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Transmission of *Mycobacterium tuberculosis* in four prisons in Colombia

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Abstract

Our study aimed to describe the transmission dynamics and genotypic diversity of *Mycobacterium tuberculosis* in people deprived of liberty (PDL) in four Colombian prisons. Our cohort study included 64 PDL with bacteriologically confirmed pulmonary tuberculosis diagnosed in four Colombian prisons. The 132 isolates were genotyped using 24-mycobacterial interspersed repeated units-variable number tandem repeats (MIRUs-VNTR). A cluster was defined when ≥2 isolates from different PDL had the same genotype. Tuberculosis acquired in prison was considered when ≥2 persons were within the same cluster and had an epidemiological link. We mapped the place of residence before incarceration and within prisons. We assessed overcrowding and ventilation conditions in the prison that had clusters. We found that the most frequent genotypes were LAM (56.8%) and Haarlem (36.4%), and 45.3% of the PDL diagnosed with tuberculosis were clustered. Most PDL diagnosed in prison came from neighborhoods in Medellin with a high TB incidence. *M. tuberculosis* infection acquired in prison was detected in 19% of PDL, 9.4% had mixed infection, 3.1% reinfection, and 1.6% relapse. Clusters only appeared in one prison, in cell blocks with overcrowding >100%, and inadequate ventilation conditions. Prisons require the implementation of effective respiratory infection control measures to prevent *M. tuberculosis* transmission.

Introduction

Tuberculosis is one of the top causes of death due to infectious diseases in the world (only surpassed by COVID-19 in recent years), with 10.6 million people who fell ill in 2022 [1]. People deprived of liberty (PDL) are at the highest risk of contracting *Mycobacterium tuberculosis* infection and progressing to tuberculosis disease [2]. A systematic review reported an incidence of *M. tuberculosis* infection inside prisons of 1 to 144 infections per 100 person-years [2]. This incidence can be explained by the high tuberculosis prevalence in prisons (320 to 1810 per 100,000 PDL) [2], overcrowding (up to 454.4% was reported in 2023) [3], lack or limited exposure to sunlight, vitamin D deficiency [4], drug use, smoking, and lack of an effective healthcare system, among others.

In Central and South American countries, tuberculosis in prisons is concerning. The number of PDL has increased, and the number of reported people diagnosed with tuberculosis has also increased, up to 269% [5]. In Colombian prisons, tuberculosis has a similar trend, with an annual tuberculosis prevalence of 1,026 per 100,000 PDL [6] and incidence rates that range between 244.2 per 100,000 PDL [7] to 517 per 100000 PDL per year [8].

Prisons amplify and spread tuberculosis to the community [9]. Understanding the patterns of tuberculosis transmission within prisons can help prevent the spread of the disease to the community [10].

Our study aimed to determine the transmission dynamics and genotypic diversity of *M. tuberculosis* in PDL and to evaluate two environmental conditions (overcrowding and ventilation) inside four Colombian prisons.

Original Paper

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Methods

Setting

The study was conducted in two female and two male prisons in Bucaramanga and Medellin, Colombia. Inside the prisons, each cell block (with around 1000 to 1700 PDL) had between one and 12 accommodation wings, and inside each wing, there was a variable number of cells. PDL must stay inside each wing between 4 p.m. and 8 a.m. Between 8 a.m. and 4 p.m., PDL were allowed to do some activities such as spending time with people from other wings or exercise in the outdoor recreation area within the cell block, and study or work outside the cell block.

Study design

In this prospective cohort study, among 1305 PDL incarcerated in four Colombian prisons and systematically screened for respiratory symptoms, 72 were bacteriologically confirmed pulmonary tuberculosis by acid-fast bacilli examination and Lowenstein-Jensen, thin layer or mycobacterial growth indicator tube (MGIT) 960 BACTEC cultures as previously published [11]. Seven PDL had positive sputum smear but negative culture, and one person died at diagnosis and we could not access the clinical isolate. Therefore, this paper reports all 64 PDL diagnosed with tuberculosis by culture.

Participants and follow-up

Sixty-four PDL were diagnosed with tuberculosis between April 30, 2010 and December 23, 2012. Participants were followed up monthly during tuberculosis treatment, then every 2 months for 6 months, and every 3 months during the second year. The total follow-up for each person was 2 years. At baseline and each follow-up, we collected demographic, clinical and microbiological characteristics, and collected spontaneous and induced sputum samples [11]. Each *M. tuberculosis* isolate detected on each follow-up was processed for first- and second-line drugs' phenotypic testing on 7H11 Middlebrook agar using the proportion and for 24-mycobacterial interspersed repeated units-variable number tandem repeats (MIRU-VNTR) genotyping. Participant screening, tuberculosis diagnosis, and follow-up details are published elsewhere [8,11].

Genotyping

DNA extraction

DNA was extracted using the CTAB/NaCl and stored at −20 °C until the genotyping processing.

24 MIRU-VNTR technique and analysis

Isolates were genotyped using polymerase chain reaction (PCR) amplification (DNA Engine®, BioRad, CA, USA) of a standard set of 24 MIRU-VNTR loci with specific primers flanking regions of each VNTR region according to reference [12] with modifications. Each MIRU-VNTR analyzed by PCR included a negative control (PCR water) and a positive control (*M. tuberculosis* H37Rv DNA). We run the PCR products on 2% agarose gels (Invitrogen, CA, USA) by electrophoresis at 130 V for 3 h. We used 50 bp and 100 bp molecular weight markers (Invitrogen, Carlsbad, CA, USA) to determine the sizes of the amplified fragments. Sizes of amplified fragments were compared with tables established to determine the number of alleles for each MIRU-VNTR analyzed [13]. The results were analyzed using the BioNumerics® (Applied Maths) V.7.0 software.

