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Brief communication

Estimation of COVID-19 basic reproduction ratio in a large urban jail in the United States

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A R T I C L E I N F O

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ABSTRACT

Purpose: To estimate the basic reproduction ratio () of SARS-CoV-2 inside a correctional facility early in the COVID-19 pandemic.

Methods: We developed a dynamic transmission model for a large, urban jail in the United States. We used the next generation method to determine the basic reproduction ratio We included anonymized data of incarcerated individuals and correctional staff with confirmed COVID-19 infections in our estimation of the basic reproduction ratio () of SARS-CoV-2.

Results: The estimated is 8.44 (95% Credible Interval (CrI): 5.00-13.13) for the entire jail. *Conclusions*: The high of SARS-CoV-2 in a large urban jail highlights the importance of including

correctional facilities in public health strategies for COVID-19. In the absence of more aggressive mitigation strategies, correctional facilities will continue to contribute to community infections.

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Introduction

Jails are epicenters of COVID-19 transmission in the United States. Early in the pandemic, Cook County Jail had one of the largest cluster outbreaks in the country, and the infection rate at Rikers Island was nearly five times that of New York City. With 11 million new admissions yearly, jails present an ideal setting for infections to spread. Incarcerated individuals are at higher risk for infection due to unsanitary living conditions and inability to so-cially distance [1]. Furthermore, correctional officers rarely have public health training, and correctional health systems are chronically underfunded.

The conditions making correctional facilities prone to disease outbreaks have long been present. In 1918, a person infected with the H1N1 virus caused a massive outbreak in California's San Quentin prison. The basic reproduction ratio (R_0) for the virus was

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estimated to be close to three in the prison population, far higher than for the general population [2]. Yet, jails remain largely excluded from public health strategies to mitigate the spread of infectious diseases. For example, in the 2009 H1N1 pandemic, more than half of jails did not receive vaccine supplies [3]. Further, the Centers for Disease Control and Prevention (CDC) guidelines do not classify correctional officers as first responders, despite the fact that they come into "close contact with persons with confirmed or possible COVID-19 in the course of their work [4]."

We estimate the R_0 of the novel SARS-CoV-2 virus in a large urban jail in the United States. This estimate can help inform public health policies toward mitigation of COVID-19 in correctional systems.

Methods

We used a dynamic transmission model to calculate R_0 for a large urban jail in a U.S. city with an ongoing COVID-19 outbreak. The model is a modified SEIR model and includes the following COVID-19 disease states: susceptible (*S*), exposed (*E*), infected symptomatic (I_{sym}), infected asymptomatic (I_{asym}), quarantined (*Q*), hospitalized (*H*), recovered (*Rec*), and dead (*Dead*).





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Individuals enter the jail as susceptible at a net rate *b*. Susceptible individuals become exposed at rate β due to contact with infected symptomatic or asymptomatic individuals. Exposed individuals are infected but not yet infectious and transition to either symptomatic or asymptomatic infection at rate ε . The proportion of infected individuals who are asymptomatic is represented by α . We assume that infected individuals who are symptomatic will be moved to quarantine after one day, while those who are asymptomatic will not be moved to quarantine. All infected individuals recover at rate γ . Infected individuals who are in quarantine either recover or become hospitalized with probability η . Those who are hospitalized recover from hospitalization at rate λ . Equations (1)-(9) define the model.

$$\frac{dS}{dt} = bS - \frac{\beta S}{N} \left(I_{sym} + I_{asym} \right) \tag{1}$$

$$\frac{dE}{dt} = bE + \frac{\beta S}{N} \left(I_{sym} + I_{asym} \right) - \varepsilon E$$
(2)

$$\frac{dI_{sym}}{dt} = (1 - \alpha)\varepsilon E - I_{sym} \tag{3}$$

$$\frac{dI_{asym}}{dt} = bI_{asym} + \alpha \varepsilon E - \gamma I_{asym} \tag{4}$$

$$\frac{dQ}{dt} = I_{sym} - (1 - \eta)\gamma Q - \eta \left(\frac{1}{\gamma} - \frac{1}{\mu}\right)^{-1} Q$$
(5)

$$\frac{dH}{dt} = \eta \left(\frac{1}{\gamma} - \frac{1}{\mu}\right)^{-1} Q - \mu H \tag{6}$$

$$\frac{dRec}{dt} = (1 - d_I)(1 - \eta)\gamma Q + (1 - d_I)\mu H + \gamma I_{asym}$$
(7)

$$\frac{dDead}{dt} = d_I(1-\eta)\gamma Q + d_I\mu H \tag{8}$$

$$N = S + E + I_{svm} + I_{asvm} + Q + H + Rec$$
(9)

