Supplementary Appendix

This appendix has been provided by the authors to give readers additional information about their work.

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SUPPLEMENTARY APPENDIX

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Risk Factors for SARS-CoV-2 in a Statewide Correctional System

BACKGROUND

Following a respiratory disease outbreak in Wuhan, China, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) was confirmed as the pathogen causing novel coronavirus disease 2019 (COVID-19). [1] Prior reports have suggested that congregate settings are high-risk environments for the transmission and complications of COVID-19, but multivariate analyses identifying risk factors in these populations are lacking. [2 3 4 5 6 7 8] Worldwide, about 10.4 million individuals are incarcerated with the most being in the United States (about 2.2 million), many of whom are medically vulnerable due to preexisting chronic conditions and at high-risk for infectious diseases, including COVID-19. [9 10 11 12] In this study, we performed multivariate analyses to identify individual and facility-level risk factors associated with SARS-CoV-2 prevalence and outcomes in a statewide correctional population that underwent nearly universal testing.

METHODS

Study Population

The Connecticut Department of Correction (CTDOC) is an integrated correctional system that includes prisons and jails, which house mainly sentenced and unsentenced inmates, respectively. CTDOC is comprised of 17 facilities located throughout the state with a combined average daily census of nearly

ten thousand. Onsite clinical staff provide general medical care to the inmate patient population, with outside referrals made as needed for emergency and/or specialty care.

Laboratory Testing

In March 2020, CTDOC issued initial clinical guidelines for COVID-19 testing of symptomatic patients (e.g., fever, cough, shortness of breath). For suspected cases, nasopharyngeal specimens were collected and real-time reverse transcriptase-polymerase chain reaction (rRT-PCR) for SARS-CoV-2 was performed by Quest Diagnostics Laboratory. [13] [14] On March 13th, the first confirmed COVID case among CTDOC inmates was identified. Since the initial roll-out of clinical guidelines for the agency, symptom-based testing has been ongoing. However, in mid-May, mass testing began of all assenting inmates and continued through the end of June, with final follow-up through mid-July. By the end of this point-prevalence survey, the cumulative total tested was 10,304.

Data Variables

This study considered the following outcomes: SARS-CoV-2 prevalence; subsequent hospitalization; intensive care unit (ICU) admission; and death. Potential covariates included age, sex, race/ethnicity and chronic conditions identified through the electronic health record (hypertension, heart disease [coronary artery disease, congestive heart failure, atrial fibrillation], diabetes mellitus, lung disease [asthma, chronic obstructive pulmonary disease, chronic fibrosis], liver disease, cancer, HIV, autoimmune disease [systemic lupus erythematosus, rheumatoid arthritis, inflammatory bowel disease, multiple sclerosis]) as well as body mass index. Facility-level factors were also considered: type of

facility (prison, jail, or both) and predominant housing category at a given facility (cell, dormitory, or both).

Follow-up

For the study population, individuals had 14 or more days of follow-up. Laboratory-confirmed SARS-CoV-2 cases were considered recovered if they were afebrile without antipyretics for at least 72 hours, other symptoms had improved, and it had been at least 14 days since symptom onset, or 14 days since testing if asymptomatic.

Data Analysis

To determine the risk factors associated with each outcome, logistic regression analysis was performed using Stata version 12 (College Station, Texas, 2011). First, odds ratios (ORs) and 95% confidence intervals (CIs) were determined for each outcome and covariate combination using the "*penlogit*" command for penalized likelihood estimation as previously described (univariate fixed effects). [15] For example:

penlogit outcome1 covariate1, or

Second, all covariates with an OR 95% CI excluding one were entered into a multivariate model for the given outcome (multivariate fixed effects). For example:

penlogit outcome1 covariate1 covariate2, or

Third, random-effects intercept terms for housing and facility were added to these multivariate models in order to account for potential clustering in the data (multivariate mixed effects) using the "*xtmelogit*" command. For example:

xtmelogit outcome1 covariate1 covariate2 || cluster1: || cluster2: , or

These models were compared with corresponding multivariate models that included only one random-effects intercept term—that is, for facility. The latter models showed better fit with the data, based on lower AIC and BIC values. Therefore, these were the final multilevel models and associations are reported as ORs with 95% CIs. The widths of confidence intervals have not been adjusted for multiplicity and should not be used to draw inferences about definite associations. Regression models for the outcome, SARS-CoV-2 prevalence, included the male study population only (n = 9,699), since no female inmates tested positive. For the hospitalization, ICU admission, and death outcomes, the regression models included only those individuals testing positive for SAR-CoV-2 (n = 1,240).

