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Rapid transmission of coronavirus disease 2019 within a religious sect in South Korea: A mathematical modeling study

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ABSTRACT

Rapid transmission of coronavirus disease 2019 (COVID-19) was observed in the Shincheonji Church of Jesus, a religious sect in South Korea. The index case was confirmed on February 18, 2020 in Daegu City, and within two weeks, 3081 connected cases were identified. Doubling times during these initial stages (i.e., February 18 – March 2) of the outbreak were less than 2 days. A stochastic model fitted to the time series of confirmed cases suggests that the basic reproduction number (R_0) of COVID-19 was 8.5 [95% credible interval (CrI): 6.3, 10.9] among the church members, whereas ($R_0 = 1.9$ [95% CrI: 0.4, 4.4]) in the rest of the population of Daegu City. The model also suggests that there were already 4 [95% CrI: 2, 11] undetected cases of COVID-19 on February 7 when the index case reportedly presented symptoms. The Shincheonji Church cluster is likely to be emblematic of other outbreak-prone populations where R_0 of COVID-19 is higher. Understanding and subsequently limiting the risk of transmission in such high-risk places is key to effective control.

1. Introduction

Coronavirus disease 2019 (COVID-19) has become a global pandemic since it was first reported in Wuhan, China in December 2019 with the name of novel coronavirus disease (Li et al., 2020a). The causative agent, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), transmits mainly through human-to-human contact (Chan et al., 2020), which can happen even during the infector is asymptomatic (Rothe et al., 2020; Yu et al., 2020). Infection with the virus causes diseases with varying degree of symptoms including death (Fu et al., 2020; Guan et al., 2020). Infection mortality ratio is lowest among children aged between 5 and 9 years and increases loglinearly with age (O'Driscoll et al., 2021).

One key characteristic of COVID-19 pandemic is that transmission events in high-risk settings such as super-spreading events (SSEs) contribute to most transmissions (Adam et al., 2020; Lemieux et al., 2020). The risk of COVID-19 transmission is believed to high in places with high occupancy and poor ventilation (Jones et al., 2020). One extreme example is the outbreak in the Diamond Princess cruise ship, where 17% (619/3711) of the passengers were infected from January 25 to February 20, 2020 (Russell et al., 2020). Other examples include

transmission events in bars and wedding (Adam et al., 2020) in Hong Kong, nursing homes in U.S. (Chen et al., 2021), telemarketers working in group in closed places (Park et al., 2020) and fitness classes (Jang et al., 2020) in South Korea, and also religious gatherings, which we describe below.

Explosive spread of COVID-19 was observed in the Shincheonji Church of Jesus ("Shincheonji"), a religious sect in South Korea. The index case was confirmed on February 18, 2020 and within two weeks, 3081 connected cases were identified (Korea Disease Control and Prevention Agency, 2020a). A simple calculation reveals that the outbreak size doubled in less than every 2 days ($14/\log_2(3081) \approx 1.21$), which is smaller than doubling times reported in the early stages of the COVID-19 outbreak in China (2.5 and 3.1 days in Hubei Province and Hunan Province, respectively) (Muniz-Rodriguez et al., 2020), Spain (2.8 days) (Guirao, 2020), the US (2.7 days) (Lurie et al., 2020), and Korea (2.8 – 10.2 days) (Shim et al., 2020b). A total of 6684 confirmed cases were reported in Daegu City as of March 31, 2020 of which 4467 (66.8%) were Shincheonji members, representing close to half (47.9%, 4467/9334) of the city's total Shincheonji membership.

Previous studies highlighted that COVID-19 transmissions involve SSEs (Xu et al., 2020), which can play a key role in sustained community

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transmissions (Adam et al., 2020; Lemieux et al., 2020). However, there have been no attempts to model the dynamics of COVID-19 transmission within high-risk settings and their interaction with the general community. In this study, we modeled the outbreak in the Shincheonji community while accounting for its interaction with the rest of population. We used the stochastic model to account for the stochastic nature of the transmission events. We used the model to explore the differences in the basic reproduction number (R_0) between the high-risk setting and the general community, and quantify uncertainties related to the initial conditions and dynamics of transmission under the dynamic intervention programs.

