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Factors Associated with Recently Transmitted *Mycobacterium tuberculosis* strain MS0006 in Hinds County, Mississippi

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Abstract

Objective—The objective of this study was to investigate risk factors associated with tuberculosis (TB) transmission that was caused by *Mycobacterium tuberculosis* strain MS0006 from 2004 to 2009 in Hinds County, Mississippi.

Methods—DNA fingerprinting using spoligotyping, mycobacterial interspersed repetitive unit, and IS6110-based restriction fragment length polymorphism of culture-confirmed cases of TB was performed. Clinical and demographic factors associated with strain MS0006 were analyzed by univariate and multivariate analysis.

Results—Of the 144 cases of TB diagnosed during the study period, 117 were culture positive with fingerprints available. There were 48 different strains, of which 6 clustered strains were distributed among 74 patients. The MS0006 strain accounted for 46.2% of all culture-confirmed cases. Risk factors for having the MS0006 strain in a univariate analysis included homelessness, HIV co-infection, sputum smear negativity, tuberculin skin test negativity, and noninjectable drug use. Multivariate analysis identified homelessness (odds ratio 7.88, 95% confidence interval 2.90-21.35) and African American race (odds ratio 5.80, 95% confidence interval 1.37-24.55) as independent predictors of having TB caused by the MS0006 strain of *M. tuberculosis*.

Conclusions—Our findings suggest that a majority of recently transmitted TB in the studied county was caused by the MS0006 strain. African American race and homelessness were significant risk factors for inclusion in the cluster. Molecular epidemiology techniques continue to provide in-depth analysis of disease transmission and play a vital role in effective contact tracing and interruption of ongoing transmission.

Keywords

tuberculosis; HIV; Mississippi; homeless; molecular epidemiology

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In 2009, approximately 9.4 million new cases of tuberculosis (TB) were reported globally (8.9-9.9 million), representing a case rate of 137 cases per 100,000 population; the majority of the cases occurred in regions of Africa and Asia.¹ Concentrated efforts in the United States to control TB transmission have resulted in a decrease in the overall case rate (3.8/100,000 in 2010, down from 4.2/100,000 in 2009), but there is less success in controlling TB in foreign-born individuals, and they pose a challenge to the overall elimination of TB.²⁻⁴

In the southeastern US states, people born in the United States account for the majority of new TB cases.⁴ It is not entirely clear why TB predominates in the US-born population in some states. Researchers in South Carolina identified alcohol and drug abuse as major contributors to the continual transmission of *Mycobacterium tuberculosis* in their state.⁵ Other studies identified factors such as homelessness, excessive alcohol usage, HIV infection, and being African American as associated with an increase in TB transmission in US-born populations.^{2,6,7}

Mississippi has a long-standing directly observed therapy program and has benefited from a 19-year-long decrease in the incidence of TB (14.6/100,000 in 1986 to 3.5/100,000 in 2005)⁸; however, in 2007, an unexplained increase (4.7/100,000) in the rate of new TB cases was noted.^{3,4} A particular *M tuberculosis* strain initially identified as PCR00225 and later named MS0006 appeared to be a major cause of transmitted disease in the state (unpublished health department data). In addition, a sociodemographic analysis conducted in Hinds County by the Mississippi State Department of Health (MSDH) showed an increase in TB cases in the homeless population, from 12% in 2008 to 19.8% in 2009; a large number of cases were identified as having the MS0006 strain.⁹ DNA fingerprinting is performed on all *M tuberculosis* isolates in Mississippi and serves as a tool to differentiate recent transmission from reactivation of remote exposures. Identification of the locally predominant MS0006 strain allowed for the prompt introduction of aggressive public health measures to interrupt further transmission.

In this population-based study, we investigated the risk factors associated with TB transmission in Hinds County. Hinds County is the most populous in the state, with 66% African American, 47.2% male, 98.9% US born, and 23% of the population living below the poverty line¹⁰; the county has a homeless population of approximately 700 to 1000 individuals.⁹ In 2009, the HIV case rate for the county was reported as being 54.9/100,000 population.¹¹ According to MSDH data, the case rates for Hinds County were 6.5 in 2008 and 19.8 in 2009. The objective of the present study was to investigate the risk factors that were associated with *M tuberculosis* strain MS0006 TB transmission from 2004-2009 in Hinds County.

Methods

Study Population

Between January 2004 and December 2009, 147 unduplicated TB cases from Hinds County were reported to the MSDH Office of Tuberculosis and Refugee Health. All of the cases were diagnosed and classified according to the Centers for Disease Control and Prevention (CDC) case and laboratory definition for active TB. Demographic, social, and clinical data were obtained from the MSDH *M tuberculosis* database (Communicable Disease Control Information System). Molecular data and cluster designation was provided by the CDC regional laboratory for Mississippi. The study was reviewed and approved by the institutional review board for studies on human subjects at the MSDH.

