Effectiveness of quarantine measure on transmission dynamics of COVID-19 in Hong Kong

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Abstract

The rapid expansion of COVID-19 has caused a global pandemic. Although quarantine measures have been used widely, the critical steps among them to suppress the outbreak without a huge social-economic loss remain unknown. Hong Kong, unlike other regions in the world, had a massive number of travellers from Mainland China during the early expansion period, and yet the spread of virus has been relatively limited. Understanding the effect of control measures to reduce the transmission in Hong Kong can improve the control of the virus spreading.

We have developed a susceptible-exposed-infectious-quarantined-recovered (SEIQR) meta-population model that can stratify the infections into imported and subsequent local infections, and therefore to obtain the control effects on transmissibility in a region with many imported cases. We fitted the model to both imported and local confirmed cases with symptom onset from 18 January to 29 February 2020 in Hong Kong with daily transportation data and the transmission dynamics from Wuhan and Mainland China.

The model estimated that the reproductive number was dropped from 2.32 to 0.76 (95% CI, 0.66 to 0.86) after an infected case was estimated to be quarantined half day before the symptom onset, corresponding to the incubation time of 5.43 days (95% CI, 1.30-9.47). If the quarantine happened about one day after the onset, community spread would be likely to occur, indicated by the reproductive number larger than one. The results suggest that the early quarantine for a suspected case before the symptom onset is a key factor to suppress COVID-19.

Introduction

The coronavirus SARS-CoV-2 outbreak, originally occurred from Wuhan, China, in December 2019 has caused a global pandemic in March 2020 [1,2]. Regions in East Asia, such as Hong Kong, Taiwan, Korea and Japan, all faced an extremely high risk of community outbreak due to a massive number of travellers from Mainland China during the Chinese new year [3,4]. However, comparing to many other countries until now (March 2020), the coronavirus outbreak was still considered limited in Hong Kong and Taiwan [5]. The low number of transmission can be due to a successful public health control strategy. To understand how coronavirus can be contained in these places is of great importance to limit the global spread of the virus happening right now.

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Presently, nonpharmaceutical interventions including both mitigation and suppression strategies have been proposed to control the outbreak [6]. Suppression strategies were often intensive that can be challenging to fully implemented in many countries such as transportation restriction or city lockdown [4, 7]. How Hong Kong successfully prevent the outbreak without shutting down most of the public services thus offers us a different perspective on how to choose a containing strategy.

As most countries, quarantine and border control policies were taken in order to stop the spread of the coronavirus 16 from Wuhan. During the Chinese New Year festival, which started on 24 January in 2020, more than one million 17 of travellers (some were Hong Kong residents) arrived Hong Kong from Mainland in a week [8]. Local spread 18 occurred starting from this critical moment when only few initial travellers who carried the disease. Therefore, 19 infected individuals were reported almost every day with travel history from Wuhan or Mainland China from 20 18 January 2020 until 4 February 2020, when most of the border crossings were closed [9]. After 28 January, 21 most the travellers from Mainland require 14 days self-quarantine. Quarantine and border control were the major 22 control measures performed during this period in Hong Kong. 23

Assessing the effect of quarantine measures during this period in Hong Kong may provide an opportunity to understand how an outbreak can be suppressed (indicated by a reproductive number below one), by quarantine measures without extremely intensive interventions. However, challenge exists in assessing the effect on transmissibility in Hong Kong using classical transmission models, such as susceptible-infectious-recovered (SIR) or susceptible-exposed-infectious-recovered (SEIR) models, because many confirmed cases were identified as imported cases. To obtain the reproductive number, an indication of the transmissibility of the virus, the number of secondary infections of a given infected individual should be estimated. However, with many imported 31

cases, the observed changes in numbers of cumulative cases are not totally due to those secondary infections ³² happened locally. Because current models cannot distinguish the imported and local infections, overestimation ³³ of the reproductive number can be easily happened. ³⁴

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In order to estimate the reproductive number and other epidemiological parameters of COVID-19 in Hong Kong, ³⁶ here we developed a susceptible-exposed-infected-quarantined-recovered (SEIQR) meta-population model embedded with passenger data from Mainland China, that can stratify imported and local cases. We used Hong ³⁸ Kong as an example to demonstrate that the model can successfully recapture the transmission dynamics of both ³⁹ imported and local infections and estimate the reproductive number. Furthermore, the minimum timing and ⁴⁰ intensity of quarantine to suppress the outbreak were estimated. ⁴¹

