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MAJOR ARTICLE

Genomic Epidemiology of Severe Acute Respiratory Syndrome Coronavirus 2 in a County Jail

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Background. In the coronavirus disease 2019 (COVID-19) pandemic, correctional facilities are potential hotspots for transmission. We examined the genomic epidemiology of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) early in the pandemic in one of the country's largest urban jails.

Methods. Existing SARS-CoV-2 isolates from 131 detainees at the Cook County Jail in Chicago, Illinois, from March 2020 through May 2020 were analyzed by whole-genome sequencing. Contemporaneous isolates from Rush University Medical Center (Chicago, Illinois) and the Global Initiative on Sharing All Influenza Data (GISAID) were used to identify genetic clusters containing only jail isolates. Transmission windows were identified for each pair of detainees using the date of the SARS-CoV-2–positive test and location data to determine if detainees overlapped in the jail, within a specific building, or within particular living units during transmission windows.

Results. We identified 29 jail-only clusters that contained 75 of the 132 SARS-CoV-2 isolates from detainees; of these clusters, 17 (58.6%) had individuals who overlapped in the jail during putative transmission windows. Focusing on specific buildings revealed that 2 buildings, a single- and double-cell style of housing. were associated with having detainees infected with similar SARS-CoV-2 genomes during their infectious time period ($P < .001$).

Conclusions. Our findings suggest that there was transmission of SARS-CoV-2 in the jail, in the setting of extensive importation of COVID-19 from the community. Numerous infection control practices at intake and during incarceration were implemented in the jail to limit viral spread. Our study shows the importance of genomic analysis in this type of settings and how it can be utilized within infection control protocols.

Keywords. genomic epidemiology; jail; pandemic; SARS-CoV-2; transmission.

The current global impact of the coronavirus disease 2019 (COVID-19) pandemic is >630 million cases, more than half in the United States (US) [1]. Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is primarily spread through exposure to respiratory droplets and/or aerosols [2]. Close contact of individuals interacting in shared spaces has been identified as a risk factor for SARS-CoV-2 transmission, which is common in congregate settings such as correctional facilities, long-term care facilities, and schools/daycares [3]. These settings may have inadequate ventilation and variable access to adequate hygiene; these features could potentially contribute to transmission of the virus. In addition, congregate settings such as jails may promote disease spread and increase the risk of severe outcomes due to a greater presence of medically vulnerable individuals [4–6].

Prisons and jails have had many COVID-19 outbreaks and cases during this pandemic. The prison COVID-19 cumulative incidence rate was 30 780.1 per 100 000 in comparison to the overall US COVID-19 cumulative incidence rate of 9350.6 per 100 000 between April 2020 and 2021 [3]. To combat COVID-19 in institutional settings, prisons and jails employed infection control approaches such as physical distancing, isolation/quarantine, masking, frequent testing, and reducing the number of visitors [3, 7–10] (Supplementary Table 1). However, even these interventions did not entirely eliminate the spread of COVID-19. Many infection control interventions rely on compliance to be effective. In addition, it is hard to quantify the exact impact of interventions due to challenges in distinguishing imported COVID-19 cases from within-facility transmission. Genomic sequencing is needed not only to understand COVID-19 spread, but also to actively modify the interventions taken to control transmission of the virus.

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Historically, genomic characterization of SARS-CoV-2 in jails has been limited, with most studies from outside the US or having a limited phylogenetic analysis of isolates [7, 8, 10]. In this study, we used whole-genome sequencing (WGS) to examine the genomic epidemiology of SARS-CoV-2 strains circulating among detainees incarcerated at the jail during the early phase of the COVID-19 pandemic.

METHODS

Study Population

The study was conducted at the Cook County Jail (Chicago, Illinois), in which approximately 59 000 total individuals were detained in 2019 with an average daily census of 5800, making it one of the largest single-site jails in the US [7]. The average daily census of detainees from 1 March 2020 to 1 May 2020 was 4884 [7].

