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Strain-Specific Differences in Two Large *Mycobacterium tuberculosis* Genotype Clusters in Isolates Collected from Homeless Patients in New York City from 2001 to 2004

Michelle Macaraig,[1]* Tracy Agerton,[1,2] Cynthia R. Driver,[1] Sonal S. Munsiff,[1,2] Jalaa' Abdelwahab,[2] Julie Park,[1] Barry Kreiswirth,[3] Jeffrey Driscoll,[4] and Benyang Zhao[1]

New York City Department of Health and Mental Hygiene, New York, New York[1]; Centers for Disease Control and Prevention, Atlanta, Georgia[2]; Public Health Research Institute, Newark, New Jersey[3]; and Wadsworth Center, New York State Department of Health, Albany, New York[4]

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We studied two large *Mycobacterium tuberculosis* genotype clusters associated with recent outbreaks in homeless persons to determine factors associated with these tuberculosis (TB) strains. Isolates from all culture-positive TB cases diagnosed from 1 January 2001 to 31 December 2004 were genotyped. Patients whose isolates had identical restriction fragment length polymorphism patterns and spoligotypes were considered clustered. Health department records were reviewed and reinterviews attempted for clustered cases. Patients with the Cs30 and BEs75 strains were compared to other genotypically clustered cases and to each other. The two largest genotype clusters among homeless persons were the Cs30 strain ($n = 105$) and the BEs75 strain ($n = 47$). Fifty-one (49%) patients with the Cs30 strain and 28 (60%) with the BEs75 strain were homeless. Compared to patients with the BEs75 strain, patients with the Cs30 strain were less likely to be respiratory acid-fast bacillus smear positive (51% versus 72%). Furthermore, patients with the BEs75 strain were more likely to be HIV infected (74% versus 42%), which suggests that most patients with this strain advanced to disease after recent infection. Cases in clusters of strains that have been circulating in the community over a long time period, such as the Cs30 strain, require additional investigation to determine whether clustering is a result of recent transmission or reactivation of remote infection.

Although the tuberculosis (TB) case rate in New York City (NYC) has been declining for 10 years, from 52 per 100,000 persons in 1995 to 13.5 in 2002, it remains almost three times higher than the national average. Similar to the distribution in other large metropolitan areas, the distribution of TB is not even throughout the city; rather, TB exists in communities or settings where localized transmission can occur, such as in social networks and among homeless persons (2, 25, 32). An increase in TB cases over the expected number in a specific location or social network may indicate TB transmission.

Genotyping has been a useful tool in recognizing an increase of TB cases in congregate settings. Unlike traditional contact investigation, which mainly establishes transmission from person to person, examining cases with identical genotypes (i.e., clustered cases) reveals potential sites of transmission that might not otherwise have been known. The advent of genotyping in TB programs has assisted in disease control and surveillance by directing efforts to interrupt the spread of disease, especially among the homeless (2, 14, 17, 18, 22, 23, 31). From 2002 to 2003, a 5% increase in TB incidence in NYC was partly attributed to an increase of TB in homeless persons (26). The number and proportion of homeless TB patients increased from 49/1,084 (5%) in 2002 to 86/1,140 (8%) in 2003 (26). From 2001 to 2003, the average annual age-adjusted TB rate among adult homeless persons in Department of Homeless Services (DHS) shelters was 176 per 100,000 population (95% confidence interval [CI], 128 to 223), 44 times the citywide average annual age-adjusted adult TB rate of 4 per 100,000 population (95% CI, 17 to 18) (NYC Department of Health and Mental Hygiene [DOHMH], unpublished data).

During 2001 to 2003, homeless persons with TB in NYC were more likely than nonhomeless TB patients to have an isolate with a genotype that matched that of another case: 62% of homeless patients compared to 21% of nonhomeless patients (P value < 0.001) (NYC DOHMH, unpublished data). Two of the largest genotype clusters, Cs30 and BEs75, were associated with recent outbreaks of TB in homeless persons in NYC. However, only one of these clusters, BEs75, was highly localized in one single-room-occupancy hotel. We examined demographic, clinical, and social factors associated with these TB strains in order to direct prevention efforts among the homeless.

