Transmission Dynamics of Large Coronavirus Disease Outbreak in Homeless Shelter, Chicago, Illinois, USA, 2020

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Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has the potential for rapid transmission in congregate settings. We describe the multidisciplinary response to an outbreak of coronavirus disease (COVID-19) in a large homeless shelter in Chicago, Illinois, USA. The response to the outbreak included 4 rounds of mass PCR testing of all staff and residents and subsequent isolation of persons who tested positive for SARS-CoV-2. We further describe the dynamics of the shelter outbreak by fitting a modified susceptible-exposed-infectious-recovered compartmental model incorporating the widespread SARS-CoV-2 testing and isolation measures implemented in this shelter. Our model demonstrates that rapid transmission of COVID-19 in the shelter occurred before the outbreak was detected; rates of transmission declined after widespread testing and isolation measures were put in place. Overall, we demonstrate the feasibility of mass PCR testing and isolation in congregate settings and suggest the necessity of prompt response to suspected COVID-19 outbreaks in homeless shelters.

The coronavirus disease (COVID-19) pandemic, caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), has disproportionately affected persons living in congregate settings, including homeless shelters (*1*,*2*). People experiencing homelessness are at increased risk for SARS-CoV-2 infection because of shared living spaces and difficulty maintaining physical distance and are at increased risk for severe COVID-19 because of the high prevalence of underlying medical conditions (*3*,*4*).

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Previous studies of COVID-19 in homeless shelters have reported testing results from 1 or 2 cross-sectional time points of an outbreak (*1*,*2*), but data are limited regarding the dynamics of SARS-CoV-2 transmission in homeless shelters. Community transmission was documented in Chicago, Illinois, USA, in early March (*5*), and a statewide stay-at-home order was implemented on March 14, 2020. During March–May 2020, many homeless shelters in Chicago experienced COVID-19 outbreaks (*4*). We describe an outbreak of COVID-19 in Chicago's largest homeless shelter, including the results of repeated rounds of SARS-CoV-2 reverse transcription PCR (RT-PCR) testing. On the basis of these data, we developed a compartmental mathematical model to characterize the extent and temporal dynamics of SARS-CoV-2 infection within this shelter.

Methods

Study Population and Setting

Pacific Garden Mission (PGM) in Chicago is the largest homeless shelter in the midwestern United States, having a capacity for 950 residents. Most residents (referred to as overnight residents) sleep at night in large, gender-separated dormitories capable of accommodating ≤200 residents. During the day, these residents leave the shelter or stay collectively in large gender-separated day rooms before returning to sleep in the same dormitories but with changed bed allocations. Before the statewide stay-at-home order, the maximum length of stay for residents was 30 days. A smaller number of residents (referred to as program residents) sleep at night in smaller dormitories (ranging from 4 to 20 beds) and spend their days in the dormitories, day room, accessing services, or outside

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the shelter; these residents can stay in the shelter for up to 2 years depending on the services they are accessing. When the stay-at-home order was mandated, ≥50 residents and staff left PGM. After the statewide stay-at-home order, no residents were permitted to leave or return to the shelter, except for a select few in essential roles (e.g., employment in critical infrastructure). A total of 445 residents and staff remained at PGM.

Origin of the Outbreak at PGM

On March 14, 2020, COVID-19 was diagnosed in a female overnight resident in her 40s at an acute-care hospital. A total of 9 other PGM residents subsequently became symptomatic and sought clinical care in March; SARS-CoV-2 infection was confirmed in 10 persons by March 31. Of these, 7 were male overnight residents, 2 were female overnight residents, and 1 was a male staff member.

Clinical and Public Health Investigation and Response

For the purposes of this analysis, the investigation and response are divided into 4 phases (Figure 1). In phase 1, during March 1–29, 2020, no routine symptom screening or SARS-CoV-2 testing was conducted at PGM. Residents who sought care from staff after experiencing COVID-19–related symptoms were taken to nearby acute-care hospitals for diagnostic testing and clinical care.

In phase 2, during March 30–April 4, 2020, infection control measures were enhanced, including cleaning of frequently touched surfaces, improving the availability of hand hygiene products (e.g., alcohol-based hand sanitizer), implementing physical distancing policies, and providing facemasks to all residents (sufficient masks for universal masking were obtained by April 2). In addition, daily temperature checks and symptom screens were introduced. Residents with possible COVID-19 symptoms (persons under investigation [PUIs]) were isolated onsite. Consistent with the Centers for Disease Control and Prevention (CDC) definition at the time, residents were determined to be PUIs if they had a measured fever of ≥37.8C or reported a subjective fever, dry cough, shortness of breath, myalgia, sore throat, headache, fatigue, or close contact with a person who had confirmed SARS-CoV-2 infection.

In phase 3, during April 5–7, 2020, PUIs were transferred for offsite isolation at a hotel with individual rooms. Newly symptomatic residents were transferred to the hotel, on average, 1 day after reporting symptoms and were isolated onsite in the interim. Simultaneously, residents at high risk for severe disease (because of age or underlying medical conditions, as determined by an onsite physician) were also transferred offsite for protective housing in individual hotel rooms. A stricter shelter-in-place was instigated on April 7, 2020; after this date, residents were strongly discouraged from leaving, and residents who left for any reason were not permitted to return.

Phase 4 was characterized by recurrent rounds of widespread testing for SARS-CoV-2. During April

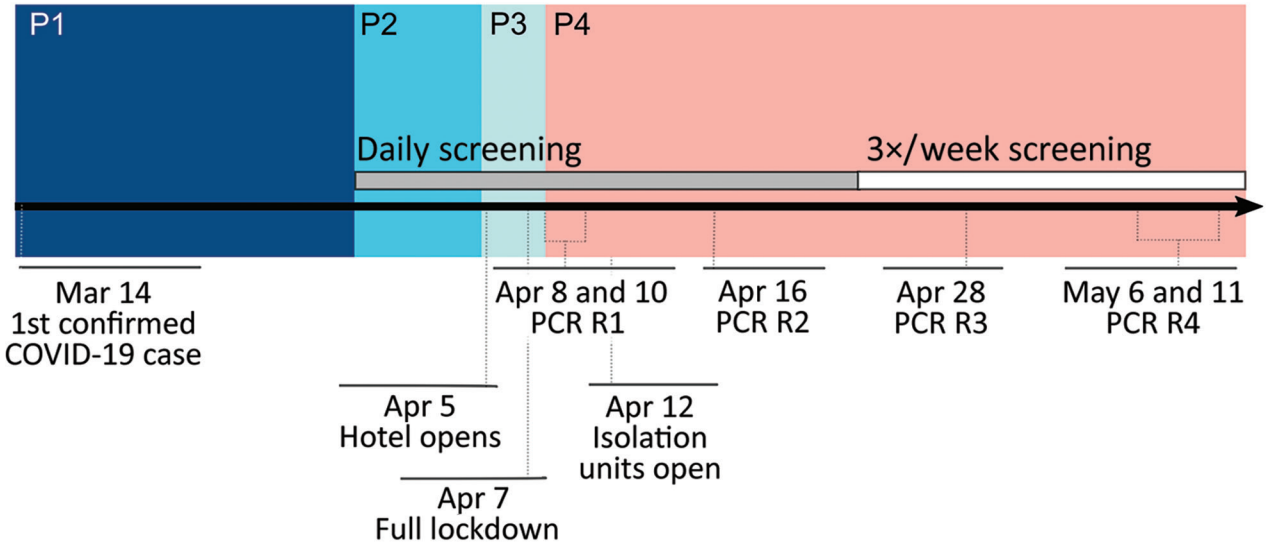

Figure 1. Summary timeline of COVID-19 outbreak and response at Pacific Garden Mission, a homeless shelter in Chicago, Illinois, USA, 2020. P1, prescreening (March 14–March 30); P2, symptom screening (March 30–April 5) and temporary isolation; P3, hotel opening with continued symptom screening (April 5–8); P4, mass RT-PCR testing rounds and isolation units (April 8–May 11). COVID-19, coronavirus disease; P, phase; RT-PCR, reverse transcription PCR.

