model in order to reflect the characteristics of COVID-19, and our sensitivity analyses also demonstrated that the results were comparatively robust to uncertainty of parameters. For example, infectiousness of COVID-19 varies by each case [22]. We took such heterogeneity into consideration by examining the simulation results with wide variety of infectiousness at population level.

In conclusion, evacuation by aircraft might be an effective countermeasure against an emerging infectious disease outbreak such as the current COVID-19 pandemic. Further investigation is needed to assess the impact of this countermeasure more precisely.

We recognise several limitations of our analysis. First, we assumed homogeneity between Wuhan’s Japanese and Chinese residents, but presumably the two populations have some differences in lifestyle and behaviour and if that is the case, frequency of effective contact would be different. A previous study showed that Japanese have more frequent social contact than people in European countries [23,24], but there is no evidence on social contact in China in the literature. Accordingly, both overestimation and underestimation should be considered when interpreting our results. Second, we fixed some of the parameters in accordance with a previous modelling study. Because these parameter values vary due to each model’s assumption, it is not clear whether fixed parameter

Fig. 5. Estimated cumulative number of Japanese cases in Wuhan and the 95% CI for each combination of parameter values. Red, blue, green, and black dots represent the mean numbers on Feb 15 under each combination of parameter values and bars indicate 95% CIs.
values appropriately reflect reality or not. Nevertheless, the results of the sensitivity analyses indicate the validity of our analyses. Third, it is difficult to assess true “effectiveness” of evacuation as a countermeasure against a COVID-19 outbreak. The Japanese government restricted the movement of evacuees after their check-up at NCGM, and this is thought to have prevented the spread of COVID-19 inside Japan. Restriction of movement is another effect of evacuation, but our estimation did not take it into consideration. This might be another topic appropriate for modelling studies in the future.

**Ethics approval and consent to participate**

This study was approved by the Ethics Committee of National Center for Global Health and Medicine, Tokyo, Japan (Approval Number NCGM-G-003475-00).

**Consent for publication**

Not applicable.

**Availability of data and materials**

The datasets used and/or analysed during the current study are available from the corresponding author on reasonable request.

**Funding**

No funder supported this study.

**Author contributions**

ST and YA conceived the study. YA, ST and CY collected a part of data used in this study. ST, YA and SK conceived the study. YA and ST constructed the model and performed simulations. SK, KH and ST critically reviewed the manuscript and all authors approved the final version of the manuscript.

**Declaration of competing interest**

We declare no competing interests.

**Acknowledgments**

Not applicable.

**Abbreviations**

COVID-19: coronavirus disease 2019
MHFW: Ministry of Health, Labour and Welfare Japan
WHO: World Health Organization
NCGM: National Center for Global Health and Medicine, Tokyo, Japan
SEIAR: susceptible-exposed-transitional-asymptomatic-infectious-recovered
SEIR: susceptible-exposed-infectious-recovered
CI: confidence interval

**Appendix A. Supplementary data**

Supplementary data to this article can be found online at https://doi.org/10.1016/j.jiac.2020.12.011.

**References**

[1] World Health Organization. Novel Coronavirus (2019-nCoV) situation reports. n.d. https://www.who.int/emergencies/diseases/novel-coronavirus-2019/situation-reports. [Accessed 4 February 2020].

[2] Zhu N, Zhang D, Wang W, Li X, Yang B, Song J, et al. A novel coronavirus from patients with pneumonia in China. 2019 N Engl J Med 2020. https://doi.org/10.1056/NEJMoa2001017. 0 null.

[3] Chan JF-W, Yuan S, Kok K-H, To KK-W, Chu H, Yang J, et al. A familial cluster of pneumonia associated with the 2019 novel coronavirus indicating person-to-person transmission: a study of a family cluster. Lancet 2020. https://doi.org/10.1016/S0140-6736(20)30154-9.

[4] Shimazu S. Nikkei business online (in Japanese). Returnee from Wuhan city by the chartered flights were “not isolated” n.d. https://business.nikkei.com/atl/genr/19000002/012801051/. [Accessed 4 February 2020].

[5] Wu P, Hao X, Lau EHY, Wong JY, Leung KSM, Wu JT, et al. Real-time tentative assessment of the epidemiological characteristics of novel coronavirus infections in Wuhan, China, as at 22 January 2020. Euro Surveill 2020:25. 2000044. https://doi.org/10.2807/1560-7917.ES.2020.25.3.2000044.

[6] Hayakawa K, Kutsuna S, Kawamata T, Suigki Y, Nonaka C, Tanaka K, et al. SARS-CoV-2 infection among returnees on charter flights to Japan from Hubei, China: a report from National Center for Global Health and Medicine. Glob. Health Med. 2020:2:107–11. https://doi.org/10.35772/ghm.2020.01036.