Study Design

This retrospective cohort study included any individual reported to the MSDH as having active TB based on clinical or radiologic disease and/or positive mycobacterial culture. We reviewed demographic, social, and clinical data for each case. Individuals were excluded if their sputum cultures were positive for *Mycobacterium* other than TB, those with TB not diagnosed in Mississippi, and individuals with nonpulmonary TB. Variables such as homelessness and drug and alcohol usage were self-reported. Only patients with culture-confirmed TB with available DNA fingerprinting data were included in the analysis. Individuals with positive cultures were designated as MS0006 (PCR00225) or non-MS0006. The designation MS was selected by the CDC laboratory to represent Mississippi, the state where the strains were identified; the numbers were assigned by the CDC regional laboratory. Polymerase chain reaction identification was performed and reported to the MSDH by the CDC. The non-MS0006 group included strains that were found primarily in Mississippi and other strains not primarily associated with Mississippi (non-MS).

Molecular Analysis and Cluster Information

All of the positive *M tuberculosis* cultures reported to the state laboratory were confirmed and grown in the state laboratory. These cultures were then submitted to the CDC designated regional laboratory for genotypic and strain identification. Spoligotyping, mycobacterial interspersed repetitive unit (MIRU), and IS6110-based restriction fragment length polymorphism (RFLP) methods were used by the CDC; RFLP was performed when strains with the same spoligotyping and MIRU pattern were found and further analysis was needed. Lineage and sublineage data were provided using long sequence polymorphism and single nucleotide polymorphisms. These results were then reported to the MSDH *M tuberculosis* division and entered into the Communicable Disease Control Information System database. Two or more individuals with the same strain information were considered a cluster, and strains causing disease in only one subject were considered to be unique.¹²⁻¹⁴

Statistical Analysis

The data were analyzed using Stata version 11.1 (StataCorp, College Station, TX). Descriptive analyses were conducted to summarize the demographic, clinical, and treatment data among strain type and culture-positive and -negative groups. Categorical variables were compared using the χ^2 test or the Fisher exact test, where appropriate. Difference in age among MS0006 strain and non-MS0006 group was compared using the *t* test. A multivariable analysis was performed for all statistically significant values ($P \leq .05$), using stepwise logistic regression analysis to test for independent association with the MS0006 strain type; a subset analysis also was performed on individuals born in the United States. Odds ratio (OR) with a 95% confidence interval (CI) was calculated using the likelihood method and a *P* value $\leq .05$ was deemed statistically significant.

Results

Study Population

During the 5-year period, 147 active TB cases were reported in the county (Figure). Three individuals were excluded from the study; one patient had missing data needed for analysis and two were diagnosed as having nontuberculous mycobacteria. A total of 144 (98%) individuals met the inclusion criteria. Of the 144 cases, 117 (81%) were culture confirmed by the MSDH mycobacterial laboratory. Spoligotyping and MIRU data were available for each of the 117 patients. RFLP data were available for 34 cases requiring further identification.

Of the 144 patients included in the study, the mean (SD) age at presentation was 46.4 (19.0) years (range, 1-94 years). One hundred nine (76%) were male patients, 115 (79.9%) were

African American, 44 (31%) were homeless, and 133 (97%) individuals were born in the United States. The majority of the homeless patients, 36/44 (81.8%), were African American and 41/44 (93.2%) were men. Of the 136 patients with HIV test results available, 34 (25%) were infected with HIV and of these, 33 (97.1%) were African American and 32 (94.1%) had culture-positive disease. Of the 143 patients who had chest x-ray results available, 137 (96%) were read as abnormal and 37 (27%) had cavitary disease. From 2004-2009, 16 patients died during TB treatment (2004: 1, 2005: 3, 2006: 5, 2007: 1, 2008: 3, and 2009: 3); they ranged in age from 24 to 83 years, with an average age of 55.69. Forty-four percent (7/16) belonged to the MS0006 cluster and 31% (5/16) were HIV positive. In our study population, there were 11 foreign-born individuals representing 7 different countries: 3 were from India, 3 from Mexico, and other countries had 1 case each.

Comparison of Patients with Culture-Positive and Culture-Negative TB

Important differences in epidemiological and clinical profiles (Table 1) were noted between individuals with culture-positive disease and those with culture-negative disease. The mean age was significantly higher in the culture-positive compared with the culture-negative group (49.12 years vs 34.37 years; $P < .01$). Sixty-two percent of the culture-positive cases were smear positive, and 73% of the culture-positive cases and 74% of the culture-negative cases had a positive tuberculin skin test (TST; Table 1). There was no significant difference noted between the culture-positive and the culture-negative patients based on race. The proportion of men, non-injectable drug use, and alcohol use were significantly larger in the culture-positive group. In addition, the patients with culture-confirmed TB were more likely than those with culture-negative TB to be homeless (35.0% vs 11.1%; $P = .02$).