MATERIALS AND METHODS

All culture-positive TB cases reported to the NYC DOHMH from 1 January 2001 to 31 December 2004 were assessed for eligibility for analysis. Demographic and clinical information for each patient was obtained by both patient interview and medical record review by trained Bureau of Tuberculosis Control staff using standard data collection forms. The information obtained includes presence and onset of symptoms; prior TB history; risk factors for TB, such as homelessness; outcome of contact investigation; and medical evaluation information, including chest radiograph results, tuberculosis treatment, and laboratory studies. Patients were offered human immunodeficiency virus (HIV) testing by their medical providers as part of routine care; however, not all patients accepted HIV testing. HIV test results were obtained from patient interviews and medical record reviews as part of routine TB control program activities and used for this study. HIV status was coded as negative if there was a negative HIV test result within

* Corresponding author. Mailing address: New York City Department of Health and Mental Hygiene, 225 Broadway, 22nd Floor, New York, NY 10007. Phone: (212) 442-9932. Fax: (212) 442-9997. E-mail: mmacarai@health.nyc.gov.

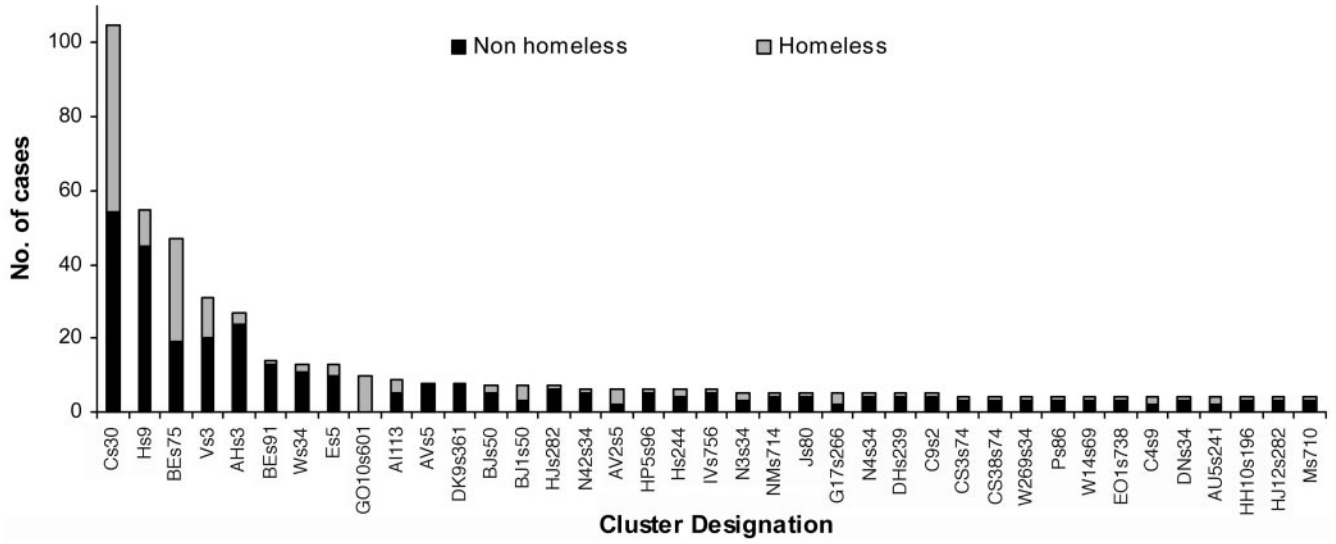


FIG. 1. Number of homeless TB patients in 39 large genotype clusters (≥4 cases; $n = 474$) in NYC from 2001 to 2004.

the year before the diagnostic evaluation for TB documented by laboratory or physician report. HIV status was coded as positive if the patient gave a history of a positive HIV test or AIDS or if there was documentation in the medical history or a laboratory result of a positive HIV test result. If neither of these criteria were met, patients were classified as having unknown HIV status for these analyses.