Materials & Methods

Data collection

We collected the date of symptom onset time for each daily newly infected case of COVID-19 from 18 January to 44 29 February 2020 in Hong Kong from the Centre for Health Protection, Government of the Hong Kong Special 45 Administrative [10]. Number of daily newly infected COVID-19 cases in Wuhan City and Mainland China 46 outside Wuhan from 16 January to 29 February 2020 were collected from the National Health Commission of 47 China [11]. Daily passenger data from Mainland China during the corresponding period were obtained from the 48 Hong Kong Immigration Department [12]. 49

SEIQR Meta-population model

The meta-population model was fitted first to the data from Wuhan and Mainland China (outside Wuhan). Using 51 the reconstructed transmission dynamics from source regions, the model was next fitted to the confirmed cases 52 with symptom onset in Hong Kong with transportation data. Assuming the newly emergence of COVID-19 53 causes an outbreak at location i, during the emergence, the changes of the numbers of infectious cases I_i at a 54 different location *j* can be determined using a meta-population framework with a mobility matrix (contact mixing 55 at the population level) such that $I_j = I_{j_imp} + I_{j_loc}$, where the subscripts *imp* and *loc* represent imported and 56 local cases and the number of $I_{j_{imp}}$ is dependent on the mobility matrix. We developed an SEIQR model to 57 include dynamics of both imported and local cases at a target location (Hong Kong), and linked this model to 58 the meta-population framework: 59

$$\frac{dS}{dt} = -\beta \frac{S}{N} \left(I_{imp} + I_{loc} + qQ_{imp} + qQ_{loc} \right) \tag{1}$$

$$\frac{dE_{imp}}{dt} = E_{impW}^{+} + E_{impC}^{+} - \frac{1}{\tau}E_{imp}$$
(2)

$$\frac{dI_{imp}}{dt} = \frac{1}{\tau} E_{imp} - \frac{1}{T_{qr}} I_{imp} - \gamma I_{imp}$$
(3)

$$\frac{dQ_{imp}}{dt} = \frac{1}{T_{qr}}I_{imp} - \gamma Q_{imp} \tag{4}$$

$$\frac{dR_{imp}}{dt} = \gamma \left(I_{imp} + Q_{imp} \right) \tag{5}$$

$$\frac{dE_{loc}}{dt} = \beta \frac{S}{N} \left(I_{imp} + I_{loc} + qQ_{imp} + qQ_{loc} \right) - \frac{1}{\tau} E_{loc} \tag{6}$$

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$$\frac{dI_{loc}}{dt} = \frac{1}{\tau} E_{loc} - \frac{1}{T_{qr}} I_{loc} - \gamma I_{loc} \tag{7}$$

$$\frac{dQ_{loc}}{dt} = \frac{1}{T_{qr}} I_{loc} - \gamma Q_{loc} \tag{8}$$

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$$\frac{dR_{loc}}{dt} = \gamma \left(I_{loc} + Q_{loc} \right) \tag{9}$$

where β is the transmission rate, τ is the latent periods, γ is the recovery rate, Tqr is the time to quarantine after 67 being infectious and q is the recontact ratio of quarantined to unquarantined individuals. I_{imp} , I_{loc} , Q_{imp} , Q_{loc} 68 are the infectious imported cases, infectious local cases, infectious imported cases that are under quarantined 69 and infectious local cases that are under quarantined. Please see Table 1 and Table 2 for detailed definitions of 70 each variables and parameters. Our SEIQR meta-population model stratifies the imported and local cases and is 71 embedded with border control and quarantine measures given daily passenger data from Wuhan and Mainland 72 China. E_{impW}^+ and E_{impC}^+ are the daily newly number of imported cases from Wuhan (denoted as W) and 73 Mainland China outside Wuhan (denoted as C). These numbers are determined by the daily passenger numbers 74 and incubation period: 75

$$E_{impW}^{+} = \eta M_{HW} \beta \frac{S_W}{N_W} \frac{I_W}{R_{pt}}$$
(10)

$$E_{impC}^{+} = \eta M_{HC} \beta \frac{S_C}{N_C} \frac{I_C}{R_{pt}}$$
(11)

where M_{ji} is the mobility rate from i to j, subscripts H, W, C indicates Hong Kong, Wuhan, Mainland China 77 (outside Wuhan), respectively. We used daily passenger data from the source regions divided by the population 78 size in the source regions to refer to M_{ji} (Table S1). Among all the passengers from Mainland China, the 79 proportion of them coming from Wuhan to Hong Kong during the study period can be calculated using the 80 International Air Transport Association (IATA) database [13]. We estimated 2.92% of the total passenger from 81 Mainland China to Hong Kong was from Wuhan. We assumed only the patients without symptom onset can 82 pass the border to Hong Kong. Thus the terms $\beta \eta M_{HW} \frac{S_W}{N_W} \frac{I_W}{R_{pt}}$ and $\beta \eta M_{HC} \frac{S_C}{N_C} \frac{I_C}{R_{pt}}$ represent the daily newly 83 imported cases from Wuhan and Mainland China (outside Wuhan) where η is a function to calculate the number 84 of infected cases before symptom onset [14] and R_{pt} is the reporting ratio. 85