2. Materials and methods

2.1. Background on the Shincheonji Church of Jesus

Shincheonji was founded by Man-hee Lee in 1984 and has approximately 245,000 members including 30,000 foreigners (Chung and Hill, 2020). At Shincheonji gatherings, worshipers used to sit close together on the floor and facial coverings, such as glasses and face masks, are forbidden. Members were expected to attend services despite illness (Choe, 2020). The index case of the Daegu City outbreak was identified as a Shincheonji member and some 1000 people were reported to have attended worship together (Yonhap, 2020). Further tracing of church members identified clustering in apartment complexes. Of 142 residents in a particular Daegu apartment block, 94 (66%) were Shincheonji members of whom 46 (38.9%) tested positive for the virus (Myung, 2020).

2.2. Data

Time series of patients confirmed with COVID-19 in Shincheonji community and the overall Daegu City over the period of 18 February – 31 March 2020 was compiled based on the daily reports from Korea

Disease Control and Prevention Agency (KDCA) (Korea Disease Control and Prevention Agency, 2020a) (Fig. 1). The reports provide the number of cases confirmed with SARS-CoV 2 based on reverse transcription polymerase chain reaction (RT-PCR) by category (Shincheonji or non-Shincheonji). We made some adjustments to the existing data before we fit the model. First, in the beginning of the outbreak, KDCA provided both daily and cumulative numbers of cases confirmed for SARS-CoV 2, which did not agree always. If there is a discrepancy between these numbers, we prioritized cumulative numbers as this figure was reported continuously throughout the outbreak. Second, data were missing for some days for the number cases for Shincheonji members. We imputed missing values using the cubic spline method (Fig. S1 in the Supplementary Material).

2.3. Doubling time

The epidemic doubling time (T_d) represents the duration in which the cumulative incidence doubles. Assuming exponential growth with a constant epidemic growth rate (r), the epidemic doubling time can be calculated by the following equation (Anderson et al., 2020; Lurie et al., 2020; Muniz-Rodriguez et al., 2020)

$$T_d = \frac{\ln(2)}{r} \quad (1)$$

Epidemic growth rate (r) may be estimated based on the data. For example, $r(t)$ can be estimated by the following equation:

$$r(t) = \frac{\ln(C(t)) - \ln(C(t - \Delta t))}{\Delta t}, \quad (2)$$

where $C(t)$ indicates the cumulative number of infected people at time t and Δt is the duration over which $r(t)$ is assumed to be constant. $r(t)$ can be calculated over the fixed time interval (e.g., 1 day or 1 week) (Ebell and Bagwell-Adams, 2020; Patel and Patel, 2020) or variable time intervals (e.g., days on which the number of cases doubles,

Fig. 1. The daily number of confirmed COVID-19 cases from Daegu City, South Korea between 18 February and 31 March 2020. White bars represent overall cases from Daegu City including Shincheonji (Total) and gray bars represent cases associated with Shincheonji. Key events during the outbreak are described in the boxes. *Data on Shincheonji-associated cases are missing.

quadruples, etc.) (Muniz-Rodriguez et al., 2020; Shim et al., 2020b). We calculated doubling based on prior 7 days or 1 day from 18 February to 5 March 2020, when the epidemic peaked and no further doubling of cumulative number of cases occurred onward.

The basic reproduction number (R_0) is defined as the average number of secondary cases caused by a single infected case in an entirely susceptible population and it provides sufficient information to produce doubling times in the beginning of an outbreak. However, estimating R_0 requires additional information such as generation time or developing a mechanistic model, and its estimates come with higher degree of uncertainty (Anderson et al., 2020). Calculating doubling times requires fewer assumptions and also allows us to compare our results with estimates from different settings where doubling times, but not reproduction numbers, are available.

2.4. Mechanistic model of COVID-19 transmission

We developed a stochastic model of COVID-19 transmission within the Shincheonji community and the overall population of Daegu City. The model includes six disease states: susceptible (S), exposed but not infectious (E), pre-symptomatic but infectious (P), symptomatic and infectious (I), asymptomatic but infectious (A), confirmed and isolated (C), and recovered (R). The model includes two patches to model Shincheonji and non-Shincheonji people, separately. Transmission rates may differ for each patch and person from one patch may infect people from the other patch. (Fig. 2).