Genotyping of the first isolate of all TB cases has been performed in NYC since 1 January 2001. Isolates were genotyped using both restriction fragment length polymorphism (RFLP) with the insertion sequence IS*6110* and spacer oligonucleotide (spoligotyping) analysis (6, 9, 13, 16). Genotype results were entered into the molecular epidemiology database. Case isolates having identical RFLP and spoligotype patterns were defined as clustered and assigned a unique cluster number. Only cases that had genotypes matching another case diagnosed within the study period were included in the study. These analyses were based on available genotyping results as of June 2005.

Cluster investigations. All clustered patients were investigated to find epidemiologic links between patients and to locate potential sites of TB transmission-where additional measures to find and treat infected contacts could be implemented to interrupt the spread of disease. The traditional contact investigation records were reviewed. If an epidemiologic link was not revealed during initial contact investigation, a cluster investigation was initiated.

In cluster investigations, medical records, contact investigation results, and information on current and prior home addresses, work and other frequented sites, activities such as attendance of religious services, prior hospitalization or long-term care admissions, and admissions to drug treatment or rehabilitation centers or other health care institutions were reviewed. DOHMH records of the patients' contacts, such as household members, friends and family, work or school contacts, social workers, or other individuals the patient spent time with prior to or during the infectious period, were reviewed for demographic and clinical characteristics. If an epidemiologic link was not found after reviewing the above information and the patient was still in treatment or completed treatment less than 1 year before the cluster investigation, a telephone reinterview of the patient by an epidemiologist was performed using a standard interview guide to obtain additional information or clarify information already collected during the initial phase of the investigation.

In addition to record review and patient reinterview, a housing history was obtained from the DHS and HIV/AIDS Service Administration (HASA) for all identified homeless TB patients. Dates of stay for all patients that resided in a shelter or single-room-occupancy hotel were examined in order to identify overlapping stays with an infectious TB case and tuberculin skin test conversions.

According to the Centers for Disease Control and Prevention guidelines for reporting of TB cases, a homeless person is defined as someone without fixed, regular, and adequate nighttime residence or whose primary nighttime residence is that of a supervised publicly or privately operated shelter designed to provide temporary housing or who sleeps in a place not intended for regular sleeping accommodations (5, 34). For this analysis, we considered the person homeless if they met any of the above criteria at any point prior to or at the time of diagnosis of TB.

Epidemiologic links are defined as patients in a cluster having contacts in common, frequenting the same site at the same time prior to TB diagnosis, or identifying another patient in the same cluster as a contact. If the investigation did not yield any of the above links, patients were classified as not having an epidemiologic link. All data collected during the investigation were entered into the molecular epidemiology database using Microsoft Access 2000, which was used to identify clustered cases.

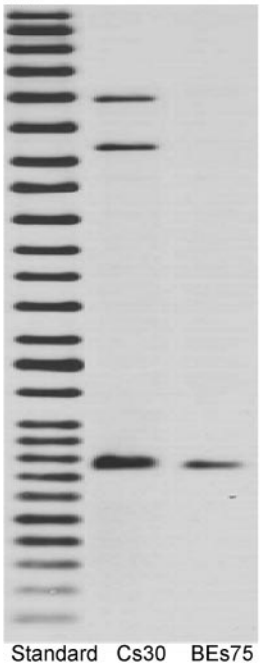
All TB cases verified in NYC from 1 January 2001 to 31 December 2004 with a genotype that was identical to that of another case during the study period were eligible for inclusion in the analysis. Subanalysis was performed by examining the two largest outbreak clusters in homeless persons, the Cs30 and BEs75 strains. Patients with the Cs30 strain were compared to patients with the BEs75 strain as well as to other clustered cases. We also compared cases in the two clusters by homeless status. The types of housing facilities in which homeless patients resided were also examined. The chi-square test was used for bivariate comparisons of discrete variables, and a P value of <0.05 was considered statistically significant. Logistic regression was used for multivariate analysis of the odds of being infected with the Cs30 and BEs75 strains compared to strains from other clustered cases and the characteristics of patients with the Cs30 strain compared to those of patients with the BEs75 strain. Variables that were significant in bivariate analysis and variables that are known to be associated with risk for clustering were included in the model. Analyses were conducted using PC SAS version 8 (SAS Institute, Inc., Cary, NC).