We parameterized our model using data from the jail and previous estimates from the literature (Table 1). The jail tracked demographics and location of those who were symptomatic daily, regardless of test results, and those who tested positive for SARS-Co-V-2.

To calibrate the transmission rate in the jail, we used 1000 Monte Carlo simulations. In each simulation, we pseudo-randomly selected a value for ε , α , and γ based on lognormal, uniform, and truncated normal distributions, respectively. For the selected parameter set, we calibrated the best-fitting value of β using an

Table 1	
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Parameter estin	nates
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exhaustive search over all values [0, 4] in increments of 0.01. We determined the best fit as the value of β which minimizes the mean squared error when comparing a five-day moving average of the incidence of symptomatic cases in the model to the daily incidence reported by the jail. Although we had thirty days of data since the outbreak began, we decided to calibrate our model using only the first eleven days of the outbreak, given that the jail implemented major interventions that may have impacted the R_0 on day twelve.

To determine R_0 , we used the next-generation method [10]. We define two matrices F and V. F describes the rate of appearance of new infections and V describes the rate of transfer of individuals in and out of compartments by all other means (Equations (10) and (11)).

$$\begin{bmatrix} 0 & 0 & 0 & -\eta \left(\frac{1}{\gamma} - \frac{1}{\mu}\right)^{-1} & \mu \end{bmatrix}$$
(11)

 R_0 is the dominant eigenvalue of the next-generation matrix, FV^{-1} . We used the preinfection susceptible population of the entire jail.

Results

Thirty days after the COVID-19 outbreak began, 5.6 percent of those incarcerated and 7.8 percent of staff had symptomatic COVID-19 infections. The mean age of incarcerated people infected with COVID-19 was 37.9 years \pm 13.6 years standard deviation, and the median length of incarceration was 233 days, interquartile range 93–475 days. The mean age of staff infected with COVID-19 was 44.9 years \pm 9.1 years.

After model calibration, the mean $\beta = 1.79$ (95%Credible Interval (CrI): 1.35, 2.22), and the estimated R_0 =8.44 (95% CrI:5.00, 13.13). The effective reproduction ratio would remain above 1 until day 30 of the outbreak. At this point, the outbreak would begin to subside largely due to a decrease in the susceptible population. For an

Name	Description	Value	Source
b	Net rate of entrance into the jail [1/day]	-0.004	Jail dataset
β	Transmission rate [1/day]		Calibrated
ε	Incubation period ⁻¹ [1/day]	0.18, Lognormal(5.1, 0.89)	Lauer et al.[5]
α	Proportion of cases that are asymptomatic	0.405, Uniform(0.25, 0.56)	Estimates from other prisons and jails[6,7]
γ	Recovery rate [1/day]	0.1, Infection period:	Rocklov, Sjödin, and Wilder-Smith[8]
		Truncated Normal (10, 6.25, min5, max20)	
η	Proportion of symptomatic infections that are hospitalized	0.14	Jail dataset
μ	Recovery rate from hospital [1/day]	0.2 Length of hospitalization: Lognormal(5, 1)	Thevarajan et al.[9]
d _I	Probability of death due to symptomatic infection	0.01	Jail dataset

outbreak of this magnitude, we predict 5695 cases in the jail over 30 days. This would result in 3388 symptomatic infections, 474 hospitalizations, and 34 deaths.

Discussion

This is the first estimation of an R_0 for COVID-19 in a large jail system. Notably, it is of higher magnitude to that reported for other congregate settings, such as the Diamond Princess cruise ship, despite the younger age of those incarcerated [11]. Further, although they are not considered first responders by the CDC, correctional staff are also significantly impacted by and exposed to COVID-19.