[7] Kermack WO, McKendrick AG. Contributions to the mathematical theory of epidemics I. Bull Math Biol 1991:53:33–55.

[8] Tian S, Hu N, Lou J, Chen K, Kang X, Xiang Z, et al. Characteristics of COVID-19 infection in Beijing. J Infect 2020. https://doi.org/10.1016/j.jinf.2020.02.018.

[9] Tong Z-D, Tang A, Li K-F, Li P, Wang H-L, Li J-P, et al. Potential presymptomatic transmission of SARS-CoV-2, Zhejiang Province, China, 2020. Emerg Infect Dis 2020:26. https://doi.org/10.3201/eid2605.200198.

[10] Bai Y, Yao L, Wei T, Tian F, Jin D-Y, Chen L, et al. Presumed asymptomatic carrier transmission of COVID-19. J Am Med Assoc 2020. https://doi.org/10.1001/jama.2020.2565.

[11] Guan W, Ni Z, Hu Y, Liang W, Ou C, He J, et al. Clinical characteristics of coronavirus disease 2019 in China. N Engl J Med 2020. https://doi.org/10.1056/NEJMoa2002032. 0 null.

[12] Kam K, Yung CF, Cui L, Lin Tzer Pin R, Mak TM, Maiwald M, et al. A well infant with coronavirus disease 2019 (COVID-19) with high viral load. Clin Infect Dis 2020. https://doi.org/10.1093/cid/czaa201.

[13] Hethcote HW. The mathematics of infectious diseases. SIAM Rev 2000;42: 599–653. https://doi.org/10.1137/S0036144400371907.

[14] Huang C, Wang Y, Li X, Ren L, Zhao J, Hu Y, et al. Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China. Lancet 2020. https://doi.org/10.1016/S0140-6736(20)30183-5. 0.

[15] Yu P, Zhu J, Zhang Z, Han Y. A familial cluster of infection associated with the 2019 novel coronavirus indicating possible person-to-person transmission during the incubation period. J Infect Dis 2020. https://doi.org/10.1093/infdis/jiaa077.

[16] Wang W, Tang J, Wei F. Updated understanding of the outbreak of 2019 novel coronavirus (2019-nCoV) in Wuhan, China. J Med Virol 2020:92:441–7. https://doi.org/10.1002/jmv.25689.

[17] Li Q, Guan X, Wu P, Wang X, Zhou L, Tong Y, et al. Early transmission dynamics in Wuhan, China, of novel coronavirus--infected pneumonia. N Engl J Med 2020. https://doi.org/10.1056/NEJMoa2001316. 0 null.

[18] Roux J, Althaus CL. Patterns of early human-to-human transmission of Wuhan 2019 novel coronavirus (2019-nCoV), December 2019 to January 2020. Euro Surveill 2020:25.2000058. https://doi.org/10.2807/1560-7917.ES.2020.25.4.2000058.

[19] Chen N, Zhou M, Dong X, Qu J, Gong F, Han Y, et al. Epidemiological and clinical characteristics of 99 cases of 2019 novel coronavirus pneumonia in Wuhan, China: a descriptive study. Lancet 2020. https://doi.org/10.1016/S0140-6736(20)30211-7. 0.

[20] He X, Lau EHY, Wu P, Deng X, Wang J, Hao X, et al. Temporal dynamics in viral shedding and transmissibility of COVID-19. Nat Med 2020:26:672–5. https://doi.org/10.1038/s41591-020-0865-9.

[21] Zheng H-Y, Jian S-W, Liu D-P, Ng T-C, Huang W-T, Lin H-H. Contact tracing assessment of COVID-19 transmission dynamics in Taiwan and risk at different exposure periods before and after symptom onset. JAMA Intern Med 2020. https://doi.org/10.1001/jamainternmed.2020.2570.

[22] Lewis NM, Chui VT, Ye D, Conners EE, Gharghure R, Laws RL, et al. Household transmission of SARS-CoV-2 in the United States. Clin Infect Dis 2020: ciaa1166. https://doi.org/10.1093/cid/ciaa1166.

[23] Mossong J, Hens N, Jit M, Beutels P, Auranen K, Mikolajczyk R, et al. Social contacts and mixing patterns relevant to the spread of infectious diseases. PLoS Med 2008:5:e74. https://doi.org/10.1371/journal.pmed.0050074.

[24] Ibuka Y, Ohkusa Y, Sugawara T, Chapman CB, Yamin D, Atkins KE, et al. Social contacts, vaccination decisions and influenza in Japan. J Epidemiol Community Health 2016;70:162–7. https://doi.org/10.1136/jech-2015-205777.