Transmission dynamics in source regions

To obtain the number of imported cases, the model has to generate the transmission dynamics (I_W and I_C) ⁸⁸ at source regions and estimated the imported cases using transportation data. We used a simple SIR model to ⁸⁹

| NPopulation size in Hong Kong S Susceptible cases E_{imp} Exposed imported cases I_{imp} Infectious imported cases Q_{imp} Quarantined infectious imported cases R_{imp} Recovered imported cases E_{loc} Exposed local cases I_{loc} Infectious local cases Q_{loc} Quarantined infectious local cases R_{loc} Recovered local cases N_W Population size in Wuhan S_W Susceptible cases in Wuhan I_W Infected cases in Wuhan N_C Population size in Mainland China (non-Wuhan) S_C Susceptible cases in Mainland China (non-Wuhan) I_C Infected cases in Mainland China (non-Wuhan) | Variables | Descriptions | | | | |
|---|-----------|---|--|--|--|--|
| S Susceptible cases E_{imp} Exposed imported cases I_{imp} Infectious imported cases Q_{imp} Quarantined infectious imported cases R_{imp} Recovered imported cases E_{loc} Exposed local cases I_{loc} Infectious local cases Q_{loc} Quarantined infectious local cases R_{loc} Recovered local cases N_W Population size in Wuhan S_W Susceptible cases in Wuhan I_W Infected cases in Wuhan N_C Population size in Mainland China (non-Wuhan) S_C Susceptible cases in Mainland China (non-Wuhan) I_C Infected cases in Mainland China (non-Wuhan) | N | Population size in Hong Kong | | | | |
| $\begin{array}{lll} E_{imp} & \mbox{Exposed imported cases} \\ I_{imp} & \mbox{Infectious imported cases} \\ Q_{imp} & \mbox{Quarantined infectious imported cases} \\ R_{imp} & \mbox{Recovered imported cases} \\ E_{loc} & \mbox{Exposed local cases} \\ I_{loc} & \mbox{Infectious local cases} \\ Q_{loc} & \mbox{Quarantined infectious local cases} \\ R_{loc} & \mbox{Recovered local cases} \\ N_W & \mbox{Population size in Wuhan} \\ S_W & \mbox{Susceptible cases in Wuhan} \\ I_W & \mbox{Infected cases in Wuhan} \\ N_C & \mbox{Population size in Mainland China (non-Wuhan)} \\ S_C & \mbox{Susceptible cases in Mainland China (non-Wuhan)} \\ I_C & \mbox{Infected cases in Mainland China (non-Wuhan)} \\ \end{array}$ | S | Susceptible cases | | | | |
| I_{imp} Infectious imported cases Q_{imp} Quarantined infectious imported cases R_{imp} Recovered imported cases E_{loc} Exposed local cases I_{loc} Infectious local cases Q_{loc} Quarantined infectious local cases R_{loc} Recovered local cases N_W Population size in Wuhan S_W Susceptible cases in Wuhan I_W Infected cases in Wuhan N_C Population size in Mainland China (non-Wuhan) S_C Susceptible cases in Mainland China (non-Wuhan) I_C Infected cases in Mainland China (non-Wuhan) | E_{imp} | Exposed imported cases | | | | |
| Q_{imp} Quarantined infectious imported cases R_{imp} Recovered imported cases E_{loc} Exposed local cases I_{loc} Infectious local cases Q_{loc} Quarantined infectious local cases R_{loc} Recovered local cases N_W Population size in Wuhan S_W Susceptible cases in Wuhan I_W Infected cases in Wuhan N_C Population size in Mainland China (non-Wuhan) S_C Susceptible cases in Mainland China (non-Wuhan) I_C Infected cases in Mainland China (non-Wuhan) | I_{imp} | Infectious imported cases | | | | |
| R_{imp} Recovered imported cases E_{loc} Exposed local cases I_{loc} Infectious local cases Q_{loc} Quarantined infectious local cases R_{loc} Recovered local cases N_W Population size in Wuhan S_W Susceptible cases in Wuhan I_W Infected cases in Wuhan N_C Population size in Mainland China (non-Wuhan) S_C Susceptible cases in Mainland China (non-Wuhan) I_C Infected cases in Mainland China (non-Wuhan) | Q_{imp} | Quarantined infectious imported cases | | | | |
| E_{loc} Exposed local cases I_{loc} Infectious local cases Q_{loc} Quarantined infectious local cases R_{loc} Recovered local cases N_W Population size in Wuhan S_W Susceptible cases in Wuhan I_W Infected cases in Wuhan N_C Population size in Mainland China (non-Wuhan) S_C Susceptible cases in Mainland China (non-Wuhan) I_C Infected cases in Mainland China (non-Wuhan) | R_{imp} | Recovered imported cases | | | | |
| I_{loc} Infectious local cases Q_{loc} Quarantined infectious local cases R_{loc} Recovered local cases N_W Population size in Wuhan S_W Susceptible cases in Wuhan I_W Infected cases in Wuhan N_C Population size in Mainland China (non-Wuhan) S_C Susceptible cases in Mainland China (non-Wuhan) I_C Infected cases in Mainland China (non-Wuhan) | E_{loc} | Exposed local cases | | | | |
| Q_{loc} Quarantined infectious local cases R_{loc} Recovered local cases N_W Population size in Wuhan S_W Susceptible cases in Wuhan I_W Infected cases in Wuhan N_C Population size in Mainland China (non-Wuhan) S_C Susceptible cases in Mainland China (non-Wuhan) I_C Infected cases in Mainland China (non-Wuhan) | I_{loc} | Infectious local cases | | | | |
| R_{loc} Recovered local cases N_W Population size in Wuhan S_W Susceptible cases in Wuhan I_W Infected cases in Wuhan N_C Population size in Mainland China (non-Wuhan) S_C Susceptible cases in Mainland China (non-Wuhan) I_C Infected cases in Mainland China (non-Wuhan) | Q_{loc} | Quarantined infectious local cases | | | | |
| N_W Population size in Wuhan S_W Susceptible cases in Wuhan I_W Infected cases in Wuhan N_C Population size in Mainland China (non-Wuhan) S_C Susceptible cases in Mainland China (non-Wuhan) I_C Infected cases in Mainland China (non-Wuhan) | R_{loc} | Recovered local cases | | | | |
| $\begin{array}{ll} S_W & & \text{Susceptible cases in Wuhan} \\ I_W & & \text{Infected cases in Wuhan} \\ N_C & & \text{Population size in Mainland China (non-Wuhan)} \\ S_C & & \text{Susceptible cases in Mainland China (non-Wuhan)} \\ I_C & & \text{Infected cases in Mainland China (non-Wuhan)} \end{array}$ | N_W | Population size in Wuhan | | | | |
| I_W Infected cases in Wuhan N_C Population size in Mainland China (non-Wuhan) S_C Susceptible cases in Mainland China (non-Wuhan) I_C Infected cases in Mainland China (non-Wuhan) | S_W | Susceptible cases in Wuhan | | | | |
| N_C Population size in Mainland China (non-Wuhan) S_C Susceptible cases in Mainland China (non-Wuhan) I_C Infected cases in Mainland China (non-Wuhan) | I_W | Infected cases in Wuhan | | | | |
| $ S_C \qquad \qquad \text{Susceptible cases in Mainland China (non-Wuhan)} \\ I_C \qquad \qquad \text{Infected cases in Mainland China (non-Wuhan)} $ | N_C | Population size in Mainland China (non-Wuhan) | | | | |
| <i>I_C</i> Infected cases in Mainland China (non-Wuhan) | S_C | Susceptible cases in Mainland China (non-Wuhan) | | | | |
| | I_C | Infected cases in Mainland China (non-Wuhan) | | | | |