Definitions

We used the following definitions using the genotyping results and the patient information:

- *Cluster*: Two or more persons diagnosed with tuberculosis with an identical genotype determined by the MIRU-VNTR method.
- *Unique pattern*: Those who did not meet the criteria for the cluster.
- *Index person*: The first person diagnosed in each cluster.
- *Secondary infections*: Second or subsequent tuberculosis diagnoses within a cluster. People should have met the definition of "infected inside prison."
- *Infected inside prison*: Two or more people diagnosed with tuberculosis who were in a cluster (had the same genotype) and had an epidemiological link, defined as people who shared space and time of incarceration in the same cellblock or cell as the other people diagnosed with tuberculosis within the cluster.
- *Infection acquired in the community* (outside the prison): A person with a unique pattern, the index person in a cluster, or people with the same genotype as others, but there was no epidemiological link between them.
- *Relapse*: People with two different diagnoses of pulmonary tuberculosis, were cured at the end of the first tuberculosis treatment (negative acid-fast bacilli examination and tuberculosis cultures in the last 2 months of treatment) and had identical genotypes in both diagnoses.
- *Reinfection*: People with two different diagnoses of pulmonary tuberculosis, were cured at the end of the first tuberculosis treatment, and had a different genotype in both diagnoses. In addition, a person with a different *M. tuberculosis* genotype was detected during antituberculosis treatment, and the genotype was in a cluster.
- *Mixed infection*: a person with a different *M. tuberculosis* isolate during antituberculosis treatment, and the genotype was not in a cluster.

Georeferencing people diagnosed with tuberculosis inside and outside prison

We used ArcGIS software v.10 to generate all maps and to geo locate each PDL place of residence in Medellin at the time of incarceration. We georeferenced each diagnosis only in Medellin due to a lack of information about the road network in Bucaramanga. We used the road network of the city obtained from the Geodatabase of Medellin, 2011 [14]. We used the reported tuberculosis incidence density in Medellin at the time of study [15].

The urban area of Medellin is divided into 16 communes. The data were entered into tables created in ArcMap [16], where the attributes of each person were described (commune code, description of the commune, number of persons diagnosed with tuberculosis per commune). Then, we obtained a range of colors given by the incidence density in each commune.

To evaluate tuberculosis distribution inside each prison and identify the places with a higher incidence, we measured each prison, cell blocks, accommodation wings, corridors, and cells. We manually drew each courtyard and where the person diagnosed with tuberculosis slept. Subsequently, we made the maps of each

prison using the Sweet Home 3D® software. Then, we used the ArcGIS® v.10 software to locate the spatial distribution of people diagnosed with tuberculosis inside the four prisons, considering both the clustered and nonclustered diagnoses. We uploaded all information into ArcMap and edited the shape and color of each person to distinguish each cluster.

Evaluation of overcrowding conditions

To determine overcrowding conditions, the research team measured the width, height, and length of cells and corridors within each accommodation wing within each cell block, and the number of people sleeping in each cell, corridor, accommodation wing, and daily census of each prison. To calculate the overcrowding in each cell block, the number of people confined per cell block was multiplied by 100 and divided by the capacity of the cell block. Later, the image of each prison was loaded into ArcMap, and a range of colors was selected to represent the per cent of overcrowding.

Data sources and analysis

We used a questionnaire to collect sociodemographic information, history of prior incarceration, prior history of tuberculosis diagnosis and contact with a person diagnosed with tuberculosis inside or outside prison, any other concomitant disease, days of respiratory symptoms, place of incarceration at tuberculosis diagnosis and during follow-up. All statistical analyses were performed using STATA v.14 (Stata Corp, College Station, TX, USA). Descriptive statistics was used to report the variables of interest.

Ventilation simulation

We used computational fluid dynamics (CFD) to simulate the airflow of the accommodation wing with the highest number of people diagnosed with tuberculosis and the most overcrowded conditions in Prison 1. To evaluate the air flow conditions inside the accommodation wing, we measured the speed of the air entering the area according to the ASHRAE 111 (practices for measurement, testing, adjusting and balancing of building heating, ventilation, air-conditioning and refrigeration systems) [17] using the method of equal areas. The airspeed was measured using a hot-wire anemometer (Testo®, Pennsylvania, USA), and the speed was recorded in three windows of the corridor where the conditions allowed. Sometimes, the hammocks, hanging clothes, or sealed windows prevented air entry into the corridor.

Inside prisons, there was only natural ventilation, and the average air speed could vary due to environmental conditions. For the qualitative simulations, we used a conservative speed of approximately 0.3 m/s, which was the lowest average of the registered measurements.

Geometry

The computational domain of the simulation was developed for Prison 1. For the CFD simulation, we built two models, one for external aerodynamics and its impact on boundary conditions (incoming air), and another model for the evaluation of internal flow conditions and pollutant dispersion. The qualitative results of the analysis inside the building are presented in this paper.

Discretization and boundary conditions

To generate the mesh, we used the cut-cell method. The parameters for mesh generation correspond to those published by Franke et al. [18], and Ramponi et al. [19]. The computational domain size was 1300000 nodes. The boundary conditions used were inlet type for the air that enters the windows at the entrance of the accommodation wing, symmetry for the middle plane of the corridor, and outlet for the end of the accommodation wing.

Model solution

We used the program Code Saturne v.3 [20] for this simulation. The turbulence model used was $k - \omega$ *SST*, as recommended by Ramponi et al. [19]. The SIMPLE algorithm was also used for