Our estimation has several limitations. We estimated R_0 based on a dynamic transmission model, which assumes homogeneous mixing within the population, but jails are transient and heterogeneous places. Also, parameter values and distributions may differ between a jail population and the populations of previous studies.

These limitations notwithstanding, our R_0 estimate indicates that outbreaks of COVID-19 in correctional facilities will continue and community rates of infection will not decrease if jails are not a central focus of public health strategies to mitigate the spread of the epidemic. Such measures would include wide-scale testing in jails inclusive of correctional officers [12], providing protective equipment and public health education for correctional officers as first responders, and coordinating large-scale release of individuals from jails to allow for adequate social distancing prior to future outbreaks.

CRediT authorship contribution statement

Lisa B. Puglisi: Conceptualization, Methodology, Resources, Writing - original draft, Writing - review & editing. Giovanni S.P. Malloy: Formal analysis, Methodology, Writing - original draft, Writing - review & editing. Tyler D. Harvey: Methodology, Writing - original draft, Writing - review & editing, Project administration. Margaret L. Brandeau: Methodology, Formal analysis, Writing original draft, Supervision. Emily A. Wang: Conceptualization, Methodology, Resources, Writing - original draft, Writing - review & editing, Supervision.

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References

- [1] Bick JA. Infection control in jails and prisons. Clin Infect Dis 2007;45(8): 1047-55.
- [2] Vynnycky E, Trindall A, Mangtani P. Estimates of the reproduction numbers of Spanish influenza using morbidity data. Int J Epidemiol 2007;36(4):881–9.
- [3] Receipt of A(H1N1) pdm09 Vaccine by Prisons and Jails United States, 2009–10 Influenza Season. https://www.cdc.gov/mmwr/preview/mmwrhtm l/mm6051a3.htm. [Accessed 26 April 2020].
- [4] CDC. Coronavirus Disease 2019 (COVID-19). Centers for Disease Control and Prevention. https://www.cdc.gov/coronavirus/2019-ncov/hcp/guidance-forems.html. [Accessed 26 April 2020].
- [5] Lauer SA, Grantz KH, Bi Q, Jones FK, Zheng Q, Meredith HR, et al. The incubation period of Coronavirus disease 2019 (COVID-19) from publicly reported confirmed cases: estimation and application. Ann Intern Med 2020;172: 577–82.
- [6] Oran DP, Topol EJ. Prevalence of asymptomatic SARS-CoV-2 infection: a narrative review [Epub ahead of print]. Ann Intern Med 2020;173:362–7.
- [7] Arons MM, Hatfield KM, Reddy SC, Kimball A, James A, Jacobs JR, et al. Presymptomatic SARS-CoV-2 infections and transmission in a skilled nursing facility. N Engl J Med 2020;382(22):2081–90.
- [8] Rocklöv J, Sjödin H, Wilder-Smith A. COVID-19 outbreak on the diamond princess cruise ship: estimating the epidemic potential and effectiveness of public health countermeasures. J Trav Med 2020;27:taaa030.
- [9] Thevarajan I, Nguyen THO, Koutsakos M, Druce J, Caly L, van de Sandt CE, et al. Breadth of concomitant immune responses prior to patient recovery: a case report of non-severe COVID-19. Nat Med 2020;26(4):453–5.
- [10] Diekmann O, Heesterbeek JA, Metz JA. On the definition and the computation of the basic reproduction ratio R0 in models for infectious diseases in heterogeneous populations. J Math Biol 1990;28(4):365–82.
- [11] Zhang S, Diao M, Yu W, Pei L, Lin Z, Chen D. Estimation of the reproductive number of novel coronavirus (COVID-19) and the probable outbreak size on the Diamond Princess cruise ship: a data-driven analysis. Int J Infect Dis 2020;93:201–4.
- [12] Gandhi M, Yokoe DS, Havlir DV. Asymptomatic transmission, the Achilles' heel of current strategies to control Covid-19. N Engl J Med 2020;382:2158–60.