Swab Collection

Individuals who entered the jail or who were incarcerated already who developed influenza-like illness were tested for SARS-CoV-2. Collected specimens during incarceration were processed in the Stroger Hospital laboratory using the m2000 system (Abbott Laboratories, Chicago, Illinois) [7]. Newly detained individuals were tested using the ID NOW COVID-19 assay (Abbott) starting on 20 April 2020; however, these specimens were not available for analysis. Swabs collected during incarceration for a variety reasons available for genomic analysis included: (1) people under investigation, (2) as part of intake clearance at day 14, (3) prior to prison transfer, (4) preprocedure, (5) admission to higher level of care, (6) postquarantine clearance, (7) detainee request, or (8) exposure to a case.

Whole-Genome Sequencing

Whole-genome sequencing was performed on 132 SARS-CoV-2 isolates collected between 1 March 2020 and 31 May 2020. RNA was extracted from viral transport medium using the Quick-RNA Viral kit (Zymo Research). Complementary DNA was synthesized using SuperScript IV First-Strand Synthesis System (Thermo Fisher Scientific), with an increased reverse-transcription incubation step of 50°C for 30 minutes and 55°C for 15 minutes, and without RNase H treatment. SARS-CoV-2 whole genomes were amplified, and libraries were prepared using the xGen SARS-CoV-2 Amplicon panel (Integrated DNA Technologies, formerly Swift Biosciences) using the modified multiplex polymerase chain reaction protocol for low viral input samples. Deep sequencing of libraries was performed on an Illumina NovaSeq6000 instrument with a 300-cycle SP flow cell at the DNA Services Facility at the University of Illinois at Urbana-Champaign. The SARS-CoV-2 isolates yielded full genomes (95% coverage) using a custom analysis pipeline described previously [11]. Pango lineages were determined using pangolin v3.0 [12]. A previously published set of isolates processed at Rush University Medical Center (RUMC, Chicago, Illinois) [11] was used to place jail isolates in the context of strains circulating in local communities. Globally distributed publicly available SARS-CoV-2 genomes from the early pandemic were downloaded from the Global Initiative on Sharing All Influenza Data (GISAID) and used for time-scaled phylogenetic analysis.

Data Analysis

Descriptive Analysis

We used R version 4.2.2 software to examine the demographic and clinical characteristics of detainees who had SARS-CoV-2. Frequency and proportions were used for categorical variables, the mean and standard deviation were used for continuous variables that were normally distributed, and the median and interquartile range were used for continuous variables that were not normally distributed. Geographic analysis was done using self-reported zip code (postal code) data provided by intake forms. We matched zip codes to previously used regions of Chicago. We calculated the frequency and proportions for regions in which detainees lived prior to incarceration.

Phylogenetic Analysis

Consensus genomes were aligned using MAFFT 7.475. To enhance confidence in genomic linkages, the following genomic regions were masked: (1) the first and last 20 bp of the genome; (2) regions with high variant density (likely due to incomplete primer and/or quality trimming; manual investigation confirmed that these were sequence artifacts and were often found near gaps in coverage), defined as 5 or more differences from the reference genome in a 10-bp window; and (3) regions proximate to poly-N tracts, defined as being within 5 bp from a poly-N tract of 10 N's or longer. For the time-scaled phylogenetic tree, the software package TreeTime v0.8.4 was used [13]. For the jail-only phylogenetic tree, the software package IQtree v2.0.3 [14] was used to create the tree, and the software package ggtree [15] was used to visualize the tree.