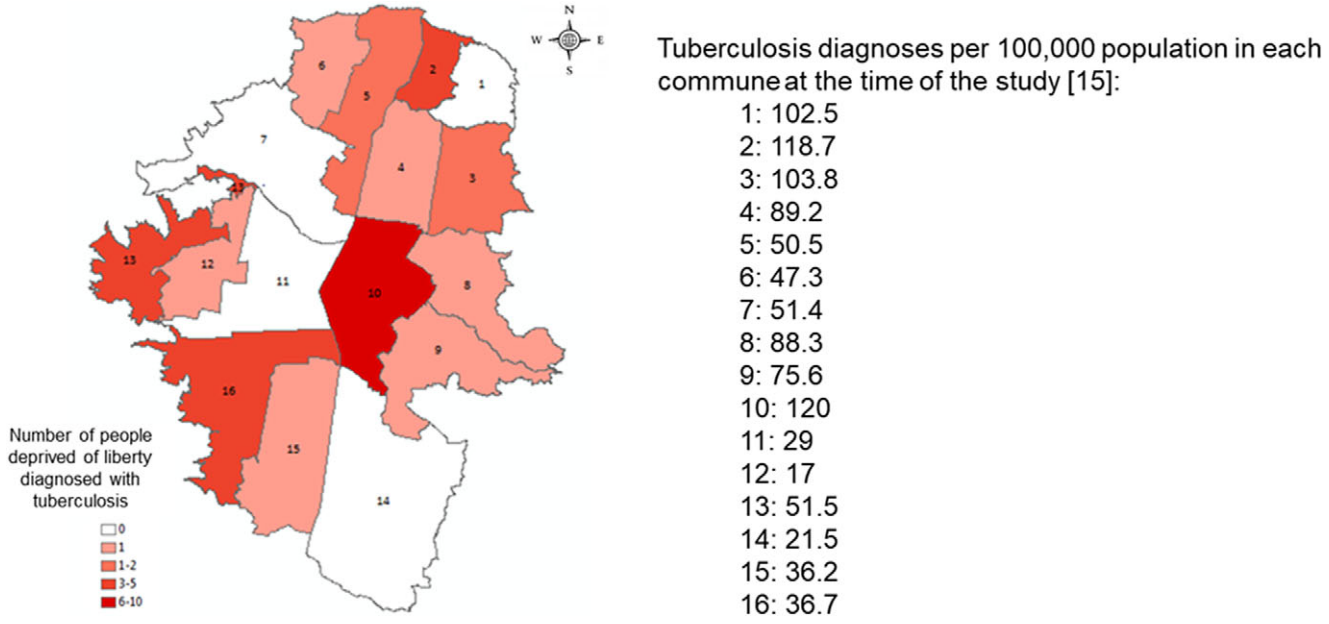

Figure 1. Place of residence before incarceration of people deprived of liberty diagnosed with tuberculosis while incarcerated between 2010 and 2012. The numbers 1–16 mean the commune (an administrative division of Medellin); the dark color means the highest number of people deprived of liberty diagnosed with tuberculosis. For comparison, we reported the tuberculosis incidence in the general population of each commune at the time of the study.

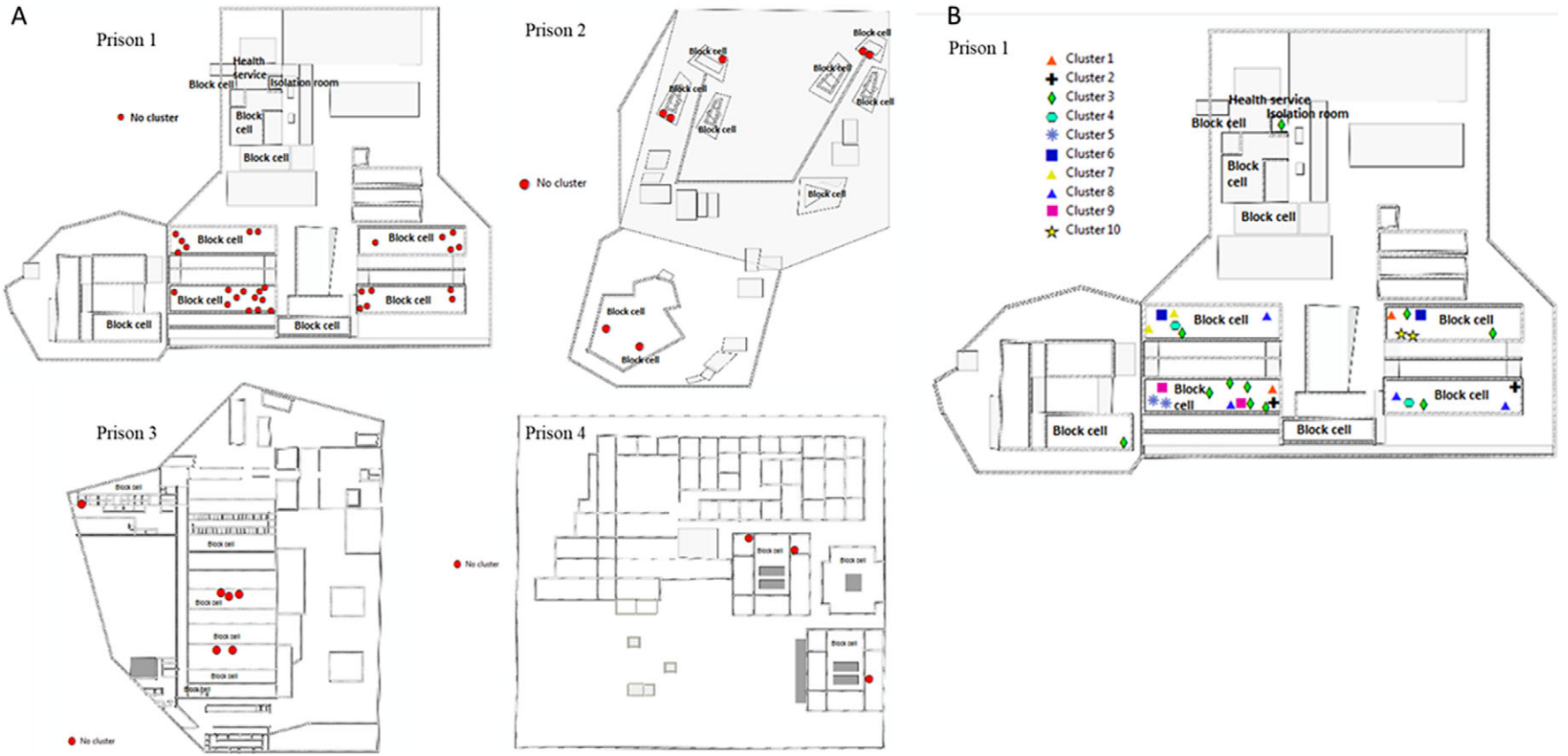

Figure 2. Distribution of people deprived of liberty diagnosed with tuberculosis with a unique pattern (a) and those in clusters with a proven epidemiological link (b). Prison 1 was the only prison that had clusters.

coupling the pressure and velocity equations, and the interpolation and discretization schemes of all the variables correspond to the second-order schemes. The convergence levels were set at 10^{-5} for the momentum and conservation variables and 10^{-4} for the turbulence variables. Since the model is considered isothermal, we did not consider an energy balance equation. Finally, pathogen dissipation mechanisms are not considered or calculated yet since only general air quality variables are considered at this stage.