The analyses received waiver from review by the NYC DOHMH Institutional Review Board because data were obtained for nonresearch purposes. In addition, the research was reviewed by the Associate Director for Science of the National Center for HIV, STD and Prevention of the CDC; the research was determined not to be human subjects research, and institutional review board review was not required.

RESULTS

From 1 January 2001 to 31 December 2004, 3,199 (92%) of 3,494 isolates of culture-positive TB cases verified in NYC were genotyped. Of these, 3,123 (98%) cases could be assessed for clustering; 1,178 (38%) had isolates with a genotype that was identical to that of another case in the study period and were eligible for this analysis. The 1,178 cases were in 291 clusters, of which 474 (40%) cases were in 39 clusters of ≥4 patients each (defined as large clusters) and 704 (60%) cases were in 252 clusters of <4 patients. Fifty percent of cases in

A



B

Strain	Spoligotype	Octal Code
Cs30	●●● ▯▯▯▯▯▯▯▯▯▯▯ ●●●● ▯ ●●●●●●●●●●●●●● ▯▯▯▯ ●●● ▯ ●●●	700036777760731
BEs75	●●●●●●●●●●●●●●●● ▯ ●● ▯▯▯▯▯ ●●●●●●●● ▯▯▯▯ ●● ▯▯▯▯ ●	777776407760601

FIG. 2. IS*6110* RFLP patterns (A) and spoligotype analysis (B) of the Cs30 strain and the BEs75 strain.

large genotype clusters were in the four largest clusters (Cs30, Hs9, BEs75, and Vs3) (Fig. 1). The Hs9 strain had been associated with nosocomial transmission (27), and patients with the Vs3 strain were primarily persons who reported substance abuse and who resided in one geographic area of NYC (NYC DOHMH, unpublished data). The Cs30 and BEs75 strains were found in recent TB outbreaks among the homeless in NYC (NYC DOHMH, unpublished data). The Cs30 and BEs75 clusters had the highest proportion of homeless-patient cases: 57% in the BEs75 cluster and 48% in Cs30, compared to 36% in Vs3 and 18% in Hs9. In addition, homeless patients with the Cs30 and BEs75 strains comprised 48% of all homeless-patient cases in the large clusters. Since patient clusters with Hs9 and Vs3 strains had a lower proportion of homeless patients and were not associated with outbreaks among homeless patients, we excluded these from our analyses. The IS*6110* RFLP pattern and octal code for Cs30 and BEs75 strain are shown in Fig. 2.

Cs30 strain. The annual number of patients with the Cs30 strain did not vary greatly during the study years: 29 (9%) cases in 2001, 25 (8%) in 2002, 31 in 2003 (10%), and 20 (9%) in 2004. The number of HIV-infected patients with the Cs30 strain was highest in 2002: there were 10 in 2001, 20 in 2002, 8 in 2003, and 6 in 2004. Fifty-one (49%) patients with the Cs30 strain were homeless; 46 (90%) patients stayed in 44 shelters, and 24 (56%) of these patients were ever in DHS facilities. All 105 cases were investigated for epidemiologic links. Four (4%) had epidemiologic links established in the initial contact investigation. Twenty (19%) had epidemiologic links found as a result of the cluster investigation. Seventy-three were eligible for reinterview; 4 (5%) refused reinterview, 12 (16%) died prior to investigation, 38 (52%) had no usable phone number or address or could not be contacted despite multiple attempts, and 19 (26%) were reinterviewed. An additional 3 cases were found to have epidemiologic links through reinterviews, bringing the total with epidemiologic links to 27 (26%).