Location Overlap Analysis

Plausible transmission pairs were identified based on overlap in the jail during epidemiologically relevant time windows for the putative source and acquirer. For the putative acquirer in a transmission pair, we defined the susceptibility window for SARS-CoV-2 as the days prior to the positive test date. For the putative source in a transmission pair, we defined the infectious period as 2 days prior to and 14 days after the positive test date [10, 16]. To determine location sharing among individuals in putative transmission pairs, we used electronic jail location data, including building and living unit data. To evaluate the concordance between genomic and epidemiologic data, we

applied single-nucleotide variant (SNV) cutoffs (eg, 0, 1, 2, 3, 4, ≥5) to identify genetically linked pairs, and quantified overlap in the jail, individual building units, and living units during the relevant time windows for putative sources and acquirers as defined above. Characteristics of each building and division block were previously reported [7]. Permutation tests were performed to identify statistically significant SNV thresholds for overlap, as previously described [17].

Cluster Analysis

To identify genetic clusters within our sample of jail and RUMC isolates, we determined the pairwise distances for each isolate in our collection using the dist.dna function of the ape package in R [18]. Cluster detection was performed by grouping together individuals where all members of a cluster harbored identical isolates. Histograms were used to show clusters containing jail and/or RUMC isolates. Singleton isolates that were not clustered with other isolates were removed from this analysis.

RESULTS

Study Population Characteristics

There were 131 unique individuals with isolates included in this study. Strains obtained from the collection of jail isolates fell into A (n = 6 [4.5%]) and B (n = 126 [95.5%]) Pango haplotypes, with the majority being Pango lineage B.1 (n = 110 [83.3%]). Most individuals were male (n = 121 [92.4%]), non-Hispanic Black (n = 99 [75.0%]), and under age 50 (n = 112 [84.8%]). Some individuals had at least 1 comorbidity (n = 26 [19.7%]) (Table 1). Due to the disproportionate number of detainees who have unstable housing, the Department of Corrections defaults those individuals to the jail zip code. The zip code for the jail was removed from our geographic analysis. The 3 most frequent areas the detainees resided in prior to incarceration were outside the Chicago area (n = 29 [22.0%]), southwest Chicago (n = 24 [18.2%]), and west Chicago (n = 24 [18.2%]) (Supplementary Figure 1).

Table 1. Characteristics of Cook County Jail Detainees With Available Severe Acute Respiratory Syndrome Coronavirus 2 Isolates Early in the Coronavirus Disease 2019 Pandemic (March–May 2020)[a]

Characteristic	No. (%) (N = 131)
Age, y, mean (SD)	35.8 (13.4)
Sex	
Female	10 (7.6)
Male	121 (92.4)
Race	
Black	99 (75.6)
White	30 (22.9)
Other	2 (1.5)
Ethnicity	
Hispanic/Latino	25 (19.1)
Non-Hispanic/Latino	106 (80.9)
BMI, kg/m^2	
Mean (SD)	32.8 (53.4)
Missing	7 (5.3)
Diabetes	
Yes	16 (12.2)
No	115 (87.8)
Dialysis in the prior year	
No	131 (100)
ICU in the last month	
No	131 (100)
Hypertension	
Yes	12 (9.2)
No	119 (90.8)
Stroke	
No	131 (100)
Chemotherapy in the last 6 mo	
No	131 (100)
Incarcerated in the past year	
Yes	43 (32.8)
No	88 (67.2)
Incarcerated ever	
Yes	94 (71.8)
No	37 (28.2)

Data are presented as No. (%) unless otherwise indicated.

Abbreviations: BMI, body mass index; ICU, intensive care unit; SD, standard deviation.

[a]All detainees answered "No" for the following variables: dialysis in the last 6 months, ICU in the last 6 months, stroke in the last 6 months, chemotherapy in the last 6 months.

Phylogenetic Tree

To understand the importation and spread of SARS-CoV-2 in the Cook County Jail, we performed a time-scaled phylogenetic analysis using isolates from the greater Chicago region and worldwide collected during the same time period (March 2020–May 2020). We observed that the most recent common ancestor for most of the jail isolates was from Europe, consistent with most US SARS-CoV-2 B lineages at the time being descended from importation from Europe. The closest genetic relative to jail isolates were most often within Illinois, supporting our capture of local circulating strains during the study period (Figure 1). Subclades harboring only jail isolates are visually detectable, consistent with the potential repeated importation and spread of SARS-CoV-2 within the jail (Figure 1).