Ethical considerations

The Ethics Committee of the Facultad Nacional de Salud Pública from the Universidad de Antioquia (acta 034/09) approved this research. The Instituto Nacional Penitenciario y Carcelario (INPEC, National Institute of Prison and Penitentiary System) also approved this research. All PDL signed written consent form and all the details are previously published [8]. All people diagnosed with tuberculosis received treatment independently of their participation in the study. We deidentified prisons as Prison 1, 2, 3, and 4 as well as the cell blocks. For this study, the INPEC authorized us to use handmade maps of the prisons.

Results

Among 64 people diagnosed with tuberculosis, 132 *M. tuberculosis* isolates were recovered during the diagnosis and follow-up.

Georeferencing tuberculosis diagnoses

Figure 1 depicts the place of residence of PDL before incarceration (Figure 1b). PDL diagnosed with tuberculosis lived in high tuberculosis incidence communes.

Prison 1 had the highest number of tuberculosis diagnoses (30 in the first year and 20 in the second year) (Figure 2).

Overcrowding conditions in prisons

The number of PDL was variable between prisons: Prison 1 had the highest level of overcrowding, with 6,000 PDL (prison capacity: 2424; overcrowding: 147.52%), Prison 2 had 800 (prison capacity: 2445, No overcrowding, −68%), Prison 3 had 2409 (prison capacity: 1234; overcrowding: 95.22%), and Prison 4 had 298 (prison capacity: 224; overcrowding: 33.03%). Also, overcrowding conditions varied within prisons (Figure 3). The highest number of

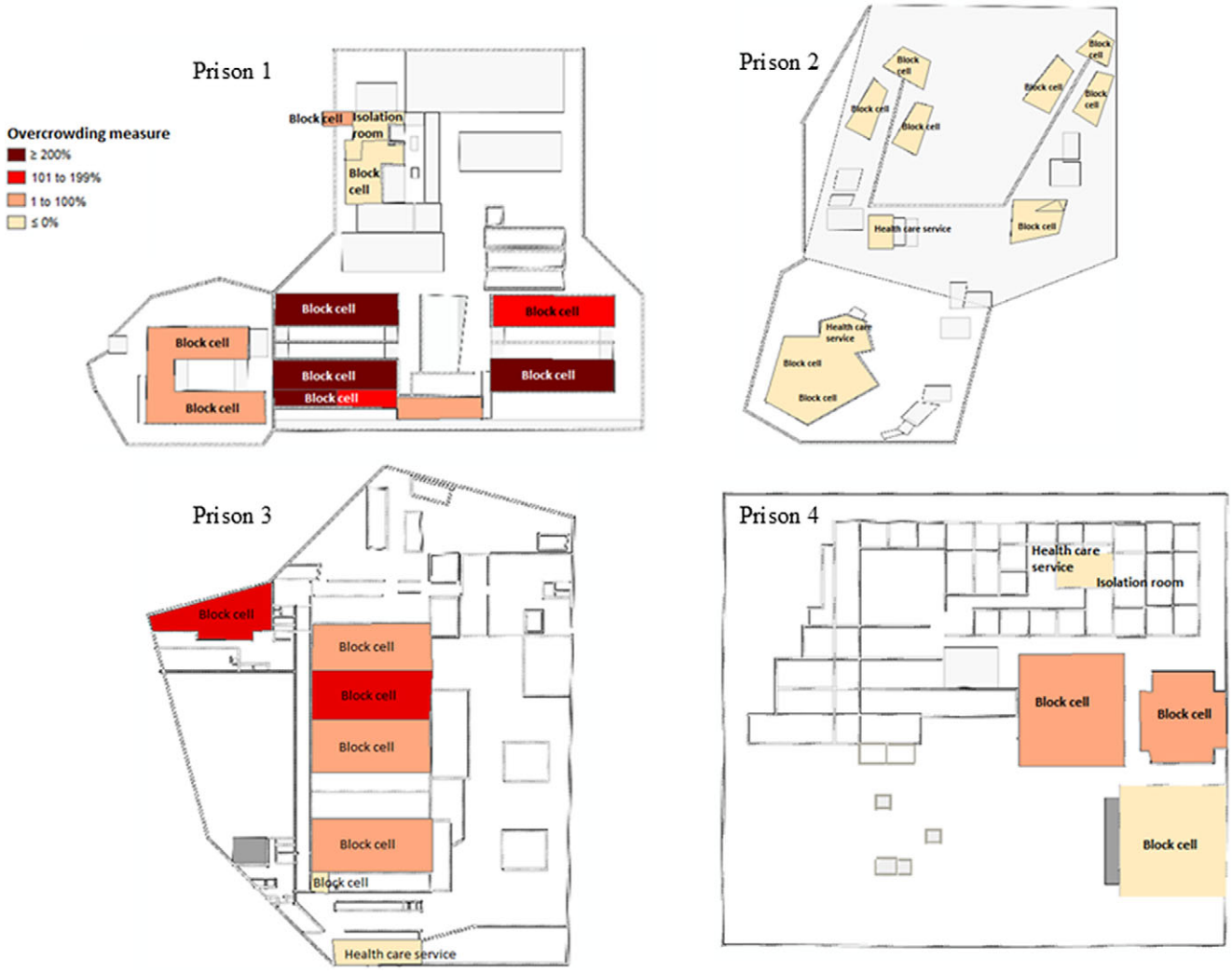

Figure 3. Per cent of overcrowding in the cell blocks of the four prisons included in the study, Colombia. The dark color means higher overcrowding per cent.

tuberculosis diagnoses (36/64) occurred in the cell blocks with the highest overcrowded cell blocks (>200%).

Mycobacterium tuberculosis genotypes

Among 132 isolates of *M. tuberculosis*, LAM (56.8%) and Haarlem (36.4%) were the most common genotypes (Figure 4). All genotypes were equally distributed in prisons 1, 2 and 3. In prison 4, only LAM genotypes were identified. Supplementary Figure S1 shows the dendrogram of the 132 isolates.