BEs75 strain. The number of patients with the BEs75 strain fluctuated during the study period: 17 (5%) in 2001, 6 (2%) in 2002, 17 (6%) in 2003, and 7 (3%) in 2004. Sixty percent of patients with the BEs75 strain were homeless and 75% were HIV infected. Nine (20%) patients had epidemiologic links identified in the initial contact investigation and were not interviewed, 5 (11%) died prior to the cluster investigation, 2 (4%) refused reinterview, 21 (45%) had no locating information or could not be contacted despite multiple attempts, and 10 (21%) were reinterviewed. Of the 47 patients with this strain, 18 (38%) were associated with one residential building where HASA clients are housed; 13 patients were HASA residents and had overlapping stays with an infectious case, 3 patients were nonresidents who were contacts of HASA resident cases and frequented the building, 1 patient shared a contact to a patient who was a HASA resident, and 1 patient lived in the building but was not a HASA client. Of the 28 homeless patients with the BEs75 strain, 26 (93%) resided in 35 different housing facilities prior to diagnosis. Twenty-five (53%) patients had epidemiologic links identified, of which 18 were found by shelter history review, 6 were found through traditional contact investigation, and 1 was found from reinterview during the cluster investigation.

Patients with the Cs30 and BEs75 strains compared to all other clustered cases. Compared to other clustered cases (n = 1,025), patients with the Cs30 strain (n = 105) were more likely

TABLE 1. Characteristics of patients with the Cs30 strain, the BEs75 strain, and other clustered strains in NYC from 2001 to 2004

Characteristic	% of patients with given characteristic[a]			Odds ratio (95% CI) for:		
	Cs30 (n = 105)	BEs75 (n = 47)	Other[b] (n = 1,025)	Cs30 versus BEs75	Cs30 versus other[e]	BEs75 versus other[f]
Median age in years (range)	45 (0–75)	47 (18–77)	40 (0–100)	0.44 (0.98–1.00)	0.99 (0.98–1.00)	0.99 (0.98–1.01)
Homelessness						
Yes	49	60	13	0.64 (0.30–1.36)	6.12 (3.93–9.55)	9.55 (4.99–18.36)
No	51	40	87			
Sex						
Female	22	38	35	0.45 (0.20–1.02)	0.51 (0.31–0.85)	1.13 (0.59–2.14)
Male	78	62	64			
Country of birth						
United States	80	85	42	0.70 (0.25–1.92)	5.43 (3.24–9.19)	7.76 (3.30–19.16)
Not United States	20	15	57			
Race and ethnicity						
Asian	3	2	16	2.00 (0.00–88.2)	0.21 (0.04–1.17)	0.14 (0.00–2.05)
Hispanic	24	19	37	1.39 (0.14–11.61)	0.77 (0.24–2.73)	0.55 (0.11–3.83)
Non-Hispanic black	51	51	28	1.13 (0.13–7.92)	2.18 (0.71–7.44)	1.94 (0.42–12.28)
Non-Hispanic white	4	4	5	Referent	Referent	Referent
Unknown	0	23	14	0.86 (0.09–7.08)	1.61 (0.48–5.90)	1.86 (0.37–12.63)
Disease site						
Any pulmonary	85	91	84	0.52 (0.14–1.79)	1.10 (0.61–2.00)	2.12 (0.72–7.05)
Extrapulmonary only	15	9	16			
Respiratory AFB smear result						
Positive	51	72	54	0.49 (0.22–1.12)	0.93 (0.60–1.44)	1.87 (0.94–3.80)
Negative	41	28	40	Referent	Referent	Referent
Unknown	8	2	7	2.42 (0.26–56.33)	1.06 (0.44–2.47)	0.44 (0.02–3.29)
Presence of cavitary lesions						
Yes	15	11	19	1.51 (0.48–5.08)	0.76 (0.42–1.35)	0.50 (0.17–1.34)
No	85	89	81			
HIV serostatus						
Infected	42	74	20	0.31 (0.13–0.73)	2.68 (1.68–4.28)	8.72 (4.17–18.61)
Uninfected	43	23	55	Referent	Referent	Referent
Unknown	15	2	25	3.91 (0.45–87.41)	0.77 (0.41–1.44)	0.20 (0.01–1.48)
Incarcerated[c]						
Yes	2	4	3	0.44 (0.04–4.51)	0.69 (0.11–3.04)	1.58 (0.25–7.82)
No	98	96	97			
Substance abuse[d]						
Yes	49	66	25	0.49 (0.22–1.05)	2.90 (1.89–4.44)	5.94 (3.08–11.57)
No	51	34	75			