Table 1: Descriptions of variables in the meta-population model.

construct newly infected numbers that reproduced the same numbers of cumulative confirmed cases in Wuhan and Mainland China (outside Wuhan) after the outbreak. Please see supplementary methods for the detailed descriptions. 92

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Parameter estimation

Prior to parameter estimation, the transmission dynamics in Wuhan and non-Wuhan Mainland China were re-94 constructed using a modified SIR model. The resulting source dynamics were used as an initial condition to 95 seed imported cases for the target region (Figure S1 and Figure S2). Second, the posterior distributions of the 96 parameters of transmission dynamics in Hong Kong were obtained using Markov Chain Monte Carlo (MCMC) 97 to fit the detected infected cases from the model to the reported cases with symptom onset. The posterior distri-98 butions were obtained from Metropolis-Hastings in Markov Chain Monte Carlo (MCMC) with 1.2×10^6 steps 99 (Figure S3 and Figure S4) to guarantee an effective sample size (ESS) of greater than 200 for all parameters. 100 The Gelman-Rubin convergence diagnostic was used and all the scores were less than 1.056 and near one, which 101 confirmed the convergence. 102

Prior distributions for all the parameters were set to uniform distributions except the generation time Tc and ¹⁰³ the recontact ratio q. The prior of the generation time was assumed to be normally distributed with mean set ¹⁰⁴ to be 7.95 days, the average from two previous studies [15, 16]. The standard deviation was 0.25. The mean ¹⁰⁵ recontact ratio of being quarantined and not quarantined in a Gaussian prior was set to be 12% with a standard ¹⁰⁶ deviation of 0.05. A recent study has estimated each individual can contact 12.5 persons on average during a ¹⁰⁷

day [17]. Assuming many self-quarantine individuals can likely contact to their household members, with a possible expected number 1.5 persons, the mean recontact ratio of quarantined individuals to unquarantined in the prior distribution can thus be determined as $q = \frac{1.5}{12.5}$.