RESULTS

The number tested for SARS-CoV-2 increased steadily once mass screening began in mid-May (Figure S1), for a cumulative total 10,304. Based on the daily census population at the start of the study, this represents a testing percentage of about 84%. Baseline characteristics of the tested population are shown in Table S1. We identified 1,240 individuals (12%) who tested positive for SARS-CoV-2 and none were female. The positivity rate was higher during the symptom-based-only testing phase (Figure S1).

Among the SARS-CoV-2 positive males, there were: 62 hospitalizations (5%), 20 ICU admissions (1.6%), and 7 deaths (0.6%).

The logistic regression analyses are summarized in Table S2. The strongest risk factor of SARS-CoV-2 prevalence was dormitory-based housing (OR 35.3, 95% CI 7.9 – 157). Hispanic/Latino ethnicity (OR 1.4 [1.2 – 1.6]) and increasing age (OR 1.2 per decade [1.1 – 1.2]) increased the likelihood of positivity. Among positive cases, the strongest predictor of hospitalization was preexisting heart disease (OR 7.2 [2.8 – 18.5]). Increasing age (OR 2.3 [1.9 – 2.9]) and dormitory housing (OR 0.22 [0.06 – 0.74]) were also associated with hospitalization. Autoimmune disease (OR 13.5 [2.2 – 82.6]), heart disease (OR 7.7 [1.8 – 33.6]), and age (OR 2.4 [1.6 – 3.5]) predicted ICU admission. The only risk factor associated with death was age (OR 3.3 [1.7 – 6.3]).

DISCUSSION

There were a number of important findings in this study. Surprisingly, while more than six hundred female inmates were tested, not a single confirmed case of SARS-CoV-2 was identified. The reasons for this are unclear. At CTDOC, all female inmates are housed in a single facility and, therefore, do not transfer between other facilities, unlike those housing male inmates, which have frequent transfers. Consequently, this may have reduced the likelihood of introducing SARS-CoV-2 into the facility. Additionally, given its structural design, the inmates at this facility may have more outdoor exposure, restricted movement between housing units, and space to promote social distancing.

Among males, we found that the strongest risk factor for SARS-CoV-2 prevalence was residing in a facility that primarily housed inmates in dormitory units. This finding may suggest that social distancing

in the former is more challenging. A previous report of inmates observed that the prevalence of SARS-CoV-2 was higher in dormitory-based than cell-based housing, but statistical testing was not performed due to the heterogeneous data sources. [8] Together, our data support current guidelines from the Centers for Disease Control and Prevention (CDC) that call for preferentially using cells, when available and feasible, for medical isolation and quarantine, to reduce SARS-CoV-2 transmission risk. [16] We also observed that dormitory-based housing was protective for hospitalization. This may suggest that sicker inmates from dormitories were identified early and housed in cells prior to testing and subsequent hospitalization.

Interestingly, we found race/ethnicity only weakly associated with SARS-CoV-2 infection but not associated with subsequent outcomes. Others have reported stronger associations by comparing the racial/ethnic proportions of SARS-CoV-2 cases with corresponding proportions in the general population from counties identified as hotspots. [17] However, the estimates of association from this prior study were not derived from population-based testing designs and, therefore, may have been subject to bias. Nevertheless, our findings may suggest that the testing and prevention efforts at CTDOC, as an integrated correctional system, reduced potential disparities compared with the general population.

This study found age weakly associated with SARS-CoV-2 positivity and moderately associated with all SARS-CoV-2 outcomes examined. Prior multivariate analyses have observed an increased risk of serious illness and complications from COVID with increasing age. [18] [19] [20] To our knowledge, the current study is the first published report demonstrating an effect of age on the likelihood of SARS-CoV-2 infection for a congregate population that underwent nearly universal testing not part of an outbreak investigation.

Importantly, of the conditions considered, only preexisting heart and autoimmune diseases were found to be associated with SARS-CoV-2 outcomes. Indeed, heart disease strongly predicted subsequent hospitalization and ICU admission; while autoimmune disease very strongly predicted ICU admission. These findings are consistent with previous reports suggesting more serious SARS-CoV-2 complications for individuals with these two conditions. [19] [21] The lack of other comorbidities identified as predictors may reflect the younger age distribution in our study population. Further, our COVID cases were closely monitored at their facilities, including 24-hour nursing and daily clinician availability, with interventions (e.g., supplemental oxygen, EKG) provided as medically indicated. Notably, the crude case fatality rate for CTDOC was less than that from correctional facilities nationwide (0.6% vs 1.3%). [4]

The prevalence of some chronic conditions was somewhat lower when compared with data from a national survey of incarcerated persons but similar to standardized general population estimates. [11] The prior investigation's reliance on inmate self-reports rather than medical chart review may have contributed to these observed differences. Additionally, during the current COVID pandemic in Connecticut, fewer individuals have been incarcerated and eligible inmates have been released early from CTDOC, in part, due to their medical vulnerability.