[a] Values for all characteristics except for age are percentages.
[b] "Other" indicates other clustered cases.
[c] Incarcerated at the time of diagnosis.
[d] Any history of injection drug use, noninjection drug use, or alcohol abuse.
[e] Excluding BEs75.
[f] Excluding Cs30.

to be homeless, male, born in the United States, and HIV infected and to have a history of substance abuse ($P < 0.05$) (Table 1). A multivariate model was used to adjust for sex, country of origin, race and ethnicity, HIV serostatus, and homelessness. In this model, compared to other clustered cases, being male, born in the United States, non-Hispanic black, and homeless was more likely to be associated with having the Cs30 strain (Table 2).

Compared to other clustered cases (n = 1,025), patients with the BEs75 strain (n = 47) were more likely to be homeless, born in the United States, and HIV infected and to have a history of substance abuse (Table 1). When country of origin, race and ethnicity, HIV serostatus, and homelessness were adjusted for in the multivariate model, patients with the BEs75 strain were more likely to be born in the United States, HIV infected, and homeless (P value < 0.05) (Table 2).

TABLE 2. Multivariate analysis of patients with the Cs30 and BEs75 strains

Characteristic	Odds ratio (95% CI) for[a]:			
	Cs30 versus other clustered cases[b]	BEs75 versus other clustered cases[c]	Cs30 versus BEs75	Homeless patients with Cs30 versus homeless patients with BEs75
Male	1.84 (1.11–3.06)§	–	2.47 (1.11–5.49)§	2.80 (0.72–10.90)
Born in the United States	3.60 (2.11–6.14)§	2.89 (1.19–7.00)§	1.32 (0.44–3.96)	–
Non-Hispanic black	1.73 (1.11–2.69)§	0.95 (0.02–4.56)	1.00 (0.39–2.59)	–
HIV infected	1.11 (0.48–5.12)	5.54 (2.67–11.50)§	0.23 (0.11–0.51)§	0.13 (0.03–0.51)§
Respiratory AFB smear	–	–	0.67 (0.29–1.56)	0.22 (0.07–0.71)§
Homeless	3.63 (2.31–5.72)§	4.01 (2.06–7.80)§	0.95 (0.40–2.25)	–

[a] The section sign (§) indicates that the result was significant in the multivariate model. Dashes indicate that variables were excluded.
[b] Excluding BEs75.
[c] Excluding Cs30.

Patients with the Cs30 strain compared to patients with the BEs75 strain. Compared to patients with the BEs75 strain, patients with the Cs30 strain were less likely to be HIV infected (Table 1). After adjusting for sex, country of birth, race and ethnicity, HIV serostatus, respiratory acid-fast bacillus (AFB) smear, and homelessness, patients with the Cs30 strain were more likely to be male and less likely to be HIV infected (Table 2).