This modeling framework of mixing between two distinct sub-populations has been adopted in previous works, ranging from sexually transmitted diseases (Koopman et al., 1988) to vector-borne diseases such as dengue (Lee and Castillo-Chavez, 2015), where formulations for mixing between patches vary. We adopted the formulation used in the work on modeling transmission of cholera between hotspot and non-hotspot areas (Azman and Lessler, 2015). Mixing between two sub-populations are defined by the 2×2 contact matrix,

$$C = \begin{pmatrix} c_{11} & c_{12} \\ c_{21} & c_{22} \end{pmatrix},$$

where c_{ij} indicates the fraction of time that individuals from patch i spends in patch j . Next, we impose two conditions on the matrix C :

- (i) Individuals must reside in either of the two patches, i.e., $c_{11} + c_{12} = 1$ for $i=1$ (Shincheonji) and 2 (non-Shincheonji).
- (ii) The population in each patch remains constant, i.e., $c_{12}N_1 = c_{21}N_2$, where N_1 and N_2 represent population size for patch 1 and 2, respectively.

The above conditions may transform the contact matrix C to the following form:

$$C = \begin{pmatrix} 1 - c_{12} & c_{12} \\ \frac{c_{12}N_1}{N_2} & 1 - \frac{c_{12}N_1}{N_2} \end{pmatrix}$$

Fig. 2. Schematic for the two-patch model. Circles with letters inside indicate compartments of mutually exclusive states; susceptible (S), exposed but not infectious (E), pre-symptomatic but infectious (P), symptomatic and infectious (I), asymptomatic but infectious (A), confirmed and isolated (C), and recovered (R).

containing only one unknown parameter c_{12} .

The force of infection for individuals from patch i at time t , $\lambda_i(t)$, is defined as follows:

$$\lambda_i(t) = \sum_j c_{ij} \beta_j \frac{\sum_k c_{kj} (P_k(t) + A_k(t) + I_k(t))}{\sum_k c_{kj} N_k(t)}, \quad (3)$$

where β_j indicates local transmission rate in patch j and $I_k(t)$ indicates number of infectious individuals from patch k .

The transitions between states are modeled using an explicit tau-leap algorithm (Gillespie, 2001) to account for stochasticity of the infection transmission process. The number of susceptible people in patch i at time $t + \Delta t$, $S_i(t + \Delta t)$, is written as follows:

$$S_i(t + \Delta t) = S_i(t) - Q_i^{SE}(t, t + \Delta t) \quad (4)$$

$Q_i^{SE}(t, t + \Delta t)$ represents the number of people who transit from state S to state E from t to $t + \Delta t$ in patch i and is a random variable with binomial distribution:

$$\text{Binom}(S_i(t), 1 - \exp[-\lambda_i(t)\Delta t]) \quad (5)$$

That is, it is represented as an integer varying between 0 and $S_i(t)$. For states from which more than one potential transition exist (e.g., P to either A or I), multinomial distributions were applied. For instance, the number of people who transit from P to either I or A are given as follows:

$$\text{Multinom}(P_i(t), \Pi), \quad (6)$$

where $\Pi = \{\pi_0, \pi_1, \pi_2\}$ represents a vector of probabilities for transitioning to P (i.e., remaining in the present state), A , and I , respectively.

$$\pi_0 = \exp\left[-\left(\frac{1}{1/\delta - 1/\epsilon}\right)\Delta t\right], \pi_1 = (1 - \pi_0)f, \pi_2 = (1 - \pi_0)(1 - f). \quad (7)$$

The number of people in other states (i.e., E, A, I, C, R) at time t can be described similarly. The model was implemented in a combination of R and C++ languages, in which the core transmission model part is expensive and was written in C++. All the computer codes that generate the results in this paper are available at the author's GitHub repository (Kim, 2021).