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Likelihood of symptom onset

The likelihood of observing onset dates of both confirmed imported and confirmed local cases in Hong Kong 113 were calculated based on Poisson distribution during MCMC. Newly detected infected cases are defined as the 114 newly infected cases with symptom onset that eventually became quarantined. We assumed all the confirmed 115 cases were quarantined. The daily newly detected imported cases with symptom onset was used as the expected 116 value of the Poisson distribution and can be derived as $\Delta I_{imp}(\sigma)D$, where $\Delta I_{imp} = \frac{1}{\tau}E_{imp}$, and D is the detec-117 tion ratio, which was defined as the proportion of the number of quarantined imported cases to the total number 118 of infectious and quarantined cases. σ represents the pre-symptomatic transmission period, which produced a 119 delay of onset after an individual has been infected. The same approach can be used to determine the expected 120 value of the Poisson distribution for the detected local cases. 121

Effective reproductive number calculation

The effective reproductive number R_e , was calculated using the next-generation matrix approach after obtaining the posterior distributions of model parameters [18]. Please see supplementary methods for the detailed descriptions. 126

Results

Dynamics of imported and local cases

Our meta-population model reproduced the COVID-19 transmission dynamics of both imported and local infec-129 tions in Hong Kong. The number of cumulative imported cases was increasing rapidly in Hong Kong after the 130 first imported case was detected, with onset day on 18 January 2020 until the end of Chinese New Year in early 131 February (Figure 1A). The risk of community spread was highlighted as the number of local cases crossed above 132 the imported cases. In order to understand the transmission dynamics of COVID-19 in Hong Kong, we devel-133 oped an SEIQR meta-population model that stratifies imported and local cases (Figure 2). The model recaptured 134 the cumulative numbers with a crossover between the local and imported cases (Figure 1B) and transient dy-135 namics (Figure 3). The predicted number of imported cases reached to a peak on 26 January (Figure 3A). These 136 imported cases immediately caused a wave of local infections. The number of daily newly detected local cases 137 reached to a peak around 2 February and decreased afterward (Figure 3B). 138

Epidemiological parameters

Epidemiological parameters of COVID-19 were obtained for Hong Kong from 18 January to 29 February. The 141 effective reproductive number R_e was 0.76 (0.66 - 0.86) (Table 2). R_0 was 2.32 (1.19 - 4.42), referring to the 142 reproductive number when the quarantine measure was not included. Latent period was 1.94 days (0.34 - 4.17). 143 The pre-symptomatic transmission period before disease onset was 3.49 days (0.48 - 5.80). The incubation time 144 was calculated as 5.43 days (1.30 - 9.47), consistent with recent findings, where a mean or median incubation 145 period of approximately 5 days was reported [16, 19, 20]. We assumed all the infected persons can pass the border 146 before disease onset, which was defined as the incubation time. The estimated time to quarantine after being 147 infectious T_{qr} in Hong Kong is 2.92 days (0.65 - 7.81) days, which is nearly two days less than the incubation 148 period. The recontact ratio of quarantined to unquarantined individuals q was 10.26% (5.32 - 17.8). The model 149 estimated only 22% (9 - 41) of total infected cases were documented in Mainland China. 150

Effect of quarantine on Reproductive Number

The timing of quarantine was an important measurement to determine the risk of community spread. The estimated T_{qr} in Hong Kong was about half day earlier than the symptom onset time and was able to reduce R_e to be less than one (Figure 4A). If T_{qr} was longer than one day after disease onset, R_e became greater than one, the community spread could happen. Furthermore, the recontact ratio of quarantined to unquarantined individuals affected the value of R_e . If the q became about two and a half larger than the estimated value, R_e was greater

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Figure 1 Number of cumulative confirmed COVID-19 cases by symptom onset date. (A) Observed cumulative confirmed cases. Light blue denotes the total imported cases. Dark blue denotes the imported cases only from China, excluding few other cases mainly from diamond princess cruise. Red denotes the local cases. (B) Predicted cumulative detected cases. Blue denotes the predicted number of cumulative detected imported cases from China. Red denotes the predicted number of cumulative detected imported cases values.