This study has several potential limitations. First, data were not available for correctional staff, who may serve as potential sources of COVID exposure to inmates. However, CTDOC took steps to mitigate this impact, including temperature checks and symptom screening of all staff before entry into a facility. Further, staff and inmates were provided with facemasks and required to wear them, especially when social distancing was not possible following an order from the governor of Connecticut, while group activities and external visits were suspended. Second, the possibility of missing prior asymptomatic cases that already cleared the virus at the time of testing cannot be excluded. Inmates who were COVID

positive and/or symptomatic were medically isolated for 14 days; exposed inmates were medically quarantined for 14 days in a different location. Together, these and other measures likely reduced the risk of spread, even among those not identified through testing. Third, the findings reported here may not be generalizable to all correctional facilities. However, our testing percentage was greater than 80%, which reduced the risk of selection bias, and the statistical analysis minimized the likelihood of spurious associations.

The experience of CTDOC suggests that both inmate and facility-level factors are associated with SARS-CoV-2. For correctional facilities in the United States as well as other countries, taking steps to ensure social distancing in dormitory housing, along with testing will likely enhance prevention efforts. Additionally, identifying medically vulnerable inmates with SARS-CoV-2, including the elderly and/or those with cardiac and autoimmune conditions, will allow for closer monitoring and prompt intervention for those at high-risk for clinical deterioration.

IDENTIFYING DATA

One of the authors (BSK) performed the data analysis. All authors had access to the data as well as autonomy regarding this study's conception, analysis, interpretation, and manuscript writing. This work was conducted as part of CTDOC's public health response to the COVID-19 pandemic and did not require research protocol IRB approval.

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TABLE S1. Baseline Characteristics of Study Population, Connecticut Department of Correction, 2020.

Variable	Total = 10,304 N (%)
Age, years	
Mean (± SD)	38.0 (±11.8)
Sex	
Male	9,699 (94)
Female	605 (6)
Race/Ethnicity*	
White	2,895 (28)
Black/African American	4,526 (44)
Hispanic/Latino	2,804 (27)
Other	79 (1)
Chronic comorbidities	
Hypertension	1,627 (16)
Heart disease	294 (3)
Diabetes mellitus	604 (6)
Lung disease	979 (10)
Liver disease	572 (6)
Cancer	91 (1)
HIV	100 (1)

Autoimmune disease	96 (1)
Body mass index, kg/m^2	
< 25	4,202 (41)
25 – 29	3,754 (36)
≥ 30	2,348 (23)
Facility	
Prison	6,468 (63)
Jail	2,309 (22)
Both	1,527 (15)
Housing	
Cell	4,493 (44)
Dormitory	2,089 (20)
Both	3,722 (36)

*Other includes Native American and Asian. Percentages may not add to 100 due to rounding.

TABLE S2. Univariate and Multivariate Logistic Regression Analyses for SARS-CoV-2 Prevalence, Hospitalization, ICU Admission and Death, Connecticut Department of Correction, 2020.

Variable	Model 1 SARS-CoV-2 Prevalence			Model 2 Hospitalization			Model 3 ICU Admission			Model 4 Death		
	Univariate Fixed Effects	Multivariate Fixed Effects	Multivariate Mixed Effects	Univariate Fixed Effects	Multivariate Fixed Effects	Multivariate Mixed Effects	Univariate Fixed Effects	Multivariate Fixed Effects	Multivariate Mixed Effects	Univariate Fixed Effects	Multivariate Fixed Effects	Multivariate Mixed Effects
	OR (95% CI)	OR (95% CI)	OR (95% CI)	OR (95% CI)	OR (95% CI)	OR (95% CI)	OR (95% CI)	OR (95% CI)	OR (95% CI)	OR (95% CI)	OR (95% C()	OR (95% CI)
Age, per 10-year increase	**1.2 (1.1 – 1.2)**	**1.2 (1.1 – 1.3)**	**1.2 (1.1 – 1.2)**	**2.4 (1.9 – 2.9)**	**2.4 (1.9 – 3.0)**	**2.3 (1.9 – 2.9)**	**2.6 (1.9 – 3.6)**	**2.6 (1.8 – 3.7)**	**2.4 (1.6 – 3.5)**	**3.4 (1.9 – 6.1)**	**3.4 (1.9 – 6.1)**	**3.3 (1.7 – 6.3)**
Race/ ethnicity												
White	1	1	1	1			1			1		
Black/African American	**0.76 (0.66 – 0.88)**	0.92 (0.78 – 1.1)	0.97 (0.82 – 1.1)	0.78 (0.42 – 1.4)			1.1 (0.40 – 3.2)			3.0 (0.34 – 27.3)		
Hispanic/ Latino	1.1 (0.96 – 1.3)	**1.3 (1.2 – 1.6)**	**1.4 (1.2 – 1.6)**	0.78 (0.42 – 1.5)			0.73 (0.22 – 2.4)			1.8 (0.16 – 19.5)		
Other	0.47 (0.19 – 1.2)	0.52 (0.20 – 1.3)	0.52 (0.20 – 1.4)	5.7 E-6 (0 – ∞)			7.5 E-6 (0 – ∞)			4.8 E-5 (0 – ∞)		