2.5. Modeling intervention program

To account for intensification of the intervention such as case isolation and contact tracing with subsequent testing during the outbreak, we assumed case isolation rate ($1 / \text{mean time between symptom onset and case isolation}$) and transmission rate of the infectious people per unit time change over time. Specifically, we assumed that the case isolation rate, $\alpha(t)$, starts increasing on February 20 from the initial value of α^{init} when 4474 out of 9334 Shincheonji members were identified and were asked to self-isolate. During model fitting, we let data suggest the duration of intervention, d in day, which is the time required for the case isolation rate to reach its maximum, $\alpha(t) = \alpha^{\text{final}}$ for $t > \text{February } 20 + d$. We assumed that the mean time between symptom onset and case isolation linearly decreases over the intervention period d . In other words, $\alpha(t)$ is formulated as follows:

$$\alpha(t) = \begin{cases} 0, & \text{if } t < \text{Feb } 17 \\ \alpha^{\text{init}}, & \text{if } \text{Feb } 17 \leq t < \text{Feb } 20 \\ \alpha^{\text{init}} + (t - \text{Feb } 20)(\alpha^{\text{final}} - \alpha^{\text{init}})/d, & \text{if } \text{Feb } 20 \leq t < \text{Feb } 20 + d \\ \alpha^{\text{final}}, & \text{if } \text{Feb } 20 + d \leq t \end{cases} \quad (8)$$

where α^{final} is assumed to be 1 day based on the experiences in Busan City in Korea and $\alpha(t)$ is assumed to be zero before February 17 when the index case was detected.

Similarly, transmission rate per unit time at time t , $\beta_i(t)$ for $i = 1$ (Shincheonji members), 2 (non-Shincheonji people in Daegu City), is

assumed to linearly decrease during the intervention period.

$$\beta_i(t) = \begin{cases} \beta_i^{\text{init}}, & \text{if } t < \text{Feb 20} \\ \beta_i^{\text{init}} + (t - \text{Feb 20})(\beta_i^{\text{final}} - \beta_i^{\text{init}})/d, & \text{if } \text{Feb 20} \leq t < \text{Feb 20} + d \\ \beta_i^{\text{final}}, & \text{if } \text{Feb 20} + d \leq t \end{cases} \quad (9)$$

Here, β_i^{init} and β_i^{final} indicate the transmission rate per unit time before the intervention and after the intervention measures fully take effect, respectively. They can be derived once $R_{0,i}$ and R^{final} are given as:

$$\beta_i^{\text{init}} = \frac{R_{0,i}}{\frac{1}{\delta} - \frac{1}{\epsilon} + \frac{f}{\gamma + \alpha\rho} + \frac{1-f}{\gamma + \alpha}} \quad (10)$$

and

$$\beta_i^{\text{final}} = \frac{R^{\text{final}}}{\frac{1}{\delta} - \frac{1}{\epsilon} + \frac{f}{\gamma + \alpha\rho} + \frac{1-f}{\gamma + \alpha}} \quad (11)$$

2.6. Parameter estimation

Our model of COVID-19 transmission requires 15 parameters (Table 1). We divided the model parameters into three classes depending on our belief on their relative certainty. The first class includes parameters related to the natural history of infection and population size and we deemed that available parameter estimates are reliable. For these parameters, we used their point estimates based on analyses of data on COVID-19 transmissions in Korea or China. For the second class, which includes parameters related to intervention programs, we used our best guesses based on supporting evidence but still acknowledged their uncertainty. Therefore, we analyzed the models under various assumptions on their values within some pre-specified ranges. Finally, we defined six parameters that are critical for characterizing dynamics of COVID-19 transmission in Shincheonji members and non-Shincheonji people. We estimated these parameters by fitting the model to daily confirmed COVID-19 cases of Shincheonji members and non-Shincheonji people.

Estimation of parameters $\theta = \{R_{0,1}, R_{0,2}, I_0, c_{12}, d, R^{\text{final}}\}$ was based on Approximate Bayesian Computation Sequential Monte Carlo (ABC-SMC) (Minter and Retkute, 2019). The ABC is a method for approximating posterior distributions given data D , $p(\theta|D)$, by accepting proposed parameter values when the difference between simulated data D^* and D , $d(D, D^*)$, is smaller than tolerance ϵ :

$$p(\theta|D) \approx p(\theta|d(D, D^*) \leq \epsilon)$$

For our model, $d(D, D^*)$ is defined as the sum of the squared differences in daily confirmed cases over the outbreak of duration T days, that is,