8–10, 2020, healthcare workers from local academic healthcare centers collected oronasopharyngeal swab specimens from all consenting staff and residents. Testing was offered to all residents and staff who had not previously tested positive for SARS-CoV-2. Specimens were tested for SARS-CoV-2 by RT-PCR, and associated clinical and epidemiologic information was collected by using a standardized questionnaire as previously described (*4*). On average, test results were returned 48 hours after specimen collection. Isolation units, staffed by clinicians 24 hours a day and with capacity for 160 persons, were established onsite for residents who tested positive for SARS-CoV-2. Isolation units were equipped with a personal protective equipment (PPE) station for medical personnel; staff and residents were regularly trained in PPE use, and the PPE station was regularly stocked with surgical and N95 masks, gloves, and gowns. Further rounds of widespread testing were conducted on April 18, April 28, and May 6. After each round, residents were isolated as described previously. Residents who became symptomatic between rounds of testing but did not have a RT-PCR–confirmed diagnosis continued to be transferred to the hotel.

Modeling Transmission Dynamics of COVID-19 at PGM

To characterize transmission dynamics, we adapted a classic propagation dynamics compartmental model, susceptible-exposed-infectious-recovered (SEIR), to incorporate isolation and mass testing measures (Appendix, https://wwwnc.cdc.gov/EID/article/28/1/21-0780-App1.pdf). The SEIR model classifies persons in a population into 4 compartments of susceptible, exposed), infected), and recovered (or removed) and applies well to the relatively closed system of a homeless shelter, particularly after the stay-at-home order and the subsequent, stricter shelter-in-place policy. Rate of transmission is governed by 3 parameters: rate of transmission between susceptible and infectious persons ($\beta = [n_{\text{contacts/infectious individual/d}} \times \text{probability}_{\text{transmission given contact}}]$), the rate of conversion from exposed to infectious ($\sigma = 1/t_{\text{incubation}}$, $t_{\text{incubation}}$ = incubation period), and the rate of recovery ($\Upsilon = 1/t_{\text{infectious}}$, $t_{\text{infectious}}$ = *duration of infectiousness*). A system of ordinary differential equations determines the temporal progression of persons within each compartment.

We adapted the SEIR compartmental model to understand the dynamics of the PGM outbreak and constructed a model consisting of 4 separate systems of ordinary differential equations corresponding to the 4 phases of outbreak response at PGM (Figure 2). In each of these phases, we altered the corresponding model parameters and compartments to represent relevant screening, testing, and isolation measures. Our model introduces a compartment for isolation units in phase 4 and a compartment for isolation dorms (before the set-up of fully staffed, PPE-stocked isolation units) in phases 2 and 3. Finally, the model includes compartments for persons who were removed to the hotel or a hospital.

Model variables including β, incubation period, infectious duration, RT-PCR–positive duration, asymptomatic percentage, and RT-PCR sensitivity were fit to early testing data (March 14–April 7, 2020) from symptomatic persons who sought care at the hospital, number of persons admitted to the hospital, number of persons moved to the hotel, and results of the 4 rounds of mass testing by using the limited memory Broyden–Fletcher–Goldfarb–Shanno (L-BFGS) optimization algorithm in R (with native R function optim) (*6*,*7*). We derived ranges of values for each optimized variable from the literature (Table 1; Appendix). Basic reproduction number (R_0), which is calculated as β/Υ in a basic SEIR model, was calculated as $\beta_0/[\Upsilon_{ap} \times [\%\ \text{asymptomatic}] + [\Upsilon_{sp} \times (\%\ \text{symptomatic})]$, where Υ_{ap} is the inverse of infectious duration for asymptomatic persons and Υ_{sp} is the inverse of infectious duration for symptomatic persons. The number of persons in different compartments at various timepoints and model parameters (representing transmission dynamics) were estimated from the fitted model (Appendix Table).

Results

Demographic and health information of residents and staff members at PGM who had an RT-PCR test performed any time during March 14–May 11, 2020, were self-reported (Table 2). The demographic distribution of PGM residents is similar to that of a broader survey of persons experiencing homelessness in Chicago (*4*); most are men (255/358, 71%) and non-Hispanic Black (219/344, 64%), and the median age is 56 years (interquartile range 45–61 years).

During phases 1, 2, and 3, SARS-CoV-2 infection was confirmed in a total of 39 persons (35 residents and 4 staff members) (Figure 3, panel A). Of those 39 positive cases, 26 were confirmed after universal symptom screening was begun in the final week before mass testing.

The first round of widespread RT-PCR testing identified 166 (45%) of 366 persons who were confirmed to be SARS-CoV-2–positive. Subsequent rounds of testing yielded substantially lower rates of positivity: 24 (11%) of 217 in round 2 (April 16), 23 (11%) of 181 in round 3 (April 28), and 1 (0.5%) of 183 in round 4 (May 6). A small percentage of residents