When stratified by homelessness, patients with the Cs30 strain were more likely to be male and less likely to be respiratory AFB smear positive and HIV infected than homeless patients with BEs75 (Table 3). After adjusting for sex, HIV status, and respiratory AFB smear, homeless patients with the Cs30 strain were less likely to be HIV infected (odds ratio [OR], 0.13; 95% CI, 0.03 to 0.51) and respiratory AFB smear positive (OR, 0.22; 95% CI, 0.07 to 0.71) than homeless patients with BEs75 (Table 2).

DISCUSSION

Our data point to important differences in the epidemiology of two large TB genotype clusters in NYC. While genotype clustering is generally thought to reflect recent transmission, characteristics of cases in the largest cluster caused by a common strain (Cs30) seen for more than 15 years in NYC (1, 10; NYC DOHMH, unpublished data) suggest that disease was due to remote infection compared to cases with the BEs75 strain. The cluster of the BEs75 strain, a more recent strain first identified in NYC in 1997, was associated with a larger proportion of patients that were infectious and HIV infected. Respiratory AFB smear positivity is associated with increased TB transmission, while HIV infection is associated with higher risk of progression to disease. AFB smear positivity increases the likelihood of transmission, since TB cases with a positive AFB smear are more likely to be infectious than respiratory smear-negative cases (4, 12, 28, 30). A study of close contacts in Finland showed a higher risk of secondary cases among contacts to AFB smear-positive cases than AFB smear-negative cases (19). Based on respiratory smear results, patients with the BEs75 strain were significantly more infectious than patients with the Cs30 strain, which increases the likelihood of transmission. In addition, 53% of patients with the BEs75 strain had epidemiologic links compared to 26% among patients with the Cs30 strain, which indicates that patients with

TABLE 3. Characteristics of homeless patients with the Cs30 strain and the BEs75 strain in NYC from 2001 to 2004

Charateristic[a]	% of patients with given characteristic[b]		Crude OR (95% CI)[c]
	Cs30 infected (n = 51)	BEs75 infected (n = 28)	
Median age in years (range)	44 (22–62)	45 (28–61)	1.02 (0.96–1.07)
Sex			
Female	**12**	**36**	**0.24 (0.06–0.86)**
Male	88	64	
Country of birth			
United States	84	93	0.41 (0.06–2.37)
Not United States	16	7	
Race and ethnicity			
Asian	2	4	1.00 (0.00–436.06)
Hispanic	8	14	n/a
Non-Hispanic black	29	54	1.00 (0.00–41.14)
Non-Hispanic white	2	4	Referent
Unknown	14	25	1.00 (0.00–47.26)
Disease site			
Any pulmonary	90	100	n/a
Extrapulmonary only	10	0	
Respiratory AFB smear result			
Positive	**51**	**82**	**0.26 (0.07–0.88)**
Negative	43	18	Referent
Unknown	6	0	n/a
Presence of cavitary lesions			
Yes	16	7	2.42 (0.42–17.95)
No	84	93	
HIV serostatus			
Infected	**53**	**89**	**0.18 (0.04–0.77)**
Uninfected	35	11	Referent
Unknown	12	0	n/a
Incarcerated[d]			
Yes	4	4	1.10 (0.07–32.27)
No	96	96	
Substance abuse[e]			
Yes	69	23	0.48 (0.13–1.65)
No	31	5	

[a] Bold rows indicate significant variables.
[b] Values for all characteristics except for age are percentages.
[c] n/a, not applicable.
[d] Incarcerated at the time of diagnosis.
[e] Any history of injection drug use, noninjection drug use, or alcohol abuse.

the BEs75 strain were in recent contact with another infectious patient with the BEs75 strain. Once infected with the TB bacteria, HIV is the greatest single risk factor for progressing to active disease (7, 20). Since patients with the BEs75 strain were more likely to be HIV infected than patients with the Cs30 strain, it is likely that patients with the BEs75 strain progressed rapidly to disease after recent infection. For these reasons, TB disease in patients with the Cs30 strain was more likely caused by reactivation of latent TB infection acquired during the epidemic years of the early 1990s, while disease in patients with the BEs75 strain was more likely the result of very recent transmission.