Tuberculosis transmission in prisons

Table 1 reports sociodemographic characteristics of people diagnosed with TB. The clusters were detected only in Prison 1, and mostly in overcrowded places exceeding 200% (Table 1). In Prison 1, 93.1% (27/29) of tuberculosis diagnoses were in the same four cell blocks where all those with a single pattern were detected (Figure 2).

Using all *M. tuberculosis* clinical isolates at diagnosis, we found 11 clusters. Seven out of 11 clusters had an epidemiological link, and included 29 people (45.3%) [21 of them with an epidemiological link] and 55 isolates (41.7%). There were four clusters with no epidemiological link. We classified 77 isolates (58.3%) as unique patterns.

Nineteen per cent (12/64) of people were considered infected inside prisons. Figure 5 shows the temporal distribution by the place of incarceration within each cluster. The cluster three had 11 people in five cell blocks. We believe there was an outbreak in the cell block I as people were diagnosed within 18 months after the index person, all had the same genotype, and they exercised together and spent time daily (Figure 5).

There were six persons with mixed infection (9.4%) and two reinfections (3.1%) (Table 2). A reinfection occurred in person 990, who was diagnosed on March 13, 2012, and placed in the isolation room at the hospital inside the prison. On March 21, person 993 was admitted to the same isolation room. After both persons shared a room for 2 months, during the follow-up on May 16, person 990 had the same genotype as person 993.

The second reinfection occurred in person 250 (Table 2). The person was diagnosed with tuberculosis, completed antituberculosis treatment as cured; and at month 22 of follow-up, he started with respiratory symptoms and was diagnosed with tuberculosis. The genotype isolated in the second episode was different from the first one, and it was the same strain isolated from person 475 in July 2011. The epidemiological link was that the person 250 lived in the same cell block as the person 475.

Person 367 had a relapse. The first tuberculosis diagnosis, he completed treatment as cured. At month seven, he had bacteriologically

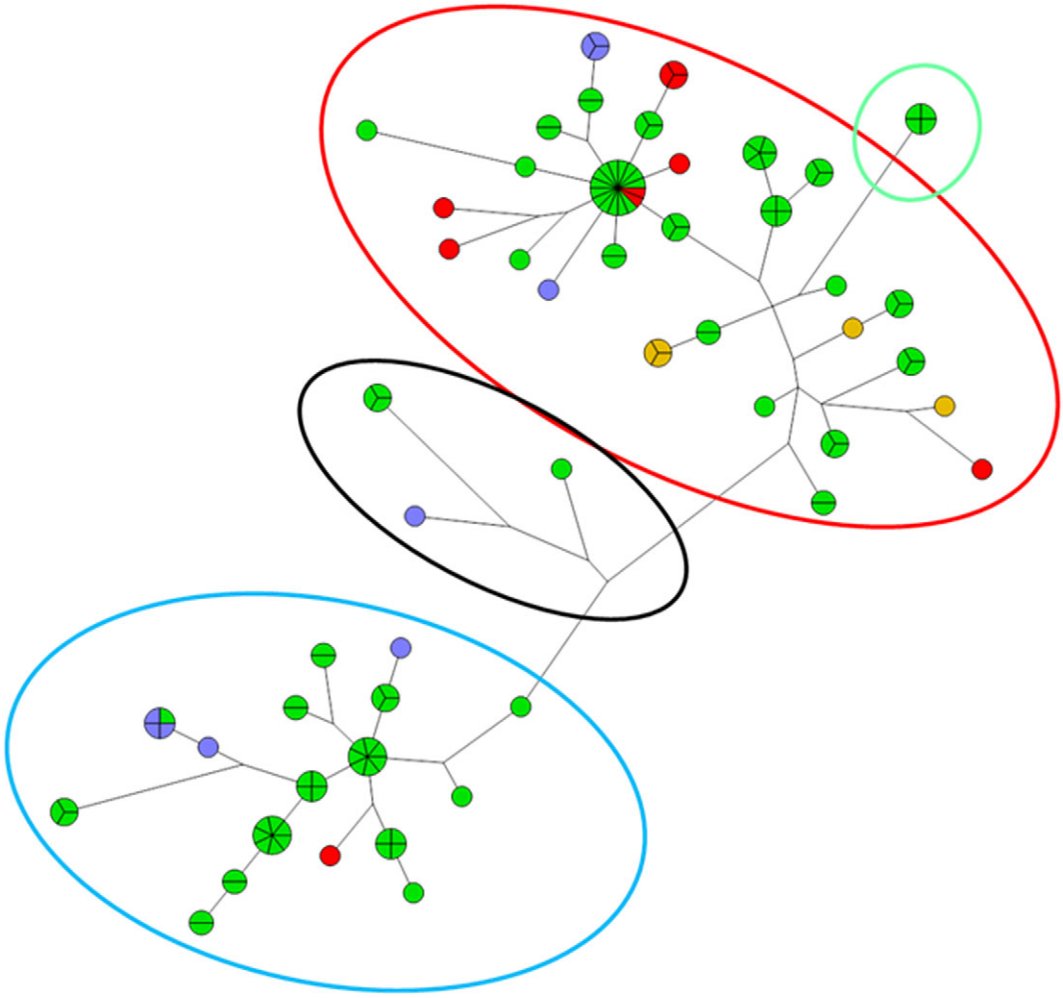

Figure 4. Distribution of *Mycobacterium tuberculosis* genotypes by prison and by family. Green color corresponds to Prison 1, red to Prison 2, purple to Prison 3, and yellow to Prison 4. The external green circle corresponds to the H37RV genotype, the red one to LAM, the black one to S, Uganda, and New-1, and the blue one to Haarlem.