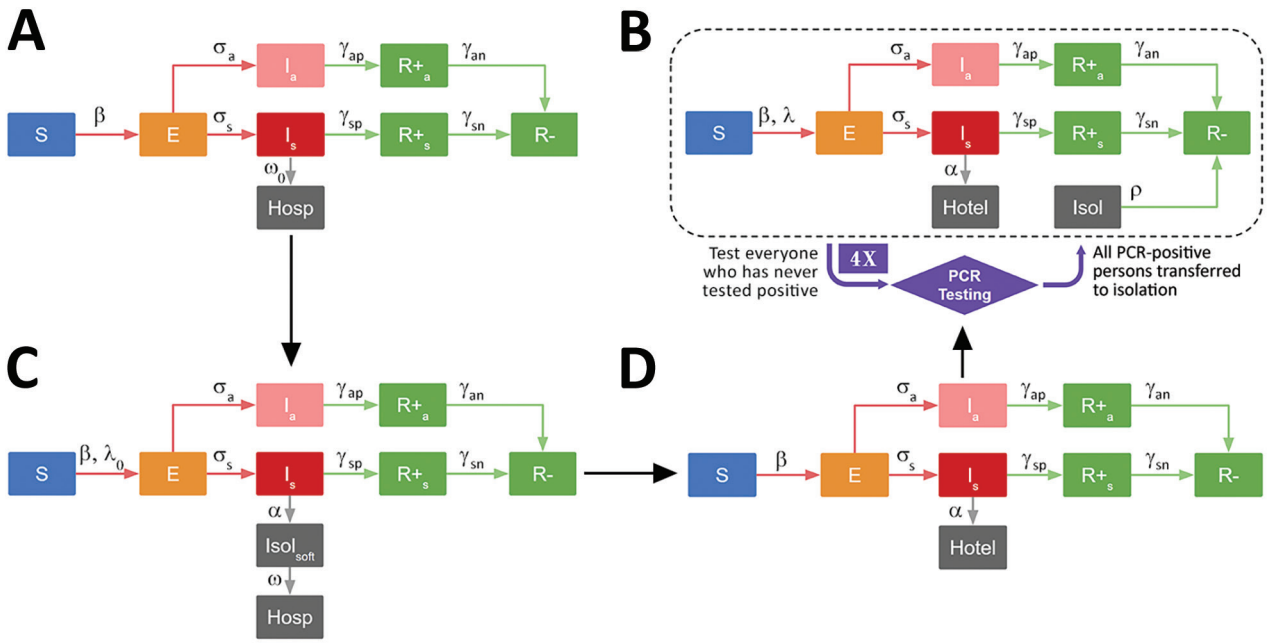

Figure 2. Sequential compartmental models corresponding to the 4 phases of the coronavirus disease outbreak response at Pacific Garden Mission, a homeless shelter in Chicago, Illinois, USA, 2020. A) Phase 1: prescreening (March 14–March 30); B) phase 2: symptom screening (March 30 – April 5) and temporary isolation; C) phase 3: hotel opening with continued symptom screening (April 5–8); D) phase 4: mass reverse transcription PCR testing rounds and isolation units (April 8–May 11). Corresponding description of compartments, systems of ordinary differential equations, and parameter descriptions are described in detail in the Appendix (https://wwwnc.cdc.gov/EID/article/28/1/21-0780-App1.pdf). E, Exposed; hosp, hospital; I, infectious; isol, isolation; R, recovered; S, susceptible

declined testing (or were not tested for other reasons) during each round; 8% (round 1), 6% (round 2), 1% (round 3), and 1% (round 4) of residents who were eligible for testing declined. Of the 322 residents tested during widespread testing rounds, 193 (60%) tested positive at some point. Of the 62 staff members tested, 17 (27%) tested positive (Figure 3, panel B). Of all persons who tested positive, 87% reported no symptoms at the time of testing.

Compartmental model trajectories are displayed for susceptible, exposed, infectious, recovered, and cumulatively infected persons over time (Figure 4). The 95% CIs of the trajectories are displayed based on model optimization across the 95% CI of initial transmission rate (β_0 = 0.60 [95% CI 0.45–0.74]). These results demonstrate widespread transmission in the early stages of the outbreak (phases 1–3); most cases were undetected before shelterwide testing, even after the implementation of screening measures in phase 2 (Appendix Figure 1). These results suggest that ≈350 persons were cumulatively infected, compared with the 253 cases detected by RT-PCR during the outbreak. This discrepancy is driven predominantly by persons who were infected (but whose illness was undetected) early in the outbreak who stopped shedding virus before mass testing. Model fitting yielded a R_0 of 4.5 (95% CI 2.7–4.8) (Appendix). Dependent model parameters are included (Table 3).

Discussion

In this study, we document a COVID-19 outbreak in a large homeless shelter involving a high number of residents; laboratory-confirmed SARS-CoV-2 infection was diagnosed in >50% of all residents and staff. Our results suggest that many others were infected before the availability of widespread testing, indicating that nearly all residents and staff were likely infected during this outbreak.

Our data represent comprehensive characterization of a COVID-19 outbreak and response in a large homeless shelter and highlight the potential for high transmission rates that could lead to rapid, exponential growth of COVID-19 outbreaks in closed, congregate settings. Our modeling results suggest that most cases were undetected before widespread testing (Figure 4; Appendix Figure 1), even after symptom screening measures began. As a result, the cumulative number of infections detected by the end of the outbreak was likely substantially underestimated.

Our modeling results yielded an R_0 value of 4.5, which is higher than R_0 estimated from analyses of early community spread (R_0 estimates 1.4–3.9) (*15*,*16*).

Table 1. Model parameters for fitting in study of transmission dynamics of coronavirus disease outbreak in homeless shelter, Chicago, Illinois, USA, 2020*

Fitted variables	Range of values fitted	Description of variable	Referenced ranges for fitting	Directly dependent model parameters	Dependent model phases	Dependent model compartments
β_0	0–445	Initial β	NA	β, R_0	1, 2, 3, 4	S, E
β_f_pct_β_0	0–1	Final β as percentage of β_0	NA	β	1, 2, 3, 4	S, E
k	0.01–2	Rate of transformation of β	NA	β	1, 2, 3, 4	S, E
t_{Trans}	1–50	Day where β reaches halfway between β_0 and β_f	NA	β	1, 2, 3, 4	S, E
Incubation period	2.8–4.0	Time between E and I compartments	(*8*)	σ	1, 2, 3, 4	E, Ia, Is
Asymptomatic percentage	0.18–0.87	Asymptomatic percentage	(*9*,*10*)	σ_s, σ_a, R_0	1, 2, 3, 4	E, Ia, Is
Infectious period for symptomatic persons, d	3–8	Infectious duration for symptomatic persons	(*11*,*12*)	Y_{sp}, R_0	1, 2, 3, 4	Is, $R+_s$
Infectious period for asymptomatic persons, d	3–8	Infectious duration for asymptomatic persons	(*11*,*12*)	Y_{ap}, R_0	1, 2, 3, 4	Is, $R+_a$
Period of RT-PCR–positivity for symptomatic persons, d	16–35	Duration of RT-PCR–positivity of symptomatic persons	(*13*,*14*)	Y_{sn}	1, 2, 3, 4	$R+_s$, $R–_s$
Period of RT-PCR–positivity for asymptomatic persons, d	3–35	Duration of RT-PCR–positivity for asymptomatic persons	(*13*,*14*)	Y_{an}	1, 2, 3, 4	$R+_a$, $R–_a$
α	0.01–1	Rate of detection of symptomatic infectious persons through screening	NA	α	2, 3, 4	Is, $Isol_{soft}$, Hotel
λ_0_pct_β	0–1	Rate of transmission between persons in $Isol_{soft}$ and S compartment, as a percentage of β	NA	λ_0	2, 3	S, E
λ_{isol}_pct_β	0–0.5	Rate of transmission between persons in isolation units and S compartment, as a percentage of β	NA	λ_{isol}	4	S, E
Isolation duration, d	14	Rate of return from isolation units to R compartment = 1/[14 d]†	NA	ρ	2, 3, 4	Isol, R
RT-PCR sensitivity	0.72–0.90	RT-PCR sensitivity	N.S. Padhye, unpub. data‡	–	1 and 2,§ 4	-
ω_0	0.05–1.0	Rate of hospital admission of Infectious symptomatic persons before screening	NA	ω_0	1	Is, Hosp
ω	0.05–1.0	Rate of hospital admission of $Isol_{soft}$ symptomatic persons during phase 2	NA	ω	2	$Isol_{soft}$, Hosp

*Details of optimization and calculation can be found in the Appendix (https://wwwnc.cdc.gov/EID/article/28/1/21-0780-App1.pdf). E, exposed; Ia, infectious asymptomatic; Is, infectious symptomatic; NA, not applicable; R+, recovered PCT-positive; R–, recovered PCR-negative; RT-PCR, reverse transcription PCR; R_0, basic reproduction number; S, susceptible.
†Value not fitted.
‡https://www.medrxiv.org/content/10.1101/2020.04.24.20078949v2.
§Fitting based on hospital-based test results.