$$d(D, D^*) = \sum_{t=1}^T (D_t - D_t^*)^2.$$

Here, D_t and D_t^* represent observed daily confirmed cases and model predicted values at time t , respectively. We computed $d(D, D^*)$ separately for Shincheonji and non-Shincheonji cluster. ABC-SMC was designed to increase efficiency of the ABC method and ABC is applied in a sequential manner by constructing intermediate distributions, which converge to the posterior distribution. Tolerance ϵ is gradually decreased and each intermediate distribution is obtained as a sample that is drawn with weights from the previous distribution and then perturbed through a kernel $K(\theta|\theta^*)$. The kernel helps keep the algorithm from being stuck in local optimum while maintaining the efficiency of the ABC-SMC method. Minimally informative uniform distributions were used as prior distributions and estimation procedure was repeated for ten different random seeds. The resulting distribution was summarized as median, 50% credible intervals (CrI; interval be-

Table 1
Model parameters.

Symbol	Parameter definition	Value	Source
<i>Parameters fixed throughout the simulation</i>			
N_2	Population size of the Daegu city excluding Shincheonji members	~2.5 million	(Korean Statistical Information Service, 2019)
N_1	Population size of the Shincheonji members	9334	(Korea Disease Control and Prevention Agency, 2020a) (Li et al., 2020a)
$1/\delta$	Mean time between infection and onset of symptoms (i.e., mean incubation period)	5.2 days	
$1/\epsilon$	Mean time between infection and infectiousness (i.e., mean latent period)	3 days	(He et al., 2020)
$1/\gamma$	Mean time between symptom onset and recovery	14 days	Assumption
τ	Time when the intense intervention measures begin to be implemented	February 20	(Korea Disease Control and Prevention Agency, 2020a) (Ki, 2020)
$1/\alpha^{\text{init}}$	Mean time between symptom onset and isolation of a patient in the beginning of the outbreak (i.e., time $t < \tau$)	4.3 days	
<i>Parameters for which a range of values explored</i>			
ρ	Rate of isolation of asymptomatic cases relative to symptomatic cases ^a	0.5 [0.1–0.9]	Assumption
f	Proportion of asymptomatic infections	0.306 [0.1–0.7]	(Kim et al., 2021)
$1/\alpha^{\text{final}}$	Mean time between symptom onset and isolation of a patient when the effect of intervention measures is highest	1–3 days	Assumption ^b
<i>Estimated parameters</i>			
c_{12}	Proportion of time that individuals from Shincheonji (N_1) spend in non-Shincheonji (N_2) ^c		
I_0	Number of infectious people in Shincheonji on February 7		
$R_{0,1}$	Basic reproduction number in the patch representing the Shincheonji members		
$R_{0,2}$	Basic reproduction number in the patch representing the non-Shincheonji people in Daegu City		
d	Time it takes for the intervention measures to be fully implemented		
R^{final}	Reproduction number (Shincheonji members and non-Shincheonji population in Daegu City) after the intervention measures are implemented. This is used to reflect the reduced transmission rate through case isolation, quarantine, and social distancing		

^a It is ρ before interventions are implemented and increases linearly reaching the maximum value of 1 when the effect of intervention measures is highest.

^b The COVID-19 outbreak in Busan City, which occurred around the same time, indicate that delays from symptom onset to isolation were close to one day around the end of February when the outbreak started to flatten (Son et al., 2020) (see Table S1 in the Supplementary Material).

^c We assume $c_{12}N_1 = c_{21}N_2$ to keep the population size constant for each patch. See the Method section for details

tween 25% and 75% percentiles) and 95% CrI (interval between 2.5% and 97.5% percentiles). More details of the algorithm such as prior distribution for each parameter, the number of steps, the tolerance values for each step, perturbation kernel appear in the Supplementary material.

3. Results

3.1. Doubling time

Over the period of February 18 – March 5, during which doubling of confirmed cases occurred 12 times, doubling times were less than 1 day in the beginning and increased subsequently with daily doubling time presenting higher variability for both Shincheonji and non-Shincheonji

Table 2

Doubling time during the Shincheonji outbreak during February 18 - March 5. On March 5, in total 4443 cases (2897 cases from Shincheonji and 1546 cases from non-Shincheonji) were identified, which may indicate 12 times of doubling, and no subsequent doubling has happened.