Table 1. Characteristics of the people deprived of liberty diagnosed with pulmonary tuberculosis in four prisons in Colombia

Variables	People in cluster *n* = 29	People with a unique pattern *n* = 35
Age in years, mean (SD)	34 (10)	30 (9)
Time (months) into the prison, median (IQR)	14 (6–25)	9 (2–35)
Previous incarceration, *n* (%)	7 (24.1)	12 (34.3)
Prior history of tuberculosis, *n* (%)	4 (13.8)	4 (11.4)
Current illicit drug use, *n* (%)	17 (58.6)	18 (51.4)
Days of respiratory symptoms, median (IQR)	20 (15–90)	15 (14–120)
People incarcerated in overcrowding conditions, *n* (%)		
≥200	22 (75.9)	14 (40.0)
101–199	6 (20.7)	3 (8.6)
1–100	1 (3.4)	8 (22.9)
≤0	0 (0.0)	10 (28.5)
Prisons, *n* (%)		
1	29 (100)	19 (54.3)
2	0	7 (20.0)
3	0	6 (17.1)
4	0	3 (8.6)
COPD, *n* (%)	3 (10.3)	5 (14.3)
HIV, *n* (%)	1 (3.4)	0 (0.0)

Abbreviations: COPD: Chronic obstructive pulmonary disease; HIV: human immunodeficiency virus; IQR: interquartile range; SD: standard deviation; TB: Tuberculosis.

confirmed tuberculosis. All genotypes were the same during all follow-ups (Table 2).

Finally, person 830 discontinued treatment after 3 months, and started respiratory symptoms 5 months after tuberculosis diagnosis. He had the same *M. tuberculosis* genotypes at diagnosis and in the fifth month (Table 2).

Air exchange inside prisons

In addition to overcrowding conditions, we did not find windows in all cells of the four cell blocks that had the highest number of tuberculosis diagnoses in Prison 1. In the corridors, many windows were blocked by hanging belongings of PDL due to limited space. In overcrowded cell blocks, PDL slept on the floor and the ceilings of bathrooms within the accommodation wings. In these places, PDL also built wooden places that hung from the windows of the corridors where they slept and stored their belongings (called "zarzos" or "busetas"). These sleeping places covered some windows and obstructed air circulation.

The simulation of the most overcrowded cell block in Prison 1 showed air recirculation inside the cells with no exchange (blue color in Figure 6); the air went from one cell to another until it exited through not blocked windows in the corridor (greenish color in Figure 6) or the entrance (red color in Figure 6). Also, there was an extremely low airflow inside the entire accommodation wing and cells (0.3 m/s) (blue color, Figure 6b). The only place with significant airflow was the entrance door to the accommodation wing (red color, Figure 6b). This simulation was similar in every accommodation wing of the four most overcrowded cell blocks in Prison 1.

Discussion

This study shows that 1. people diagnosed with pulmonary tuberculosis in prisons lived in high tuberculosis incidence neighborhoods in Medellin before incarceration; 2. there is tuberculosis transmission inside prisons as documented by new infections, reinfections and mixed infections acquired in prisons; and 3. overcrowding and poor ventilation facilitate tuberculosis transmission.

The latest Colombian tuberculosis report showed that in 2020, 6.6% of tuberculosis diagnoses were PDL (833 persons) [21]. Antioquia is the second department with the highest incidence in Colombia (33.3 per 100000 population), and in Medellin, the communes 2, 3, 8, and 10 still have tuberculosis prevalences ≥100 per 100000 population [22]. The fact that people diagnosed with tuberculosis inside prisons had unique patterns suggests that *M. tuberculosis* infection was acquired in the community, and that all of them came from neighborhoods with high tuberculosis incidence in Medellin highlights the importance of implementing effective screening strategies upon entry to prison.

One of the main challenges is that prisons are designed for security, and public health considerations are secondary priorities. It is well known that poor ventilation and overcrowding conditions increase the risk of infectious diseases transmission, in particular, by respiratory emissions. Tuberculosis transmission in prisons has been previously documented [6,23–28], and it is explained by environmental conditions and high tuberculosis prevalence in prisons. These two characteristics have been identified as amplifiers of tuberculosis within prisons, and between prisons and the community as individuals are incarcerated, transferred, and released, and there are regular visitors such as families and friends of PDL, lawyers, and prison staff. After incarceration, the risk of tuberculosis rises significantly and remains elevated for 7 to 8 years after being released from prison [27,29–31]. In Paraguay, tuberculosis notifications were often attributed to recent transmission in incarcerated and nonincarcerated people, and clinical isolates from incarcerated people were more frequently clustered (92.6% vs. 71%), likely reflecting recent transmission within prisons [27]. These findings highlight the importance of screening, testing, and treatment not only during incarceration but also before transferring PDL between locations and upon release.

In addition, there are other drivers of tuberculosis transmission in prisons such as structural environmental conditions and structural determinants of health. In our study, the only prison that had *M. tuberculosis* clusters was the prison with the highest overcrowding conditions and poor air circulation. We previously reported that PDL in these prisons lived in extremely densely populated cells (<1 m^2 per person) [8], when the ideal is to guarantee at least ≥6 m^2 per person, preferably single celling [32]. An urgent action to halt tuberculosis transmission within prisons is to decrease the overcrowding conditions by avoiding mass incarceration and decarceration strategies. Since 2000, in Central and South America, incarcerated population has grown by 206%, and over the same period, tuberculosis in prisons has increased by 269% and PDL accounted for 11% of all tuberculosis diagnoses [5]. In addition, an increase in overcrowding conditions is associated with reducing tuberculosis-free disease time [33].