than one and the community spread could also happen (Figure 4B). The epidemiological parameters and the 158 effects of quarantine measures during an infection generation was illustrated (Figure 5). Sensitivity analysis has 159 been performed to evaluate the impact of initial setting of generation time to the effective reproductive number. 160 For sensitivity analysis, we have tested two alternative model settings, with the generation time fixed at 7.5 or 161 8.4 days. Both of the settings gave the mean Re of 0.76 or 0.77 as well. 162

Effects of quarantine on Detection Ratio

The results showed that the ratio can be low during the initial period but soon reached saturated values after 3 ¹⁶⁵ weeks both for imported and local cases (Figure 6AB). Generally the detection ratios of the imported cases were ¹⁶⁶ higher than the local cases because the number of the imported cases were low. For local cases, 71%(46-90) of ¹⁶⁷ which were detected, estimated by our model. One day delay of quarantine reduced about 10% of daily detection ¹⁶⁸ ratio to 60%(39-74) (Figure 6B). Only 31%(20-39) of them could be detected or quarantined if quarantine ¹⁶⁹ was delayed 6 days. The results showed that not only early quarantine can reduce reproductive number, but also ¹⁷⁰ has a benefit on increasing overall detection ratio. ¹⁷¹

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Figure 2 Schema of susceptible-exposed-infected-quarantined-recovered meta population model. Imported cases arrive as exposed (E) status before disease onset in order to pass through the border. Imported cases then become infectious (I), quarantined (Q) or recovered (R) statuses. $\beta\eta \frac{1}{R_{pt}}M$ is the rate to produce imported cases, where η is a function to determine the probability of an ill passenger can pass the border (see Methods for the details). R_{pt} is the reporting ratio in Mainland China and M is the mobility rate. Both imported and local cases are able to infect susceptible individuals (S) and cause local transmission while quarantined cases have a lower transmission rate depending on the recontact ratio (q), indicating the ratio of the contact rates of quanratined to unquarantined individuals. Epidemiological parameters β is the transmission rate, τ is the latent periods, γ is the recovery rate, T_{qr} is the time to quarantine after being infectious. $\Delta I_{imp}(\sigma)D$ represents the newly detected imported cases, where D is the detected ratio defined as the ratio of the number of quarantined imported cases to the total number of infectious and quarantined imported cases, and σ is the pre-symptomatic transmission period, indicating the delayed time of symptom onset after being infectious. Similarly, $\Delta I_{loc}(\sigma)D$ represents the detected local cases.



Figure 3 Observed and predicted numbers of detected imported and local cases. (A) Number of observed imported and predicted number of detected imported cases. Mean, 50% and 95% prediction intervals are shown. The predicted detected cases are the daily newly cases with symptom onset that eventually become quarantined and detected. (B) Number of observed local and predicted number of detected local cases. Mean, 50% and 95% prediction intervals are shown. The definition of the detected local cases is same as (A) but for local infections.



Figure 4 Effective reproductive numbers by different timings and intensities of quarantine measures. (A) The mean and credible intervals of effective reproductive number R_e by different days of time to quarantine T_{qr} . Note the values were adjusted to time to quarantine after symptom onset. The vertical line corresponds to the average time from onset to isolation when R_e is one. Dashed line indicates the level of R_e as one. Yellow dot represents the estimated T_{qr} and the corresponded R_e . (B) The mean and credible intervals of effective reproductive number R_e by recontact ratios q. Yellow dot represents the estimated T_{qr} and the corresponded R_e . All the values were estimated from 2000 random samples from posterior distributions.



Figure 5 Epidemiological parameters during an infection generation. The effects of different times to quarantine on the effective reproductive number are illustrated.

Table 2: Values of reproductive numbers and other epidemiological parameters of COVID-19 in Hong Kong. Mean values with 95% credible intervals are produced. The basic reproductive number is defined as the expected number of secondary infections without quarantine. The effective reproductive number is derived from the posterior variables when quarantine measure is considered. The incubation time *inc* refers to the sum of latent period τ and pre-symptomatic transmission period σ .

| Parameters | Values | Descriptions |
|------------|--------------------|--|
| R_e | 0.76 (0.66 - 0.86) | Effective reproductive number |
| R_0 | 2.32 (1.19 - 4.42) | Basic reproductive number (without quarantine measure) |
| inc | 5.43 (1.30-9.47) | Incubation time (unit: day) |
| au | 1.94 (0.34-4.17) | Latent period (unit: day) |
| σ | 3.49 (0.48-5.80) | Pre-symptomatic transmission period (unit: day) |
| Tc | 7.80 (6.81-8.79) | Generation time (unit: day) |
| T_{qr} | 2.92 (0.65-7.81) | Time to quarantine after being infectious (unit: day) |
| q | 10.26% (5.32-17.8) | Recontact ratio of quarantined to unquarantined |
| Rpt | 22% (9-41) | Reporting ratio in Mainland China |