Self-reported characteristics of Pacific Garden Mission staff and residents, Chicago, Illinois, USA, 2020

Characteristic	No. (%)
All	429 (100)
Role	
Resident	362 (83)
Staff member	67 (17)
Age group, y	
20–29	22 (5)
30–39	40 (10)
40–49	81 (20)
50–59	144 (35)
60–69	109 (26)
≥70	18 (4)
Sex	
M	301 (70)
F	131 (30)
Other	1 (0)
Race and ethnicity	
Non-Hispanic Black	266 (62)
Non-Hispanic White	92 (21)
Hispanic	48 (13)
Non-Hispanic Other	22 (5)
Smoking status	
Current smoker	133 (33)
Former smoker	112 (28)
Nonsmoker	156 (39)
Medical history	
Cardiovascular disease	85 (22)
Chronic lung disease	53 (13)
Diabetes mellitus	54 (14)
Neurologic disease	20 (5)
Chronic kidney disease	13 (3)
Immunocompromised	10 (3)
Chronic liver disease	7 (2)

This rate of transmission might be explained by the difficulty of social distancing in homeless shelters, as well as higher rates of medical conditions and older age that could increase susceptibility to infection. The rate of transmission is further exacerbated by the high rate of undetected infection. In this study, 87% of those with laboratory-confirmed SARS-CoV-2 infection reported no symptoms, similar to the proportion observed in other similar populations (*2*,*4*). This low reporting rate might reflect the high prevalence of background symptoms in persons experiencing homelessness that could mask COVID-19–related symptoms or could be related to distrust of healthcare providers (*17*,*18*). The consequence of this low rate of symptom reporting is a low rate of detecting of infection and transmission in the absence of shelter-wide RT-PCR testing.

These modeling data are, however, subject to limitations. Reported parameter estimates, including the duration of viral shedding, demonstrate high population variance and are not necessarily normally distributed (*19*). A study of 21 patients experiencing mild illness demonstrated repeated negative RT-PCR tests by 10 days after symptom onset (in 90% of the patients) (*20*), and another study of 56 patients with mild-to-moderate illness reported median duration of viral RNA shedding of 24 days (*14*). Furthermore, the underlying test data were limited by the availability of widespread testing; widespread testing of congregate settings was not established in Chicago until April 2020, and no widespread testing data were available to characterize phase 1 of this outbreak. Our model accounts for this early lack of testing and fits compartmental trajectories across the entire time span of the outbreak and uses known ranges for such parameters as infectious duration and RT-PCR–positive

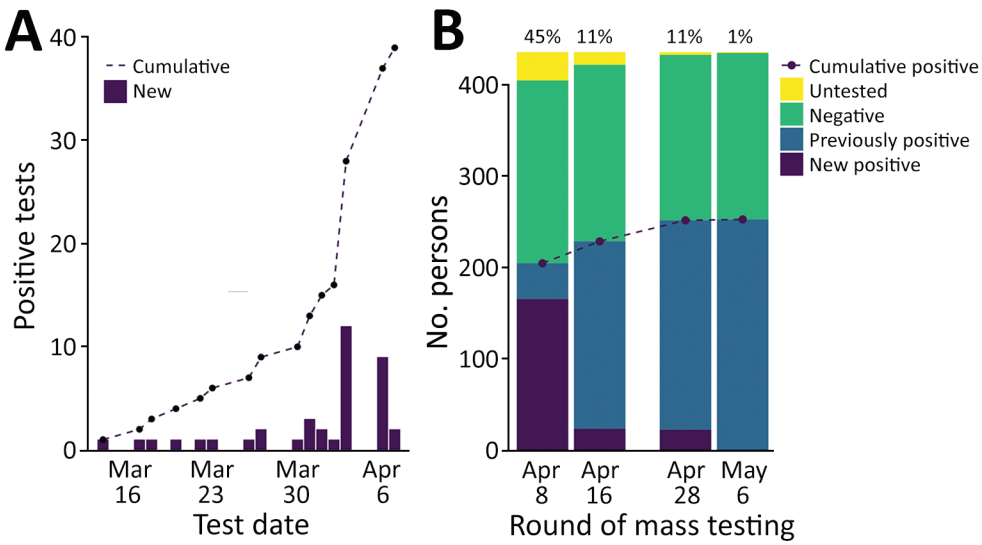

Figure 3. Coronavirus disease cases confirmed through reverse transcription PCR (RT-PCR) over time at Pacific Garden Mission, a homeless shelter in Chicago, Illinois, USA, 2020. A) Hospital-based positive tests before mass testing (March 14–April 7, 2020). Number of positive hospital-based RT-PCR tests per day (bars) and cumulatively (dashed line) are displayed for the period before mass testing. B) Results from each of 4 rounds of mass testing. Number of persons who were previously positive (and therefore not tested), newly positive, negative, and not tested for each round of mass RT-PCR testing are displayed; percentage of tests returning positive ($n_{positive}/n_{tested}$) are displayed above. During mass testing, 166 positive cases were detected in the first round, 24 positive cases were detected in the second round, 23 positive cases were detected in the third round, and 1 positive case was detected in the fourth round.

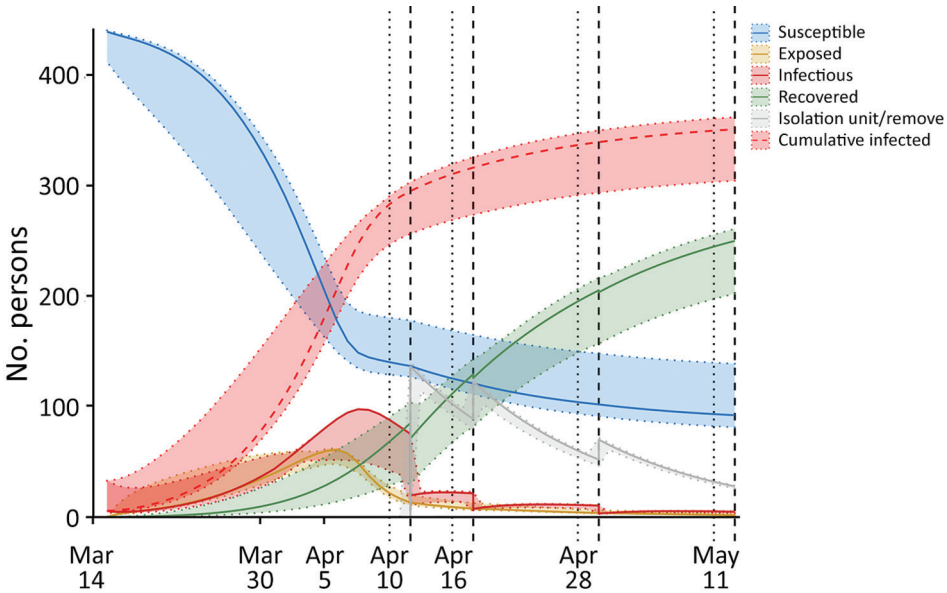

Figure 4. Compartmental modeling results of the coronavirus disease outbreak at Pacific Garden Mission, a homeless shelter in Chicago, Illinois, USA, 2020. The 4 phases of the outbreak are designated above the graph, and time points corresponding to each of the 4 rounds of mass testing and isolation are indicated by vertical dotted lines and vertical dashed lines. The susceptible compartment corresponds to persons who are estimated to have never been infected; exposed persons have been infected but are not yet infectious; infectious includes persons in both I_s and I_a; recovered include the $R+_s$, $R+_a$, and R– compartments; isolation unit/removed persons tested positive by reverse transcription PCR and either left the shelter or were moved to isolation units. The discontinuities in the isolation unit/removed, infectious, and recovered curves at each of the isolation time points (dotted lines) represent persons who tested positive by reverse transcription PCR (those in the I_s, I_a, $R+_s$, and $R+_a$ compartments) at the respective testing time point (dashed lines) being moved to the Isolation Unit compartment with each of the 4 rounds of mass testing. The 95% CIs for the compartments represent maximum and minimum values for each trajectory when reperforming model optimization with β_0 (initial transmission rate) fixed over its 95% CI (0.45–0.74) derived from initial model optimization (β_0 = 0.60). Corresponding description of compartments, systems of ordinary differential equations, and parameter descriptions are described in detail in the Appendix (https://wwwnc.cdc.gov/EID/article/28/1/21-0780-App1.pdf).