Molecular Fingerprinting Analysis

The DNA fingerprinting data using MIRU typing and spoligotyping is shown in Table 2. Of the 117 cases with molecular data available, there were 48 distinct strains: 6 clustered, 14 unique strains, and 28 non-MS strains; 19 of the 20 MS strains belonged to patients with Euro-American lineage. Only four strains had available sublineage data and these belonged to the Latin American sublineage. The 28 strains grouped into the non-MS subgroup had different spoligotype and MIRU patterns and were classified as unique (Table 3). Overall, there were 42 unique cases. Sixty-four percent of the culture-confirmed cases were clustered into 6 groups, with MS0006 strain accounting for 54 (46%) cases. There were five cases of isoniazid resistance in the non-MS0006 group and a single case of rifampin resistance in the MS0006 group.

Comparison of Patient Characteristics and Independent Risk Factors for the MS0006 Cluster

In Table 4 we identified risk factors associated with the MS0006 cluster. The patients with the MS0006 strain were more likely than those without the strain to be homeless (58.5% vs 15.6%; $P < .01$), use noninjectable drugs (34.0% vs 9.4%; $P < .01$), and be co-infected with HIV (41.5% vs 15.6%; $P = .01$). The majority of the homeless population belonged in the cluster (76%).

Independent risk factors for belonging to the TB cluster resulting from the MS0006 strain using multivariate analysis included African American race (OR 5.80, 95% CI 1.3-24.55; $P = .01$) and homelessness (OR 7.88, 95% CI 2.90-21.36; $P < 0.001$) for the entire population. Patients with MS0006 were less likely to have sputum smear-positive pulmonary TB (OR 0.47, 95% CI 0.22-0.99; $P = .05$) or have a positive TST (OR 0.37, 95% CI 0.14-0.95; $P = .04$). When the analysis was repeated with only US-born patients, homelessness (OR 5.92; 95% CI 2.2-15.27; $P < .01$) was identified as an independent risk factor for belonging to the MS0006 strain.^A

Discussion

A peak in the number and rates of TB recently was noted in Mississippi, especially in Hinds County.^{2,3,9} In the January 2010 issue of the *Mississippi Morbidity Report*, a brief report was included showing a link between the rise in TB cases in Hinds County and the rise in TB-infected homeless individuals in the state.⁹ In the present study, we examined the molecular epidemiology of TB in this predominantly urban county in Mississippi and the effects of a novel *M tuberculosis* strain (PCR00225), which was first reported in Maryland in 2003 (unpublished CDC General Equivalence Mappings database). This strain, later called MS0006, represented 10.8% of all culture-positive TB cases and 50.4% of all US-born cases in Mississippi in 2010 (unpublished CDC General Equivalence Mappings database). In the present study, the strain was responsible for 46% of all culture-positive cases in the county from 2004 to 2009, representing the largest cluster in the county during the study period. We were able to demonstrate a high degree of clustering (64% of all individuals), similar to other studies reviewed.¹⁴⁻¹⁶ This finding is consistent with reports that found a high degree of TB clusters in individuals who were born in the United States, as compared with foreign-born individuals.^{6,15,16}

In the United States, African Americans continue to have some of the highest rates of TB.^{7,15,17} In the present study, African Americans were more likely to be in the disease cluster because of the MS0006 strain. This is consistent with observations in other studies that reported a higher risk of recent transmission of TB in African Americans.¹⁴⁻¹⁶ Although Mississippi comprises 37% African Americans, they account for 71% of all of the TB cases in the state^{11,18} (Hinds County comprises 66% African Americans, who account for 80% of the county's TB cases). This trend suggests that improved control measures based on the dynamics of transmission in the African American community is necessary to accelerate TB elimination in this setting.

It has been well documented that individuals co-infected with TB and HIV are the largest group of new TB cases worldwide;^{11,19,20} they also have a higher incidence of primary and reactivation TB.²¹⁻²³ The role of HIV co-infection accelerates the disease process and complicates diagnosis and treatment.^{6,7,11,20-23} In our study, HIV-positive individuals were more likely than noninfected people to belong to the MS0006 strain^B (94% had culture-positive disease and 69% belonged to the MS0006 cluster), but there was no significant association between sputum smear and HIV status. With this in mind, one may expect a lower rate of transmission for this particular strain because smear-negative strains are less likely to be transmitted, but as indicated in other studies (San Francisco)^C transmission still occurs. This observation has been made by other researchers as they have speculated that HIV prevalence in a community leads to a higher incidence of clustering.^{24,25} The reasons are unknown but would be explained by the high incidence of clustering in our study population, meaning recent and ongoing transmission within our county, with a high HIV prevalence. HIV-positive status was associated with the MS0006 cluster, further emphasizing the need for vigilance in controlling disease transmission and progression among individuals infected with HIV.^{11,20-23}

Homelessness was identified as an independent risk factor for the MS0006 strain in univariate and multivariate analyses. The majority of the homeless patients (76%) belonged to the MS0006 cluster, 93% were men, 82% were African American, 43% admitted to illicit drug use, and 36% were HIV positive. These factors have been identified as risk factors for

^AAU: Was "cluster" rather than "strain" meant here?