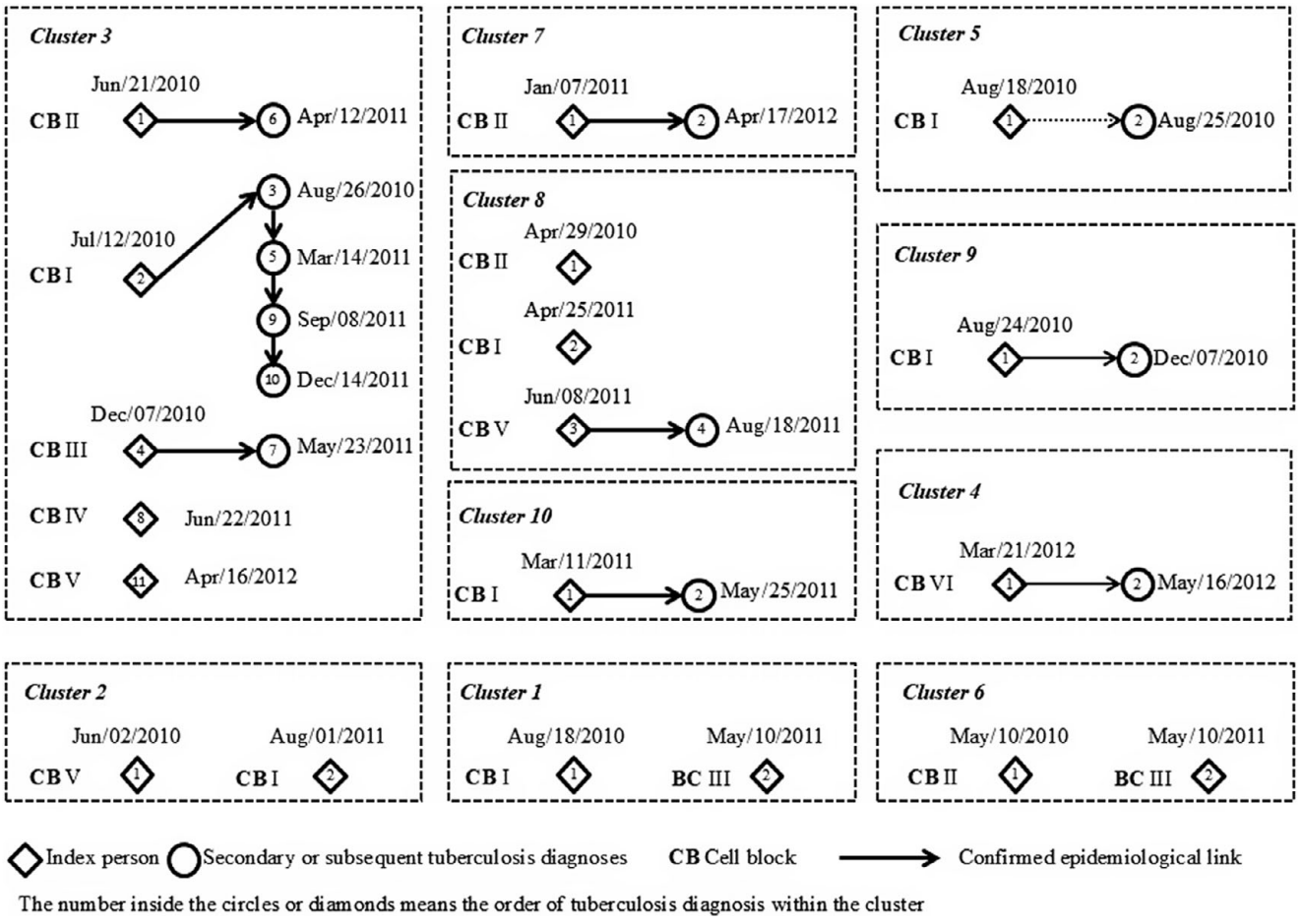

Figure 5. Dynamics of tuberculosis transmission in people deprived of liberty that were in cluster.

Table 2. People who had a change in *Mycobacterium tuberculosis* genotype during or after antituberculosis treatment

Case	Diagnosis or follow-up	Genotype by 24-MIRU-VNTR	Family	Reinfection, relapse, mixed infection	Date DD/MM/YYYY	Comments
250	Diagnosis	124326153220224633413222	LAM		21/06/2010	A person incarcerated in cell block. First person diagnosed in cluster 3
	Control 2	124326153220224633413222	LAM		20/08/2010	A person incarcerated in the hospital inside the prison
	Control 12	**2**25**3**2**5**153**32333372**34**42343**	Haarlem	Reinfection	17/04/2012	A person incarcerated in a cell block. The person was living in the same cell block with person 475, who was diagnosed with tuberculosis on 07/01/2011
	Control 14	225325153323333723442343	Haarlem		25/06/2012	A person incarcerated in the cell block
458	Diagnosis	124326153220224633413222	LAM		07/12/2010	A person incarcerated in cell block. Without epidemiological link
	Control 1	**2**25**3**2**5**153**3**20**33372**3412**34**2	Haarlem	Mixed infection	04/01/2011	A person was held in isolation. Single pattern
	Control 2	124326153220224623443222	LAM	Mixed infection	07/02/2012	A person incarcerated in the hospital inside prison. Single pattern
475	Diagnosis	225325153323333723442343	Haarlem		07/01/2011	PDL incarcerated in block cell
	Control 1	225325153323333723442343	Haarlem		15/02/2011	PDL held in isolation
	Control 4	225325153323323722443353	Haarlem	Mixed infection	12/05/2011	PDL incarcerated in block cell. Single pattern

(*Continued*)

Table 2. (*Continued*)

Case	Diagnosis or follow-up	Genotype by 24-MIRU-VNTR	Family	Reinfection, relapse, mixed infection	Date DD/MM/YYYY	Comments
549	Diagnosis	22632514332223543443363	Haarlem		11/03/2011	PDL incarcerated in block cell. The first person diagnosed in cluster 10
	Control 1	**1**26325153**2**2**02246**43443**32**3	Haarlem	Mixed infection	11/04/2011	PDL was held in isolation. Single pattern
605	Diagnosis	22422616322122484341323**2**	LAM		25/04/2011	PDL incarcerated in the cell block. Family history of TB: mother, father, uncle, sister. Also, previous TB in 2010 and abandoned tuberculosis treatment
	Control 1	22422616322122484341323**2**	LAM		30/05/2011	PDL held in isolation
	Control 2	22422616322122484341323**2**	LAM		01/07/2011	PDL held in isolation
	Control 3	22**5325153323333723442344**	Haarlem	Mixed infection	28/07/2011	PDL incarcerated in cell block. Without epidemiological link
953	Diagnosis	22532515332333623442364	Haarlem		14/12/2011	PDL incarcerated in cell block. Single pattern
	Control 1	**124326**153**2202246**334**13222**	LAM	Mixed infection acquired inside the prison	17/01/2012	PDL held in isolation. PDL was incarcerated with case 869, which was diagnosed on 08/09/2011, and he had the same genotype
990	Diagnosis	22532515332332722413342	Haarlem		13/03/2012	PDL incarcerated in block cell. Single pattern
	Control 1	**124326**153**2202246334**13**222**	LAM	Mixed infection acquired inside the prison	16/04/2012	PDL held in isolation. Before, he lived with case 458 in the same cell block
	Control 2	**2242**26153221224**84**3413**32**2	LAM	Reinfection	16/05/2012	PDL held in isolation with case 993 since 21/03/2012

Note: The bold letters and yellow color indicate the 24-MIRUs-VNTR numbers that were different from the previous *M. tuberculosis* clinical isolate.