duration, but it inevitably simplifies some complexity of the context. This simplification, in addition to the large number of fitted parameters, requires cautious interpretation of fitted parameter values. Other limitations include the assumption of a closed system; although the shelter did not allow residents to enter or leave, some high-risk residents were preemptively moved to the hotel, and some residents did inevitably

Table 3. Fitted model parameter values in study of transmission dynamics of coronavirus disease outbreak in homeless shelter, Chicago, Illinois, USA, 2020*

Parameter	Fitted value	Description of parameter
β_0	0.60	Initial β
β_f_pct_β_0	0.11	Final β as percentage of β_0
k	2.0	Rate of transformation of β
t_{Trans}	23	Day where β reaches halfway between β_0 and β_f
σ_s	0.098	Rate of transition from E to Is compartment = 1/(incubation period) × (% symptomatic)
σ_a	0.26	Rate of transition from E to Ia compartment = 1/(incubation period) × (% asymptomatic)
Asymptomatic percentage	0.73	Asymptomatic percentage
Υ_{sp}	0.15	Rate of transition from Is to Rs+ compartment = 1/(infectious period for symptomatic persons)
Υ_{ap}	0.13	Rate of transition from Ia to Ra+ compartment = 1/(infectious period for asymptomatic persons)
Υ_{sn}	0.046	Rate of transition from Rs+ to R- compartment = 1/[(duration of RT-PCR–positivity) – (infectious period)] for symptomatic persons
Υ_{an}	0.12	Rate of transition from Ra+ to R- compartment = 1/[(duration of RT-PCR–positivity) – (infectious period]) for asymptomatic persons
α	0.32	Rate of detection of I symptomatic persons through screening
λ_0_pct_β	1	Rate of transmission between persons in $Isol_{soft}$ and Susceptible compartment, as a percentage of β
λ_{isol}_pct_β	1	Rate of transmission between persons in isolation units and Susceptible compartment, as a percentage of β
ρ	1/14 d*	Rate of return from isolation units to Recovered compartment = 1/[14 d]†
PCR sensitivity	0.90	RT-PCR sensitivity
ω_0	0.75	Rate of hospital admission of Infectious symptomatic persons before screening
ω	0.39	Rate of hospital admission of $Isol_{soft}$ symptomatic persons during phase 2

*Details of optimization and calculation can be found in the Appendix (https://wwwnc.cdc.gov/EID/article/28/1/21-0780-App1.pdf). E, exposed; I, infectious; RT-PCR, reverse transcription PCR.
†Value not fitted.

leave the shelter. In addition, some staff left the shelter and returned, and the model further assumes random mixing of the shelter population (outside of isolation units).

Our data reiterate the potential for high rates of SARS-CoV-2 transmission, which could result in large COVID-19 outbreaks in congregate settings, such as homeless shelters. Our data also reinforce the CDC recommendation to perform facilitywide RT-PCR testing and effective isolation in response to cases of COVID-19 in homeless shelters (https://www.cdc.gov/coronavirus/2019-ncov/community/homeless-shelters/testing.html). Isolating several hundred residents at PGM demonstrates the feasibility of establishing supported onsite isolation even within shelter settings, although offsite supported isolation centers have also been successfully used for persons experiencing homelessness (https://chhrge.org) (*21*,*22*). Establishing robust, proactive infection prevention practices, as recommended by CDC (https://www.cdc.gov/coronavirus/2019-ncov/community/homeless-shelters/plan-prepare-respond.html), and responding rapidly with a comprehensive testing and isolation protocol are crucial to keep persons residing in homeless shelters safe from COVID-19.

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About the Author

Ms. Chang is an MD/PhD candidate in bioengineering at the University of Illinois College of Medicine. Her research focuses on system's biological approaches to characterize and predict outcomes in immune-related disease.

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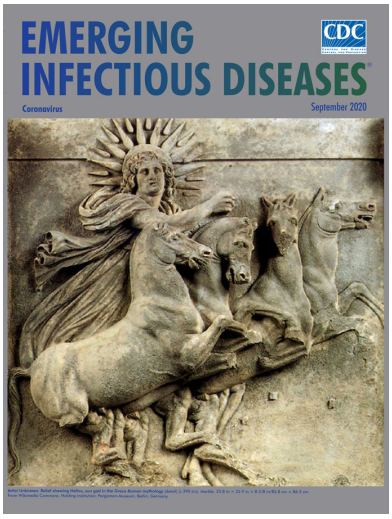

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Transmission Dynamics of Large Coronavirus Disease Outbreak in Homeless Shelter, Chicago, Illinois, USA, 2020

Appendix

Supplementary Methods: Model Construction

A total of 4 sequential compartmental models were constructed corresponding to the 4 phases of coronavirus disease (COVID-19) outbreak response at the Pacific Garden Mission homeless shelter in Chicago, Illinois, USA: phase 1: prescreening (March 14–30), phase 2: symptom screening (March 30–April 5) and temporary isolation, phase 3: hotel opening and continued symptom screening (April 5–8), phase 4: mass PCR testing rounds and isolation units (April 8–May 11) (Figure 2, https://wwwnc.cdc.gov/EID/article/28/1/21-0780-F2.htm).

Because transmission rate (β) varies as a function of the number of contacts per infectious person and probability of transmission given contact, it is expected to vary over time in our model because of removal of persons from the population (primarily into isolation units) and infection control measures. β at any given time point is thus calculated by using the transition equation below:

$$\beta = \beta_0 - \frac{\beta_0 - \beta_f}{1 + e^{(t - t_{Trans})/k}}, \text{ where}$$

β_0 corresponds to the initial transmission rate, $\beta_f = \beta_f_pct_\beta_0 \times \beta_0$ (where $\beta_f_pct_\beta_0$ corresponds to final transmission rate as a percentage of β_0), t_{Trans} represents the time point at which β reaches a value halfway between β_0 and β_f, and k represents the rate of transformation between initial and final β (Table 1, https://wwwnc.cdc.gov/EID/article/28/1/21-0780-T1.htm).