Figure 6 Detection ratios of imported and local cases by time. (A) Detection ratios of imported cases. The ratios denote the proportion of daily newly cases with symptom onset that eventually become quarantined among all infectious cases. Blue, the detection ratio estimated using the posterior distribution of the time to quarantine, denoted as no delay. Red, the detection ratio estimated using the posterior distribution of the time to quarantine with one day delay. Green, the detection ratio estimated using the posterior distribution of the time to quarantine with six days delay. Shared areas are the 95% intervals. (B) Detection ratios of local cases. The ratios denote the proportion of daily newly cases with symptom onset that eventually become quarantined among all infectious cases. Same definition of colors are used as (A) but for local infections.

Discussion

By characterizing the transmission dynamics with quarantine and border control measures across the Chinese 174 New Year festival in Hong Kong, we have identified the key aspects in containing the outbreak. This is the first 175 study to demonstrate that early time targeted quarantine measures significantly suppress the COVID-19 outbreak 176 and the proper timing of quarantine is feasible. Suppression of the outbreak during the study period is important 177 because global expansion occurred starting from this critical moment when initial travellers who carried the 178 diseases moved to different countries [21–24].

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Until now, how to suppress the outbreak of COVID-19 has been studied only in regions with many infections, ¹⁸¹ such as Wuhan or China [4, 21, 25, 26]. Although certain strict public health policies can suppress the outbreak, ¹⁸² these approaches can cause profound social and economic impacts, which may not be feasible by every country. ¹⁸³ In contrast, our study illustrated that Hong Kong can be a good model to learn how to prevent the community ¹⁸⁴ spread through quarantine before many other intensive control policies (such as transportation restriction and ¹⁸⁵ closure of public facilities) are required. ¹⁸⁶

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How to impose a large scale quarantine properly to suppress the outbreak remain largely unknown [6]. Our ¹⁸⁸ results demonstrated that quarantine of suspected individuals before symptom onset, is critical to contain the ¹⁸⁹ COVID-19 outbreak. Given that the incubation period was about 5 days and the confirmation of COVID-19 ¹⁹⁰ infection can often be delayed, to guarantee an early quarantine of all suspected cases before symptom onset is ¹⁹¹ a critical criterion to reduce the chance of community spread. ¹⁹²

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Using a model that can stratify both dynamics of imported and local infections, we demonstrated that many epidemiological parameters, including the reproductive number, latent period and incubation time, along with the reporting ratio in Mainland China can be estimated after fitting confirmed cases with symptom onset in Hong Kong with daily transportation data. Generation time we used are adopted from previous studies studies with the estimated mean of 7.8 days [15, 16]. The values, such as incubation time and reporting ratio are consistent to recent studies [7, 16, 19, 20].

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One of the major challenges to limit the COVID-19 epidemic through quarantine is pre-symptomatic transmission. Currently, little is known about when does the transmission occur before the symptom. Our model has found, an individual after latent period, can be infectious without symptoms about 3 days, similar to 1-3 203

days found by many recent studies through contact tracing and enhanced investigation of clusters of confirmed ²⁰⁴ cases [27–30]. Thus, even if a very intensive contact tracing is proposed, to identify all the contacts made by an ²⁰⁵ infectious individual before symptom onset can be difficult. Thus, how to reduce social contacts and maintain ²⁰⁶ social distancing along with quarantine measures become critical to prevent the spread. To evaluate the benefits of different approaches to reduce unnecessary contacts, such as working from home, wearing masks, etc, ²⁰⁸ becomes an important task [31, 32].

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The study highlights the importance of having a time targeted quarantine measure along with travel bans. Investigating the timing and the quality of quarantine in different outbreak regions is a critical factor for prevention and control of COVID-19 outbreak.

Declaration of Interests

All authors declare no competing interests.

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Author Contributions

H-YY designed the study. AM and GH participated in the data collection. H-YY and AM analysed and interpreted the data. H-YY wrote the paper. Everyone reviewed, revised and edited the manuscript. 228

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Supplementary Methods

Dynamics in source regions

To obtain the number of imported cases, the model has to generate transmission dynamics in source regions is to seed the target region (Hong Kong). We modified an SIR to construct newly infected numbers that were close to the observed confirmed numbers in Wuhan and Mainland China (outside Wuhan).

$$\frac{dS_i}{dt} = -\beta \frac{S_i}{N_i} - E^+_{impi} - \alpha S_i$$
$$\frac{dI_i}{dt} = \beta \frac{S_i}{N_i} - \gamma I_i$$
$$\frac{dR_i}{dt} = \gamma I_i$$

Where α is a parameter to represent the effect of reduction of social contacts after the Wuhan lockdown on 23 January 2020 and the closure of the border crossings on 4 February 2020 [1]. As a result, reduction of susceptible population happens by time. Assuming generation time is 8.4 days thus we have the recovery rate $\gamma = \frac{1}{8.4}$. Using $R_0 = 2.92$, we can obtain $\beta = R_0\gamma = 0.3476$ in Mainland China. We also assumed the recovery rate is same for γ both transmission dynamics in Mainland China and in Hong Kong.