Date	Cumulative incidence		Daily doubling time		Weekly rolling doubling time	
	Shincheonji	Non-Shincheonji	Shincheonji	Non-Shincheonji	Shincheonji	Non-Shincheonji
2020-02-18	1	0	–	–	–	–
2020-02-19	9	2	0.3	0.0	–	–
2020-02-20	26	8	0.7	0.5	–	–
2020-02-21	63	16	0.8	1.0	–	–
2020-02-22	129	20	1.0	3.1	–	–
2020-02-23	237	60	1.1	0.6	–	–
2020-02-24	376	66	1.5	7.3	–	–
2020-02-25	407	92	8.7	2.1	0.8	0.0
2020-02-26	501	176	3.3	1.1	1.2	1.1
2020-02-27	682 ^a	335	2.2	1.1	1.5	1.3
2020-02-28	962 ^a	352	2.0	14.9	1.8	1.6
2020-02-29	1356	699	2.0	1.0	2.1	1.4
2020-03-01	1870	706	2.2	69.6	2.3	2.0
2020-03-02	2152 ^a	936	4.9	2.5	2.8	1.8
2020-03-03	2339 ^a	1269	8.3	2.3	2.8	1.8
2020-03-04	2576	1437	7.2	5.6	3.0	2.3
2020-03-05	2897	1546	5.9	9.5	3.4	3.2

^a Imputed numbers using Kalman smoothing method (see Methods and [Supplementary Material](#))

values ([Table 2](#)). Doubling times calculated over sliding one-week intervals remained shorter than 3 days for the most part for both Shincheonji and non-Shincheonji population.

3.2. Comparison between observations and the mechanistic model

Our fitted model projects the trajectory of number of daily and cumulative confirmed cases in Shincheonji and in the rest of the population of Daegu City ([Fig. 3\(a\)-\(d\)](#)). The model correctly projects the decreasing trends in both patches after reaching the peak on around March 3, 2020. However, for the non-Shincheonji, daily new cases are underestimated toward the end of the outbreak. R_0 were estimated to be quite different across two patches ([Fig. 3\(e\)](#)). The local reproduction number in the patch representing Shincheonji members, $R_{0,1}$, was estimated to be 8.54 [95% credible interval (CrI): 6.30, 10.95] whereas the local reproduction number in the patch representing non-Shincheonji members, $R_{0,2}$, was estimated to be 1.87 [95% CrI: 0.38, 4.40]. The time taken for the intervention program to have exerted highest effect, d , is around 9.02 days [95% CrI: 7.85, 10.45], which leads to both reduced transmission rate per unit time and reproduction numbers ($R^{\text{final}} = 0.34$ [95% CrI: 0.18, 0.53]). The model also suggests that there were infectious people already when the first cases was symptomatic on February 7 ($I_0 = 4$ [95% CrI: 2, 11]). The proportion of time that a person from Shincheonji members spends mixing with non-Shincheonji people, c_{12} , was estimate be around 0.14 [95% CrI: 0.05, 0.22]. Posterior distribution of parameters based on 2000 samples obtained from 10 different random seeds and two-way correlations appear in [Supplementary Material](#) ([Fig. S2](#)).

4. Discussion

Rapid transmission of COVID-19 within the Shincheonji community is likely to have been facilitated by high intensity contact between individuals gathering during services and in residential areas. Our mathematical modeling analyses quantify the rapid spread of COVID-19 in Daegu City driven by a community of Shincheonji members. The median R_0 among Shincheonji members ($R_{0,1}$) was 8.5, which is over 4-fold higher than what was estimated for the rest of the population in Daegu City ($R_{0,2}=1.9$). While the R_0 in the Shincheonji community is higher than estimates from most transmission hotspots (e.g., in China ([Alimohamadi et al., 2020](#); [Imai et al., 2020](#); [Riou and Althaus, 2020](#); [Wu et al., 2020](#); [Zhao et al., 2020b](#)) and Korea ([Bae et al., 2020](#); [Choi and Ki, 2020](#); [Ki, 2020](#); [Shim et al., 2020a](#))), such high R_0 is not unusual in