The phase 1 compartments are S (Susceptible), representing the number of uninfected persons; E (Exposed), representing the number of persons who have been infected but are not yet infectious; I_s (Infectious symptomatic), representing the number of persons who are infectious and symptomatic (or will become symptomatic); I_a (Infectious asymptomatic), representing

persons who are infectious and asymptomatic; $R+_s$ (Rps, Recovered symptomatic persons, PCR-positive), representing recovered symptomatic persons who are still PCR-positive; $R+_a$ (Rpa, Recovered asymptomatic persons, PCR-positive), representing recovered asymptomatic persons who are still PCR-positive; R– (Rn, Recovered, PCR-negative), representing persons who have recovered from infection; and Hospital (Hs), representing persons who tested positive through hospital-based PCR, most of whom were admitted. These are the ordinary differential equations (ODEs) for phase 1:

$$dS = -\beta \times S \times (Is+Ia)$$

$$dE = \beta \times S^*(Is+Ia) - \sigma s \times E - \sigma a \times E$$

$$dIs = \sigma s \times E - \Upsilon sp \times Is - \omega 0 \times Is$$

$$dIa = \sigma a \times E - \Upsilon ap \times Ia$$

$$dRps = \Upsilon sp \times Is - \Upsilon sn \times Rps$$

$$dRpa = \Upsilon ap \times Ia - \Upsilon an \times Rpa$$

$$dRn = \Upsilon sn \times Rps + \Upsilon an \times Rpa$$

$$dHs = \omega 0 \times Is$$

β: rate of transmission between Susceptible and Infectious persons

σ_s: rate of transition from E to $I_s = 1 / t_{incubation} \times p_{symp}$, $t_{incubation}$ = incubation period, p_{symp} = percent symptomatic

σ_a: rate of transition from E to $I_a = 1 / t_{incubation} \times p_{asymp}$, $t_{incubation}$ = incubation period, p_{asymp} = percent asymptomatic

Υ_{sp}: rate of transition from I_s to $R_{ps} = 1/t_{infectious_s}$, $t_{infectious_s}$ = infectious period of symptomatic persons

Υ_{ap}: rate of transition from I_a to $R_{pa} = 1/t_{infectious_a}$, $t_{infectious_a}$ = infectious period of asymptomatic persons

Υ_{sn}: rate of transition from R_{ps} to R- = $1/[t_{pcrPos_s} - t_{infectious_s}]$, t_{pcrPos_s} = duration of PCR positivity for symptomatic infected persons

Υ_{an}: rate of transition from R_{pa} to R- = $1/[t_{pcrPos_a} - t_{infectious_a}]$, t_{pcrPos_a} = duration of PCR positivity for asymptomatic infected persons

ω_0: rate of hospital admission of I_s

(Eq. 1) ODEs for phase 1

The phase 2 compartments are similar to phase 1, but with the addition of an $Isol_{soft}$ (Isolation dorms, labeled "Q" in ODEs) compartment because of the beginning of symptom screening. These are the ODEs for phase 2:

$dS = -\beta \times S \times (Is+Ia) - \lambda 0p\beta \times \beta \times S \times Q$

$dE = \beta \times S \times (Is+Ia) - \lambda 0p\beta \times \beta \times S \times Q - \sigma s \times E - \sigma a \times E$

$dIs = \sigma s \times E - \Upsilon sp \times Is - \alpha \times Is$

$dIa = \sigma a \times E - \Upsilon ap \times Ia$

$dRps = \Upsilon sp \times Is - \Upsilon sn \times Rps$

$dRpa = + \Upsilon ap \times Ia - \Upsilon an \times Rpa$

$dRn = \Upsilon sn \times Rps + \Upsilon an \times Rpa$

$dQ = -\omega \times Q + \alpha \times Is$

$dHs = \omega \times Q$

β: rate of transmission between Susceptible and Infectious persons

$\lambda 0p\beta$: rate of transmission between Susceptible and $Isol_{soft}(Q)$ persons, as a percentage of β

σ_s: rate of transition from E to $I_s = 1 / t_{incubation} \times p_{symp}$, $t_{incubation}$ = incubation period, p_{symp} = percent symptomatic

σ_a: rate of transition from E to $I_a = 1 / t_{incubation} \times p_{asymp}$, $t_{incubation}$ = incubation period, p_{asymp} = percent asymptomatic

Υ_{sp}: rate of transition from I_s to $R_{ps} = 1/t_{infectious_s}$, $t_{infectious_s}$ = infectious period of symptomatic persons

Υ_{ap}: rate of transition from I_a to R_{pa} = $1/t_{infectious_a}$, $t_{infectious_a}$ = infectious period of asymptomatic persons

Υ_{sn}: rate of transition from R_{ps} to R_n = $1/[t_{pcrPos_s} - t_{infectious_s}]$, t_{pcrPos_s} = duration of PCR-positivity for symptomatic infected persons

Υ_{an}: rate of transition from R_{pa} to R_n = $1/[t_{pcrPos_a} - t_{infectious_a}]$, t_{pcrPos_a} = duration of PCR-positivity for asymptomatic infected persons

α: rate of transition from I_s to Q

ω: rate of transition from Q to Hosp

(Eq. 2) ODEs for phase 2

The phase 3 compartments are similar to phase 2, but with the replacement of the Hospital (Hosp) and $Isol_{soft}(Q)$ compartments with Hotel (Ht) because of the opening of a hotel for homeless persons suspected to have COVID-19. All symptomatic PCR-positive persons were moved to the hotel upon a positive test. These are the ODEs for phase 3:

$dS = -\beta \times S \times (Is+Ia)$

$dE = \beta \times S \times (Is+Ia) - \sigma s \times E - \sigma a \times E$

$dIs = \sigma s \times E - \Upsilon sp \times Is - \alpha \times Is$

$dIa = \sigma a \times E - \Upsilon ap \times Ia$

$dRps = \Upsilon sp \times Is - \Upsilon sn \times Rps$

$dRpa = + \Upsilon ap \times Ia - \Upsilon an \times Rpa$

$dRn = \Upsilon sn \times Rps + \Upsilon an \times Rpa$

$dHt = + \alpha \times Is$

β: rate of transmission between Susceptible and Infectious persons

σ_s: rate of transition from E to I_s = $1 / t_{incubation} \times p_{symp}$, $t_{incubation}$ = incubation period, p_{symp} = percent symptomatic

σ_a: rate of transition from E to I_a = $1 / t_{incubation} \times p_{asymp}$, $t_{incubation}$ = incubation period, p_{asymp} = percent asymptomatic

Υ_{sp}: rate of transition from I_s to R_{ps} = $1/t_{infectious_s}$, $t_{infectious_s}$ = infectious period of symptomatic persons

Υ_{ap}: rate of transition from I_a to R_{pa} = $1/t_{infectious_a}$, $t_{infectious_a}$ = infectious period of asymptomatic persons

Υ_{sn}: rate of transition from R_{ps} to R_n = $1/[t_{pcrPos_s} - t_{infectious_s}]$, t_{pcrPos_s} = duration of PCR positivity for symptomatic infected persons

Υ_{an}: rate of transition from R_{pa} to R_n = $1/[t_{pcrPos_a} - t_{infectious_a}]$, t_{pcrPos_a} = duration of PCR positivity for asymptomatic infected persons

α: rate of transition from I_s to Hotel

(Eq. 3) ODEs for phase 3

The phase 4 compartments are similar to phase 3, but with the addition of the Isol compartment because of the implementation of Isolation Units for persons who tested positive during mass PCR screens. At each of the 4 isolation time points (2 days after each testing point), the number of persons in the I_s, I_a, R_{ps}, and R_{pa} compartments who are simulated to test positive ($Sensitivity_{PCR} \times n_{individuals\ in\ each\ compartment\ on\ test\ day}$) are moved to the Isol compartment. The phase 4 ODEs are thus propagated in 4 separate phases corresponding to the 4 testing rounds. These are the ODEs for phase 4:

$dS = -\beta \times S \times (Is+Ia) - \lambda \times S \times Isol$

$dE = \beta \times S \times (Is+Ia) - \lambda \times S \times Isol - \sigma s \times E - \sigma a \times E$

$dIs = \sigma s \times E - \Upsilon sp \times Is - \alpha \times Is$

$dIa = \sigma a \times E - \Upsilon ap \times Ia$

$dRps = \Upsilon sp \times Is - \Upsilon sn \times Rps$

$dRpa = + \Upsilon ap \times Ia - \Upsilon an \times Rpa$

$dRn = \Upsilon sn \times Rps + \Upsilon an \times Rpa$

$dHt = + \alpha \times Is$

$dIsol = - \rho \times Isol$

β: rate of transmission between Susceptible and Infectious persons

$\lambda p\beta$: rate of transmission between Susceptible and Isol persons, as a percentage of β

σ_s: rate of transition from E to $I_s = 1 / t_{incubation} \times p_{symp}$, $t_{incubation}$ = incubation period, p_{symp} = percent symptomatic

σ_a: rate of transition from E to $I_a = 1 / t_{incubation} \times p_{asymp}$, $t_{incubation}$ = incubation period, p_{asymp} = percent asymptomatic

Υ_{sp}: rate of transition from I_s to $R_{ps} = 1/t_{infectious_s}$, $t_{infectious_s}$ = infectious period of symptomatic persons

Υ_{ap}: rate of transition from I_a to $R_{pa} = 1/t_{infectious_a}$, $t_{infectious_a}$ = infectious period of asymptomatic persons

Υ_{sn}: rate of transition from R_{ps} to $R_n = 1/[t_{pcrPos_s} - t_{infectious_s}]$, t_{pcrPos_s} = duration of PCR positivity for symptomatic infected persons

Υ_{an}: rate of transition from R_{pa} to $R_n = 1/[t_{pcrPos_a} - t_{infectious_a}]$, t_{pcrPos_a} = duration of PCR positivity for asymptomatic infected persons

α: rate of transition from I_s to Hotel

ρ: rate of transition from Isol to $R_n = 1/t_{isolation}$, $t_{isolation}$ = duration of isolation (14 days)

(Eq. 4) ODEs for phase 4

Supplementary Methods: Model Fitting

We constructed a function to propagate all 4 model phases sequentially, and the *optim* function within the R programming language *stats* package was used to fit model parameters with the L-BFGS optimization algorithm. The L-BFGS optimization algorithm is a quasi-Newton algorithm chosen for its stability and efficiency in handling optimization problems with large numbers of parameters. Appendix Table 1 lists the data points, values, and weights by which root mean log squared error was minimized for model fitting. Ranges of values for each optimized variable were derived from the literature. For example, reverse transcription PCR sensitivity was fit between 0.72 and 0.9 on the basis of reported ranges (*1*). Asymptomatic percentage was fit between 0.18 and 0.87 on the basis of literature estimates (*2*,*3*), as well as our results from self-reported symptoms at time of specimen collection, which showed an

asymptomatic percentage of 87%. Infectious period (separately for symptomatic and asymptomatic persons) was fit to values between 3 and 8 days on the basis of a virologic analysis assessing duration of active severe acute respiratory syndrome coronavirus 2 replication in the upper respiratory tract (*4*). Duration of PCR-positivity was fit to values from 16 to 35 days for symptomatic persons and 3–35 days for asymptomatic persons on the basis of studies with repeated PCR testing of nasopharyngeal specimens (*5*,*6*). Table 1 lists the variables that were optimized, along with the range of values supplied as boundaries to the L-BFGS optimization algorithm and the dependent model parameters. The optimization converged successfully within 500 iterations. Table 3 (https://wwwnc.cdc.gov/EID/article/28/1/21-0780-T3.htm) lists the fitted model parameter values, and Appendix Figure 2 displays the modeled data points against real data points.

Standard error of transmission rate (β_0), which is the most critical and uncertain parameter in our model, was derived as the square root of the diagonal elements of the inverse (negative) Hessian matrix evaluated at the optimum parameter values (*7*) (the Hessian matrix is returned by the *optim* function in R); the 95% CI of β_0 was thus calculated as 0.45–0.74. The Hessian derivation of CIs is only valid when the optimum parameter values are in the interior of the parameter space. This was not the case for all of our parameters, because we imposed certain narrow constraints on the basis of values reported in the literature, such as incubation period, infectious duration, and asymptomatic percentage. CIs for the basic reproduction number (R_0) were thus generated by reperforming model optimization with β_0 (initial transmission rate) fixed at equally spaced values over its 95% CI derived from initial model optimization. The R_0 CIs represent maximum and minimum values across all iterations (n = 20 equally spaced values of β_0 from 0.45–0.74) of this model optimization.

Because a bootstrapping strategy was not viable with our dataset (relatively few input data points, with certain data points of critical importance for modeling [i.e., number of positive cases from the 1st round of widespread PCR testing]), CIs for the trajectories of the different compartments were estimated in a similar manner to calculation of R_0 CIs. These intervals are represented as the maximum and minimum trajectory values across all iterations of model optimization with β_0 fixed across its 95% CI (Figure 4).

To characterize collinearity between fitted parameter values, we added noise to the input data to which our model was fitted and reperformed optimization 100 times. For each optimization, each input data point (e.g., number of PCR-positive persons during the first round of widespread PCR testing) was independently perturbed by adding a random percentage to the original data point, sampled randomly from a uniform distribution from −20% to 20%. The resultant data points used for fitting were each between 80% and 120% of their original values. We then correlated the fitted parameter values from the 100 rounds of optimization in a pairwise fashion to identify collinear parameters. Expected pairs of parameters were correlated, including an inverse correlation between symptomatic infectious period and symptomatic PCR-positive period (Pearson's correlation coefficient, $R = -0.44$); these collinearities are expected, because they contribute to the total period during which persons will test positive. However, the initial transmission rate (β_0) was only significantly correlated with symptomatic infectious period ($R = -0.23$), which was narrowly constrained in our model between 3 and 8 days. Further, the R_0 was not significantly correlated with any of the modeled parameters except for β_0.