Even though these two strains have few IS*6110* copies (Cs30 has three and BEs75 has one), they have been shown to be clonal through various strain typing methods: inverse PCR, polymorphic guanine- and cytosine-rich repetitive sequence, and variable number tandem repeat (10, 21). Furthermore, the high proportion of patients with the BEs75 strain that were linked epidemiologically also suggests that all of these cases were due to a single strain.

Molecular information, in conjunction with conventional epidemiologic methods in our study, provided insight into TB transmission patterns reported by others (8, 35). Many investigators have examined the differences between clustered cases and nonclustered cases (18, 31). However, few studies have examined characteristics of specific clusters (10, 24, 25). Our results suggest that cluster-specific differences may provide important information that is lost in aggregate analysis of clustered cases.

The high rate of tuberculosis among individuals in homeless settings is likely due to several factors that increase the risk of development of disease or transmission. First, while homeless persons have a high risk of latent TB infection (LTBI), it is difficult to screen unstably housed individuals for LTBI, which is present without symptoms. Even once LTBI is diagnosed among individuals in this population, it is often difficult to initiate and complete LTBI treatment, which usually requires taking medications for 9 months (NYC DOHMH, unpublished data). Second, when an individual has LTBI, factors such as drug abuse (29) and HIV infection increase the risk of progression to active disease (11, 15, 33). And finally, there is increased opportunity for transmission among homeless persons in congregate settings once a case is present due to the increased number and proximity of contacts.

Other investigators have recommended focusing on locations of TB exposure rather than traditional contact identification for contact tracing among homeless persons (2, 3). Housing records are an excellent source of information for location-based contact investigation. Information obtained from DHS and HASA housing histories and address matching have been useful in NYC for making additional epidemiologic links over those obtained from traditional interviews among the homeless. Furthermore, once a genotype cluster is known to be associated with transmission at a particular location, future patients having the same strain can be asked whether they frequented that location prior to diagnosis.

Our investigation was limited by several factors. Since the number of cases in these clusters was relatively small, there may have been other factors associated with having the Cs30 strain that were not detected due to limited power. As genotyping of additional culture-confirmed TB isolates is obtained, additional differences between clusters may become evident. Second, many patients in the Cs30 and BEs75 groups could not be reinterviewed to identify potential locations of common exposure; thus, epidemiologic links between cases were likely underascertained.

The health department and the DHS are collaborating to improve detection of TB among persons with a history of homelessness. Matches of the TB case registry and the DHS database are conducted at regular intervals to determine whether suspected or confirmed TB patients reside in a DHS facility. Once homelessness in a TB patient is recognized, the housing history is reviewed to ascertain the need for additional contact investigation among shelter residents. The health department also works with DHS to find homeless persons who were exposed to a TB case at one facility but moved prior to the contact investigation. Finally, our collaboration with the DHS has facilitated tracking of nonadherent patients residing in any of the DHS facilities, thereby ensuring completion of treatment among patients and contacts.

In summary, TB genotyping was useful in identifying transmission among HIV-infected homeless persons. Differences among cases in two large genotype clusters suggest differences in the dynamics of transmission of these clusters. While continuing transmission from common TB strains may occur, reactivation of TB from strains transmitted during epidemic periods is also a source of genotype clustering. All cases in a cluster do not necessarily represent recent transmission; they may represent reactivation of infection acquired more remotely. To determine if clusters of TB patients are the result of recent transmission, additional investigations are often required.

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