Cluster Analysis

To further analyze putative transmission clusters within the jail, we extracted clusters of local contextual isolates from RUMC and the jail that were genetically identical. We identified 157 such clusters, falling into 3 categories: jail-only clusters (18.5%), RUMC-only clusters (73.2%), and jail/RUMC clusters (8.2%). We identified 29 jail-only clusters that contained 75 SARS-CoV-2 isolates; of these clusters, 40 detainees from 17 of these clusters overlapped in the jail within their infectious and susceptible time periods (Supplementary Figure 2). Furthermore, of these 40 detainees, 17 overlapped in the same building. The median number of isolates within a cluster was 2 (range, 2–6). A maximum-security cell-block style

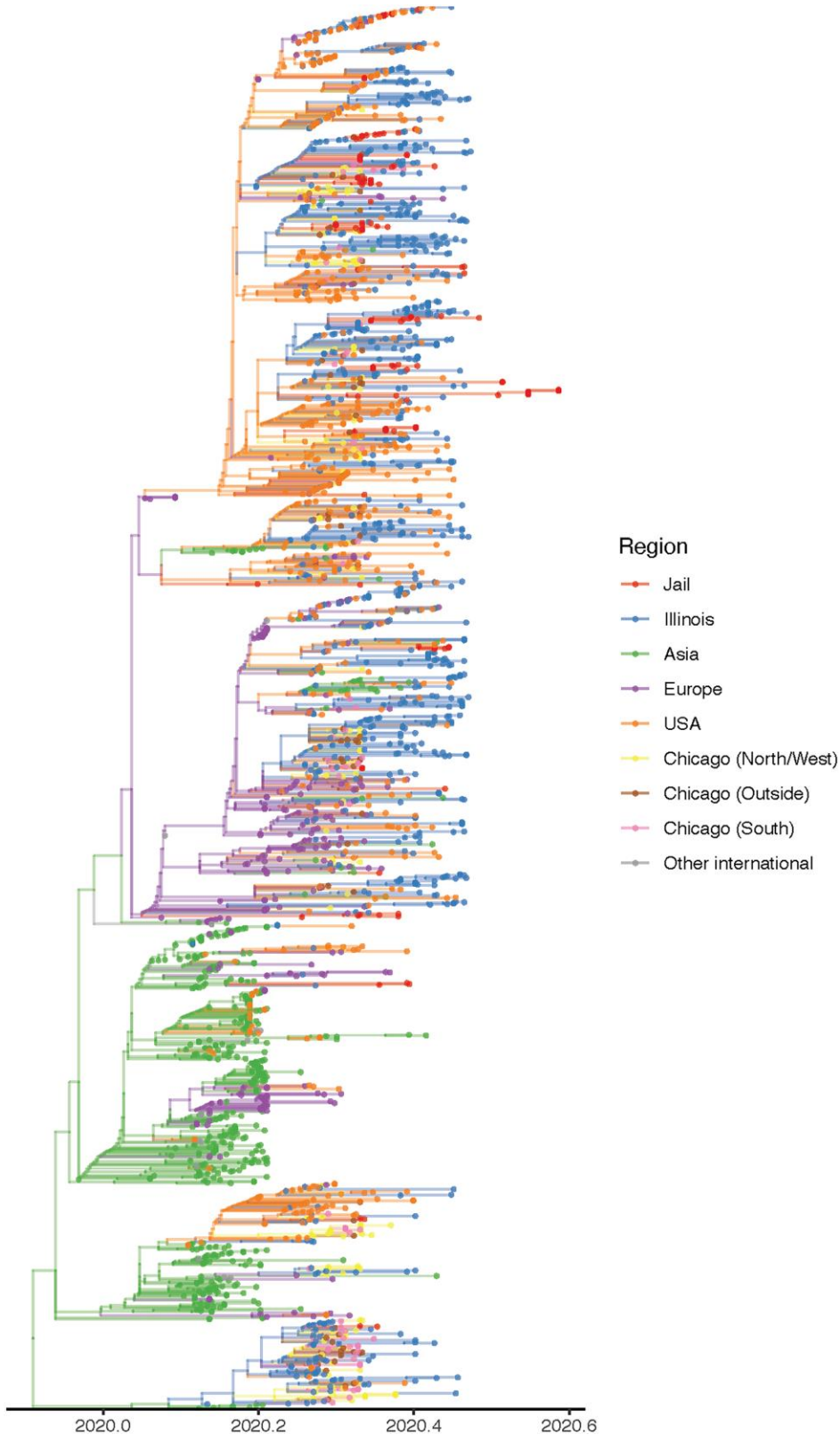

Figure 1. Time-calibrated whole-genome phylogeny of severe acute respiratory syndrome coronavirus 2 isolates taken from the jail, an urban hospital, and GISAID using TreeTime. Recombination-masked whole-genome alignment was used. The tree is midpoint rooted. The x-axis shows time points in the early phase of the COVID-19 pandemic in date decimal format.

building (buildings B and D) and a multifaceted mixed-use building (cells, dormitory style housing, medical care) (building I) were found to have the most overlap for jail-only clusters (Figure 2). Among jail/RUMC clusters, we identified 13 clusters that contained 186 SARS-CoV-2 isolates from both settings. The median number of isolates within these clusters was 4.5 (range, 2–89).

Relationship of Jail Location to SARS-CoV-2 Isolates

Having observed clusters with individuals overlapping in the same building, we next sought to determine if this was nonrandom. Among detainees who tested positive for SARS-CoV-2, detainees with isolates within 2 SNVs were more likely to be in the jail simultaneously and overlap in the same building ($P < .005$) (Supplementary Figure 3). Further analysis showed a subset of buildings with more overlap, with detainees whose isolates were in the same cluster and who overlapped in the same building having spent significantly more days in buildings B, D, and I than other detainees (n = 211/289 [73%] vs 1171/2244 [52%] for other detainees; χ^2 $P < .001$) (Figure 2). When comparing the individual buildings B, D, or I to other buildings within the jail to determine if there were associations between these buildings and genetic linkage pairs, we found that buildings B and D were significantly associated with individuals in genetic linkage pairs being located in them during their infectious time periods ($P < .001$).

DISCUSSION

Our findings suggest that there was transmission of SARS-CoV-2 in the jail, in the setting of extensive importation from the community. We identified 17 genomic jail-only clusters that contained 40 jail isolates with an overlap in the jail during plausible epidemiological time windows for transmission events. Clusters within the jails were usually small, consisting of 2 people, suggesting the infection control measures that were implemented may have prevented large outbreaks between detainees. Moreover, the significant enrichment in spatiotemporal overlap in buildings among closely related pairs further supports COVID-19 spread among detainees. Locations of overlap included both dormitory and cell-block style buildings, indicating the complexity of controlling spread in a large congregate setting.

The B.1 lineage was found to be the predominant lineage in the Cook County Jail during the first wave of the pandemic, which reflected trends seen nationally during that time period. Additionally, we observed that the majority of jail isolates belonged to 2 clades on the tree including contemporaneous global isolates, with these isolates having a European ancestor, which is consistent with other studies that report the European source of most US lineages at the time [19, 20]. Placing jail isolates in the context of contemporaneous isolates from Chicago identified a number of jail-only clusters, consistent with multiple importations and subsequent in-jail transmission. In total, 40 (30.3%) detainee isolates were part of these jail-only clusters and exhibited overlap in the jail during plausible transmission windows, although only 17 of these detainees also overlapped in the same building.