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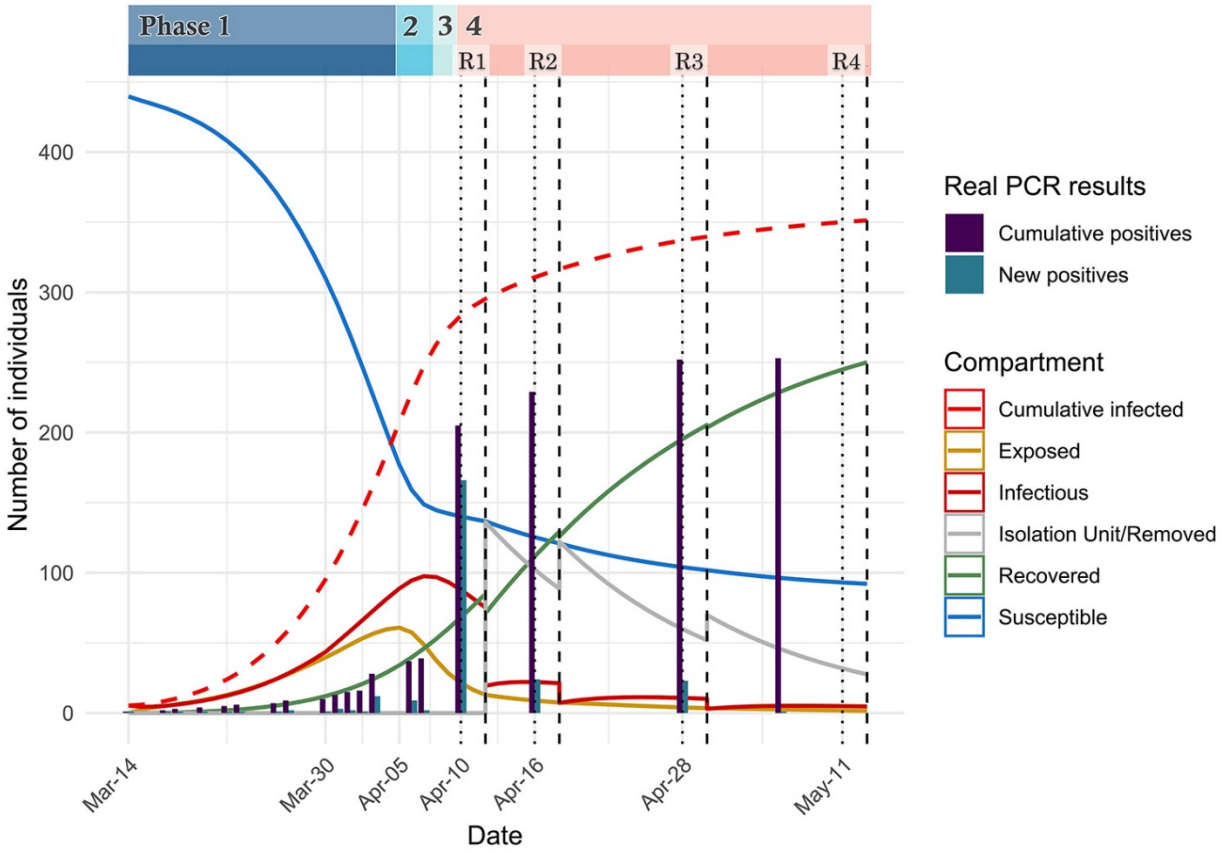
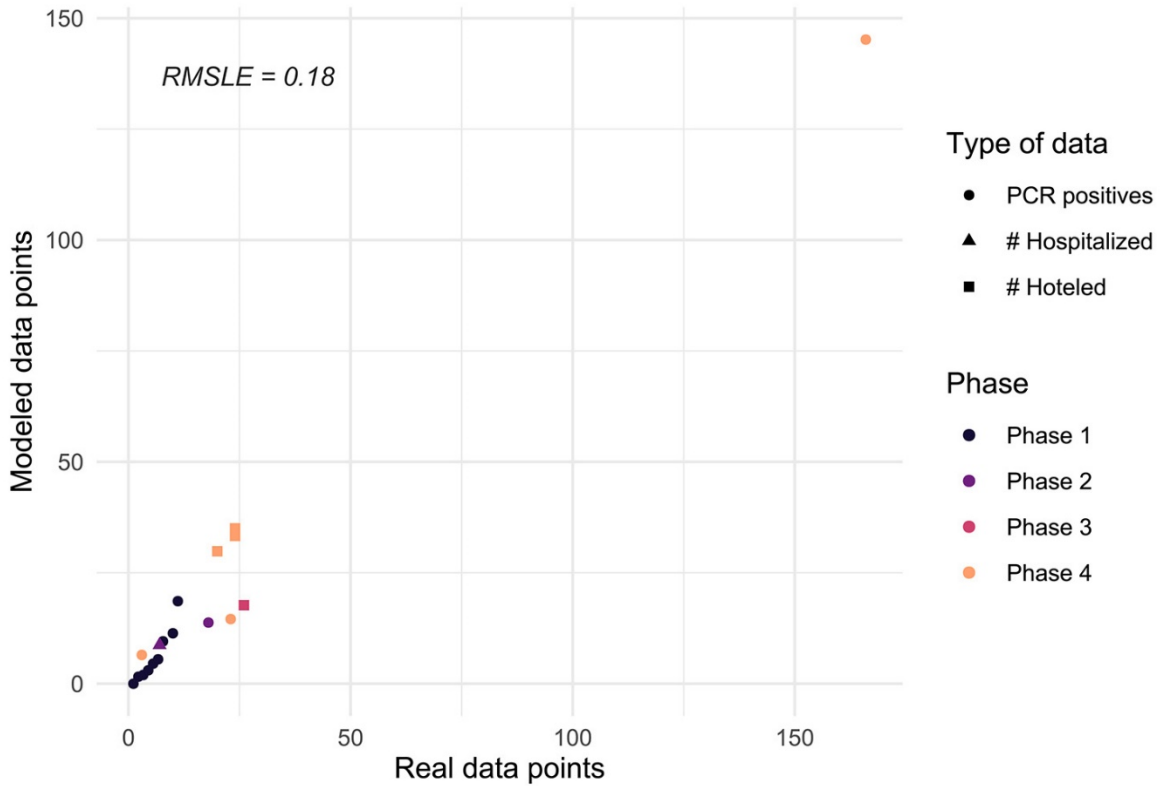
Appendix Table. Datapoints for model fitting in study of transmission dynamics of coronavirus disease outbreak in homeless shelter, Chicago, Illinois, USA, 2020

Phase	Datapoints	Values	Weight
Phase 1	Cumulative no. hospital-based PCR positives per day during March 14–30	1–10	1 (summed across dates)
Phase 2	No. persons who tested positive by PCR during phase 2 (Apr 5)	18	1
	No. persons who were admitted to the hospital during phase 2	7	1
Phase 3	No. persons moved to hotel	26	1
Phase 4	No. positives in each of 4 rounds of mass PCR testing	166, 24, 23, 1	2 (summed across 4 rounds)
	No. persons moved to hotel between rounds of mass testing	20 (between 1 and 2), 4 (between 2 and 3), 0 (between 3 and 4)	1 (summed across 3 periods)



Appendix Figure 1. Compartmental modeling results superimposed with real PCR data from coronavirus disease outbreak at homeless shelter, Chicago, Illinois, USA. Compartmental modeling results (Figure 4, https://wwwnc.cdc.gov/EID/article/28/1/21-0780-F4.htm) are superimposed with real PCR testing data, including both incident and cumulative positive cases. Positive cases before phase 4 were ascertained through hospital-based PCR testing of symptomatic persons, whereas positive cases during phase 4 represent positive results from shelter-wide testing. The gap between the cumulative positive tests (real data represented by bar plots) and the modeled cumulative infections primarily represent persons who were infected (but whose illness was not detected) early in the outbreak and recovered before mass PCR testing.



Appendix Figure 2. Modeled data points compared with real data points in study of transmission dynamics of coronavirus disease outbreak in homeless shelter, Chicago, Illinois, USA, 2020. Real data points from hospital-based PCR, shelter-wide PCR testing, and numbers of persons hospitalized or moved to the hotel are plotted against data points yielded by model fitting (Appendix Table 1). The minimized RMSLE was minimized at a value of 0.18. RMSLE, root mean square log error.