Hypertension	1.2 (0.99 – 1.4)			1.4 (0.74 – 2.5)			2.0 (0.76 – 5.3)			0.77 (0.09 – 6.4)		
Heart disease	1.2 (0.85 – 1.7)			**6.1 (2.8 – 13.4)**	**6.8 (2.7 – 17.3)**	**7.2 (2.8 – 18.5)**	**8.0 (2.5 – 25.1)**	**6.6 (1.7 – 25.3)**	**7.7 (1.8 – 33.6)**	1.9 E-6 (0 – ∞)		
Diabetes mellitus	0.93 (0.72 – 1.2)			1.5 (0.59 – 3.9)			1.9 (0.43 – 8.4)			6.8 E-7 (0 – ∞)		
Lung disease	1.1 (0.90 – 1.3)			**2.2 (1.1 – 4.2)**	1.7 (0.81 – 3.6)	1.7 (0.80 – 3.5)	0.96 (0.22 – 4.2)			6.4 E-7 (0 – ∞)		
Liver disease	1.0 (0.80 – 1.3)			0.83 (0.25 – 2.7)			0.86 (0.11 – 6.6)			6.8 E-7 (0 – ∞)		
Cancer	1.5 (0.87 – 2.6)			1.3 (0.16 – 9.8)			6.0 E-6 (0 – ∞)			1.1 E-5 (0 – ∞)		
HIV	1.2 (0.68 – 2.1)			3.1 E-6 (0 – ∞)			3.2 E-6 (0 – ∞)			4.1 E-6 (0 – ∞)		
Autoimmune disease	1.5 (0.89 – 2.6)			**4.2 (1.2 – 15.1)**	3.4 (0.74 – 15.2)	2.9 (0.60 – 14.1)	**15.2 (4.0 – 57.8)**	**14.0 (3.0 – 65.4)**	**13.5 (2.2 – 82.6)**	1.1 E-5 (0 – ∞)		
Body mass index, kg/m^2												
< 25	1	1	1	1			1			1		
25 – 29	**1.3 (1.1 – 1.5)**	1.1 (0.99 – 1.3)	1.1 (0.98 – 1.3)	1.3 (0.70 – 2.5)			1.0 (0.34 – 3.1)			0.59 (0.10 – 3.5)		
≥ 30	1.2 (0.99 – 1.4)	1.1 (0.90 – 1.2)	1.1 (0.90 – 1.3)	1.9 (1.0 – 3.8)			1.9 (0.63 – 5.7)			1.1 (0.18 – 6.4)		

Facility												
Prison	1	1	1	1			1			1		
Jail	1.1 (0.99 – 1.3)	**0.47** **(0.38 – 0.58)**	0.46 (0.04 – 5.3)	0.50 (0.24 – 1.0)			0.27 (0.06 – 1.2)			5.1 E-7 (0 – ∞)		
Both	**1.4** **(1.2 – 1.7)**	**18.5** **(13.0 – 26.2)**	4.9 (0.67 – 35.6)	1.1 (0.51 – 2.3)			5.7 E-7 (0 – ∞)			5.1 E-7 (0 – ∞)		
Housing												
Cell	1	1	1	1	1	1	1			1		
Dormitory	**7.4** **(6.2 – 8.8)**	**28.6** **(20.8 – 39.4)**	**35.3** **(7.9 – 157)**	**0.33** **(0.16 – 0.66)**	**0.29** **(0.14 – 0.61)**	**0.22** **(0.06 – 0.74)**	**1.3** **(0.27 – 6.3)**			0.37 (0.02 – 5.9)		
Both	**4.5** **(3.8 – 5.4)**	**28.4** **(20.2 – 39.9)**	**35.0** **(3.3 – 371)**	0.60 (0.32 – 1.1)	**0.39** **(0.20 – 0.78)**	**0.30** **(0.09 – 0.95)**	2.0 (0.45 – 9.3)			1.8 (0.21 – 15.8)		

OR = odds ratio; CI = confidence interval; ICU = intensive care unit. Model 1 included the male study population (n = 9,699), since no female inmates tested positive. Models 2 – 4 included SARS-CoV-2 positive individuals only (n = 1,240). Multivariate random-effects models included a random-intercept for facility to account for potential clustering in the data.

FIGURE S1. Inmate SARS-CoV-2 Testing, Connecticut Department of Correction, 2020.