When we overlaid building location data to the infectious time periods, we found the majority of the overlap of detainees (73%) occurred in 3 buildings (buildings B, D, and I). Buildings in the Cook County Jail varied from being single cell to dormitory cell, with varying levels of turnover [7]. As described previously, building I was a residential treatment unit that housed detainees with medical comorbidities (ie, medical infirmary) and may not represent actual transmission cases. Additionally, we found no association between building I and detainees with genetic linkage, underscoring the importance of incorporating robust epidemiologic data in determining potential transmission linkages. Buildings B and D were large maximum-security buildings with a lower turnover of detainees in cells and who were cleared from the initial screening process for SARS-CoV-2. Therefore, identifying the overlap of detainees with genomically similar SARS-CoV-2 isolates in these buildings suggests possible transmission events.

Our study had limitations. First, while screening for SARS-CoV-2 was performed for detainees who entered the Cook County Jail, we only had access to swabs from individuals who tested positive subsequently. Testing during incarceration was prompted for a variety of reasons including when a detainee left the 14-day intake clearance, had a temperature of >37.7°C, had other viral symptoms, was part of contact tracing after a known exposure, or requested to be tested, and may have missed potential cases that did not meet these requirements for testing. Second, we may also have missed individuals acquiring SARS-CoV-2 during incarceration who were asymptomatic, who could potentially contribute to the spread [21]. Third, even in cases where there was genetic clustering among detainees in the same building, we cannot rule out this being due to shared exposures in the community prior to incarceration or staff introduction. Fourth, despite genomic and epidemiologic support, we cannot rule out the possibility that these isolates were derived from multiple independent importation events that were not identified in these analyses, due to limited sampling of circulating strains from the community [16]. In addition, due to a lack of genetic variation of SARS-CoV-2 strains in the jail and community, we might have underestimated the number of instances of jail transmission. We also note that our analysis focused on detainees; however, staff members within the jail could have transmitted SARS-CoV-2 to detainees, which is a possible route of importation or transmission of SARS-CoV-2 within the jail [7]. Finally, due to the high clonality of SARS-CoV-2 during this period, it is likely for individuals not directly linked by transmission to harbor genetically identical strains. However, by