particular considering that R_0 can be different depending on the local settings with varying contact rates ([Temime et al., 2020](#)). Studies do report that R_0 estimates of COVID-19 that are comparable or even higher than our estimates for the Shincheonji community. During periods of intensive social contacts near the Chinese New Year in China, R_0 was estimated to be 6 ([Sanche et al., 2020](#); [Tang et al., 2020](#)). Also, R_0 estimates were around 5 among those traveled from Wuhan and were subsequently confirmed in other countries ([Zhao et al., 2020a](#)), and around 7 during the initial growth phase in the UK ([Dropkin, 2020](#)). In an extreme setting such as the Diamond Princess ship, much higher estimates ($R_0 = 14.8$) were reported ([Rocklöv et al., 2020](#)). Although the previous studies that included data on the outbreak in Shincheonji community report smaller R_0 estimates ([Choi and Ki, 2020](#); [Shim et al., 2020a](#)) than our estimates, the difference might stem from that prior studies did not model the Shincheonji community separately from the rest of the population and therefore measured the R_0 averaged across sub-population that are highly heterogeneous.

Although estimated daily doubling times show some variability (e.g., 14 days on February 28 and 69.6 days on March 1 for the non-Shincheonji population), they are short overall, which indicates rapid growth of the outbreak, and are compatible with estimates from other settings. Daily doubling times were lower than one day in the beginning of the outbreak and this is similar to the estimates from several regions in China ([Muniz-Rodriguez et al., 2020](#)). The study by [Shim et al. \(2020b\)](#) used the dataset from Daegu City, Korea including Shincheonji population produced the doubling time of 2.8 days [95% CI: 2.5, 4.0]. Our daily doubling time estimates averaged over the period of February 18 – March 5 is 2.9 days and is consistent with the study. The period from February 18 to March 5 is likely to have been used in the study by [Shim et al.](#) because the authors calculated the doubling times on the days when the reported cases doubled and during the period of February 18 – March 5 the number of cases doubled 12 times and no further doubling occurred since then. The study by [Lee et al. \(2020\)](#) used similar data, but reported seemingly inconsistent findings, doubling time of 2.9 days for the first week and 3.4 over the period around February 18 – March 4 considering that our estimate averaged over the first week is 0.9 day. One likely reason for this difference is that [Lee et al.](#) calculated the doubling time using the cumulative incidence estimated from a logistic model that used the initial value (i.e., number of infected people on February 18) as a free parameter. [Fig. 2\(D\)](#) from their study indicates that the number of infected people on 18 February is much larger than 1 and this might have led to the higher doubling time than our estimates. This may also explain why [Lee et al.](#) estimates for a similar period (i.e.,

Fig. 3. Parameter estimates and comparison between model outputs and data. Model outputs are based on 2000 simulation runs and presented with median (lines) with 50% (dark shading) and 95% (light shading) percentiles. (a) and (b) represent daily number of confirmed COVID-19 cases from the model and observations for Shincheonji and non-Shincheonji, respectively. (c) and (d) represent cumulative confirmed cases from model outputs and data for Shincheonji and non-Shincheonji, respectively. (e) shows posterior parameter estimates. Red dots represent the median, and thick and thin bars represent 50% and 95% CrI of the posterior distribution for each parameter. Median for c_{12} is 0.14 with its 50% CrI and 95% CrI being (0.11, 0.18) and (0.05, 0.22), respectively. Median for R^{final} is 0.34 with its 50% CrI and 95% CrI being (0.28, 0.40) and (0.18, 0.53), respectively.

February 18 – March 5) is higher than our estimates and those by Shim et al. (2020b).

The relationship between the doubling time and the R_0 provides two insights on our inferences on R_0 . For an SEIR model, there exists an algebraic formula that describes the inverse relationship between initial epidemic growth rate and R_0 (Ma, 2020; Ma et al., 2014). This inverse relationship suggests that short doubling times during the early phase of the epidemic we calculated using the growth rates are consistent with high R_0 for Shincheonji we estimated using the stochastic dynamic transmission model (Table S2 in the Supplementary Material). On the other hand, while doubling times may be reduced and imply high R_0 for non-Shincheonji people as well, such short doubling times can arise through mixing (i.e., positive c_{12}) with Shincheonji of high R_0 even if the R_0 for the non-Shincheonji people are not as high.