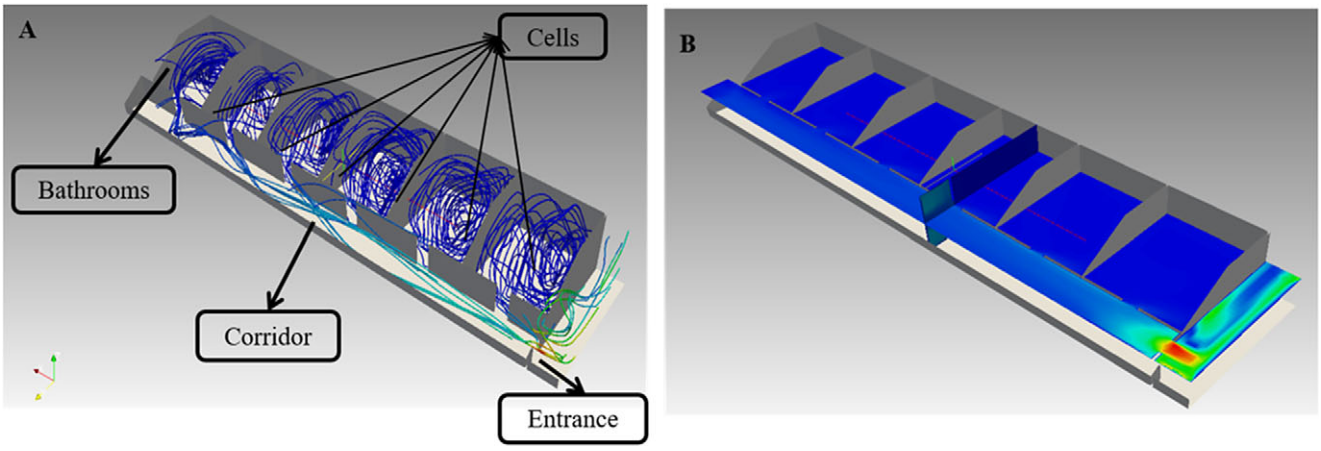

Figure 6. Airflow modeling inside an accommodation wing in Prison 1. (a) Airflow lines illustrate the air circulation inside the most overcrowded accommodation wing using computational fluid dynamics. (b) Velocity fields in the corridor and cells of an accommodation wing in Prison 1. The color means the airflow, blue means very low air circulation, and red means high air circulation.

Another urgent call to action is to address structural environmental conditions by improving the air circulation within prisons and avoiding shared isolation rooms. Previous research has shown that improving ventilation reduces tuberculosis transmission within prisons [34]. This measure will decrease not only tuberculosis transmission but also other respiratory infections that rapidly spread by respiratory emissions [35] such as influenza virus, respiratory syncytial virus, *Streptococcus pneumoniae*, measles, mumps, varicella, adenovirus, and COVID-19.

Tuberculosis transmission inside prisons also happened in the healthcare facility as reported in our study, where people diagnosed with tuberculosis acquired additional *M. tuberculosis* isolates while in shared isolation. Prisons in Colombia [36] and other countries have reported deficiencies in their infrastructures and health services [37–39], such as lack of or limited intersectoral policies between healthcare, justice, and public health systems, limited resources and staff, and lack of prison-specific guidelines with a person-centered approach, among others. Due to limited resources and spaces, some prisons isolate and quarantine PDL diagnosed with tuberculosis in shared rooms rather than single rooms. To protect people's health and avoid infectious disease outbreaks, it is essential to develop specific protocols for each prison considering health and security that include ideally single celling, increased resources and access to health care, long term, social and economic

support, and more importantly, decarceration strategies [32] as previously mentioned.

Finally, The most frequent sublineages in our study were similar to those previously reported in the general population in Medellin [40], and Colombia [41,42], and different from what was reported by Guerra et al. in Guaduas prison in Colombia (Haarlem, 68.4%; LAM, 26.3%) [6]. Transmission inside prisons has some consequences on the Mycobacterium's adaptability. A national study in Georgia showed that the high transmission rate involving PDL allows Mycobacterium isolates to acquire compensatory mutations that help them keep their ability to grow without losing their fitness capacity [43]. Also, *M. tuberculosis* isolates found in clusters have strong virulence and the ability to spread [44] threats tuberculosis control programs.

Conclusions

Our study shows tuberculosis transmission within prisons and that people also acquired *M. tuberculosis* infection before incarceration but developed tuberculosis while incarcerated. Overcrowding and poor ventilation conditions are playing a significant role in tuberculosis transmission in prisons; therefore, it is essential to reconsider mass incarceration policies and decarceration strategies. It also requires to design prisons with a public health and equity lens. Finally, it is essential to implement screening, testing and treatment upon entry to prison, during incarceration and upon release.

Supplementary material. The supplementary material for this article can be found at http://doi.org/10.1017/S0950268825000184.

Data availability statement. Individual-level data of PDL included in this manuscript after de-identification are considered sensitive and will not be shared. The study methods, statistical analyses, and results are all described in detail in the methods and throughout the manuscript.

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Author contribution. ZVR conceptualized, designed, and led the research. LMA-R and GIN-C measured all prisons. LMA-R drafted all maps. LA performed the georeferencing mapping. TR performed the laboratory testing and the MIRU-VNTR genotyping and analysis. NR performed the ventilation measurements and did the simulation. Visualization: ZVR. All authors contributed to the analysis and interpretation of data. ZVR drafted the paper. All authors reviewed it critically for important intellectual content. All authors read and approved the manuscript submitted. MPA and ZVR acquired funding. Project administration: ZVR.

Competing interest. The authors declare no conflict of interest.

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