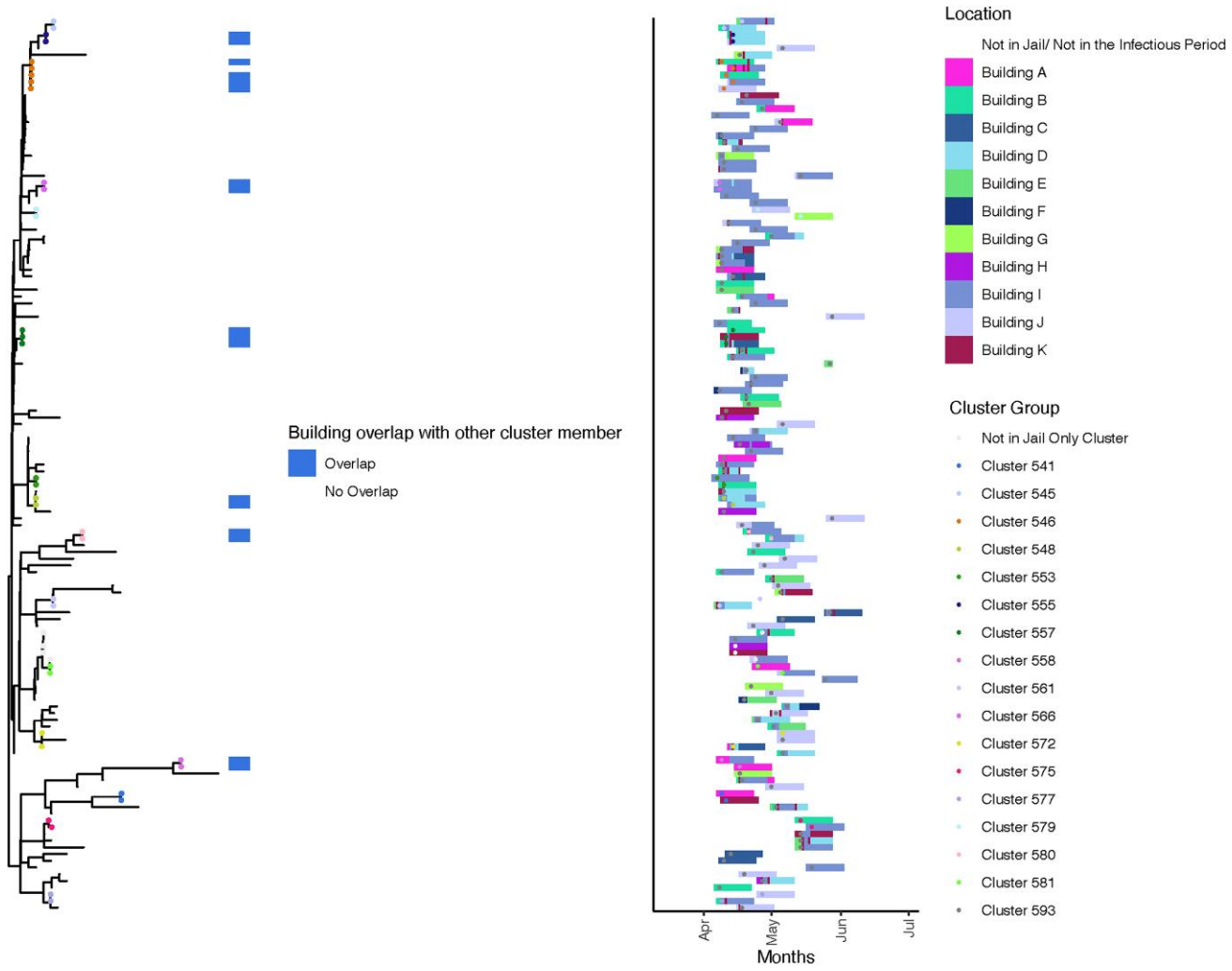

Figure 2. A whole-genome phylogenetic tree (left) of jail severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) isolates with tips colored to indicate jail-only clusters. Trace plot (right) aligned with the tree to show whether detainees were within the same building and clusters. Each line represents the location of the detainees during their infectious period, and each dot represents the collection date of the SARS-CoV-2 specimen. The collection dot is colored by which cluster group each isolate was in.

restricting our analysis to cases where genetic data enabled discrimination of jail and community (RUMC) strains, and further overlaying data on detainees' location during plausible transmission periods, we increased our confidence that we were indeed detecting within-jail transmission.

Our study described the genomic epidemiology of SARS-CoV-2 among detainees in a large, urban jail during the beginning of the COVID-19 pandemic. Genomic analyses suggest transmission of SARS-CoV-2 in the jail, in the setting of extensive importation from the community. Within-jail transmission was detected in specific buildings, which may be targeted for enhanced infection prevention. Numerous infection prevention practices at intake and during incarceration were implemented in the jail to limit the spread of SARS-CoV-2 [7, 11] (Supplementary Table 1). However, compliance with these measures was variable among detainees and staff, making containment of SARS-CoV-2 more challenging [7]. Our findings underscore the challenges with infection prevention in a congregate setting with a high importation burden of disease, but support genomic analysis being able to improve our understanding of the spread of SARS-CoV-2 in correctional facilities and allow for more tailored surveillance and infection control practices.

Supplementary Data

Supplementary materials are available at *Open Forum Infectious Diseases* online. Consisting of data provided by the authors to benefit the reader, the posted materials are not copyedited and are the sole responsibility of the authors, so questions or comments should be addressed to the corresponding author.

Notes

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Patient consent. The study was approved with waiver of consent by the Cook County Health Institutional Review Board.

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Potential conflicts of interest. All authors: No reported conflicts.

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