Parameters around asymptomatic infections of COVID-19 are largely unknown (Fox et al., 2020) and we tested the sensitivity of our inferences to our assumptions on two parameters related to asymptomatic infection, namely the proportion of asymptomatic infection, f , and relative rate of isolation of asymptomatic people, ρ (Fig. S3 in Supplementary Material). R_0 for Shincheonji people, $R_{0,1}$, and the final reproduction number, R^{final} , showed a slight increase with increasing f or decreasing ρ while other parameter estimates remain relatively constant. We also tested the sensitivity of our parameter estimates to α^{final} , maximum rate of isolation near the end of the outbreak. α^{final} showed an inverse relationship with other intervention-related parameters such as duration of intervention d , and reproduction number at the end of the outbreak, R^{final} . Overall, while there are some quantitative differences in our parameter estimates in response to the change in our assumptions on fixed parameters, $R_{0,1}$ was always over 4-fold higher than $R_{0,2}$.

While the first case was confirmed on February 18 for the Shincheonji outbreak, it was later revealed that the first case had symptoms on February 7 and even earlier transmission events were also suspected (Korea Disease Control and Prevention Agency, 2020b). This finding is consistent with our model analyses, which suggest there were 4 [95% CrI: 2, 11] infectious people on February 7. These undetected cases are likely to have contributed to the explosive outbreak in the Shincheonji community. Studies suggest that a substantial fraction of all SARS-CoV-2 infections were undetected. For Korea, it was suggested that the number of undetected cases may be larger than the number of detected cases (Lee et al., 2021). A study suggests that more than 80% of all infections were undocumented during the initial spread in China (Li et al., 2020b). In France, over the period of 7 weeks since 28 June 2020 after the first lockdown, it was estimated that around 93% of all symptomatic cases were undetected initially and later around 69% of symptomatic cases were undetected by the time when case ascertainment improved (Pullano et al., 2021).

We have shown that SARS-CoV 2 has disproportionately affected a religious community generating a large cluster of linked cases in Korea. Similar large clusters of cases in high-risk settings have been observed in Korea and elsewhere. In Korea, many similar outbreaks in high-risk settings have been reported in the news including the outbreak in a dance class (Jang et al., 2020) and a call center (Park et al., 2020). In Singapore, a total of 247 cases were confirmed as of March 17, 2020 and six clusters including the spread in a hotel and in a church accounted for 45.3% of the total cases (Tariq et al., 2020). In Hong Kong, 1038 cases were confirmed from January 23 to April 28, 2020 and among them, 51.3% of cases were associated with large clusters. Such social settings as bars, restaurants, weddings, and religious sites appeared at increased risk of large outbreaks (Adam et al., 2020).

One limitation of our analyses is that the model was fit to date of case confirmation because the date of symptom onset, which is more closely related with the date of infection, was not available. The daily number of confirmed cases can abruptly change depending on the intensity of intervention measures, of which the dynamics may not be consistent with disease transmission process. This means using the data on case

confirmation under dynamics intervention measures is challenging. We tried to mitigate this difficulty by incorporating the dynamics of intervention programs by assuming that the start date and duration of enhanced case detection vary while the case detection rate increases over time and let the data suggest the values for those parameters.

5. Conclusions

The potential for large variations in R_0 for COVID-19 has important implications for the design and effectiveness of control strategies. The efficacy of components of intervention programs, such as contact tracing and physical distancing, is dependent on various environmental and societal factors (e.g., large gatherings, physical proximity, high risk behaviors such as singing, etc.) that influence the transmissibility of disease. Our analyses provide important insights that in order to minimize the risk of sudden outbreaks, efforts to identify and preempt high transmission scenarios will be key to controlling the spread of the COVID-19. Understanding and subsequently limiting the risk of transmission in high-risk places such as the Shincheonji Church cluster in Korea is key to effective control of COVID-19 transmission.

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CRediT authorship contribution statement

Jong-Hoon Kim: Conceptualization, Methodology, Software, Original draft preparation. **Hyojung Lee:** Data curation, Writing, and Editing. **Yong Sul Won:** Data curation, Writing, and Editing. **Woo-Sik Son:** Writing, Validation. **Justin Im:** Writing, Reviewing, and Editing.

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Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at doi:10.1016/j.epidem.2021.100519.

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