Effective reproductive number calculation

The effective reproductive number R_e , was calculated using the next-generation matrix approach after obtaining the posterior distributions of model parameters. Following the same notation as in the study by Diekmann et al[2]. We obtained the transmission matrix T and the transition S. Elements in T represents the average newly infected cases in exposed group (E) transmitted by a single infected individual in infectious or quarantined group (I), which can be calculated as $\beta \frac{s}{N}$ or $q\beta \frac{s}{N}$. R_e can be calculated as the first eigenvector of $-(TS^{-1})$ with the following formulas:

$$T = \begin{bmatrix} 0 & \beta \frac{S}{N} & q\beta \frac{S}{N} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$
$$S = \begin{bmatrix} \frac{-1}{\tau} & 0 & 0 \\ \frac{1}{\tau} & -(\frac{1}{T_c} + \frac{1}{T_{qr}}) & 0 \\ 0 & \frac{1}{T_{qr}} & \frac{-1}{T_c} \end{bmatrix}$$



Supplementary Figures and Tables

Figure S1 The number of daily newly infected COVID-19 cases by onset day in China. (A) Daily newly infected COVID-19 cases in Wuhan, China. Red line represents the reconstructed curve adjusted by 10 days reporting delay after fitting the actual data in Wuhan. The x-axis denotes the case reporting day after Jan 16, 2020. (B) Daily newly infected COVID-19 cases in Mainland China (outside Wuhan). Red line represents the reconstructed curve adjusted by 10 days reporting delay after fitting the actual data outside Wuhan.



Figure S2 The number of cumulative confirmed COVID-19 cases by onset day in China. (A) Cumulative confirmed COVID-19 cases in Wuhan, China. Red line represents the reconstructed curve adjusted by 10 days reporting delay after fitting the actual data inside Wuhan. The x-axis denotes the number of days from Jan 18 to Feb 29, 2020. (B) Cumulative confirmed COVID-19 cases in Mainland China (outside Wuhan). Red line represents the reconstructed curve adjusted by 10 days reporting delay after fitting the actual data outside Wuhan.



Figure S3 Posterior distributions of model parameters.



Figure S4 Trajectories of MCMC output.

| Time | Residents(HK) | Residents(Mainland) | Time | Residents(HK) | Residents(Mainland) |
|------|---------------|---------------------|------|---------------|---------------------|
| 1/24 | 102,663 | 36,705 | 2/12 | 15,792 | 729 |
| 1/25 | 86,417 | 29,891 | 2/13 | 13,312 | 751 |
| 1/26 | 163,668 | 36,690 | 2/14 | 13,507 | 683 |
| 1/27 | 177,470 | 28,780 | 2/15 | 16,089 | 791 |
| 1/28 | 188,788 | 24,156 | 2/16 | 20,325 | 749 |
| 1/29 | 197,572 | 27,780 | 2/17 | 15,990 | 643 |
| 1/30 | 132,506 | 19,555 | 2/18 | 14,383 | 579 |
| 1/31 | 116,544 | 16,058 | 2/19 | 12,801 | 567 |
| 2/1 | 115,122 | 13,382 | 2/20 | 13,677 | 648 |
| 2/2 | 122,399 | 11,715 | 2/21 | 14,557 | 682 |
| 2/3 | 111,033 | 13,461 | 2/22 | 15,440 | 651 |
| 2/4 | 54,816 | 9,511 | 2/23 | 20,241 | 673 |
| 2/5 | 44,566 | 8,760 | 2/24 | 16,972 | 588 |
| 2/6 | 65,122 | 11,009 | 2/25 | 15,207 | 558 |
| 2/7 | 76,899 | 12,746 | 2/26 | 14,317 | 587 |
| 2/8 | 18,823 | 995 | 2/27 | 13,846 | 702 |
| 2/9 | 24,939 | 956 | 2/28 | 15,248 | 558 |
| 2/10 | 18,408 | 832 | 2/29 | 17,881 | 1,084 |
| 2/11 | 15,953 | 738 | | | |

Table S1 Daily number of passengers from outside Hong Kong

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