^BAU: Was "cluster" rather than "strain" meant here?

^CAU: This statement requires direct attribution to a reference citation. Pls provide.

TB acquisition and transmission, adding to a complicated situation in which many of these individuals are unfamiliar with the index case.^{4,6,7,15,26} The transient nature of the homeless population adds another layer of complexity to TB diagnosis and management. This is apparent in our nine cases, whose TST results were not available for interpretation, hence decreasing the chance of early detection of infection in these individuals. A study from the Netherlands identified male sex and illicit drug use, also seen in homeless individuals, as significant factors in late detection of TB.²⁶ Barnes et al.^D made the association that TB transmission in their study was linked by epidemiologic analysis to shelters and other locations where homeless individuals congregate. Methodologies used by health departments for overall case identification and contact tracing are imprecise and tend to underestimate the level of TB transmission.^{6,11,27} In an attempt to address this problem, numerous programs have been tried and implemented. In Mississippi, a targeted testing program was implemented in autumn 2008 to identify latent infections and active disease in an attempt to control disease transmission. This program focused on the homeless population and those who work with them, using the interferon- γ release assay blood test and clinical symptoms (with rapid HIV testing) as screening tools at various centers that care for this population.⁹

The overall dominance of the Euro-American lineage within our study population attests to the high degree of “homegrown” TB in Mississippi. MS0006 was identified as a member of this lineage, but sublineage information was not available. Numerous studies suggest that certain lineages have a propensity for causing active disease in humans,²⁸ with some diseases^E leading to an increased or decreased stimulation of the host immune system^{29,30}; this is an important aspect of the MS0006 strain and its role in domestic and global TB outbreaks that must be analyzed further.

A limitation of our study is its retrospective nature, which did not allow us to investigate transmission links between patients in the TB clusters. Because this was a retrospective study, some variables had missing or unknown values (TST, HIV, chest x-ray, sputum smear conversion) that may have affected statistical significance; these values were not used to calculate the significance for each group. Another limitation was recall and social desirability bias, because homelessness and alcohol and drug use were self-reported. We also must take into account that the overall increase in TB cases within the county may be the result of increased case detection methods and vigilance in contact tracing activities by the health department.

Conclusions

Molecular epidemiology, as a means of identifying clusters responsible for ongoing transmission, continues to be an important tool in the fight against TB. It also may be used to identify strains of the disease that are more likely to lead to transmission or have specific clinical characteristics. In Mississippi, strain MS0006 was an important factor in ongoing TB transmission in a major urban county. Individuals with positive sputum smears and TST were more likely to belong to the non-MS0006 group. Using a multivariate analysis method, epidemiologic risk factors associated with the MS0006 strain included African American race and homelessness.

Discounting this strain-specific outbreak, TB rates in Mississippi would have continued to decline and remained consistent with the broader national trend. This local outbreak is a stern reminder that TB will reemerge in vulnerable populations. It is also a reminder that TB

^DAU: Reference citation required. Pls provide.

^EAU: Antecedent to “some” was unclear. Is “diseases” the correct correlate to “some”?

is not merely a problem among the foreign-born population living in the United States. Recognition of distinct strains with the clinical and/or epidemiologic (as in this outbreak) factors associated with patients having these strains can permit earlier targeted testing and treatment in these populations. Continued education of people who are at highest risk of disease acquisition and transmission will remain a primary goal of MSDH to control this TB strain and others in the state.

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Key Points

- The MS0006 (PCR0025) tuberculosis (TB) strain, belonging to the Euro-American lineage, has played a major role in the outbreak of TB in Hinds County, Mississippi.
- People infected with the MS0006 strain were less likely to have sputum smear-positive disease.
- HIV co-infection, African American race, and homelessness were important risk factors in TB transmission.
- The use of molecular epidemiology continues to provide more in-depth analysis of disease transmission and plays a vital role in effective contact tracing and interruption of ongoing transmission.

Brief Description

Although tuberculosis (TB) case rates in the United States are declining, some geographic areas and subpopulations still have relatively high case rates. DNA fingerprinting is performed on all mycobacterium TB isolates in Mississippi and serves as a tool to differentiate recent transmission from reactivation of remote exposures. The authors identified a particular strain of *Mycobacterium tuberculosis* that was responsible for more than 45% of all TB cases in Hinds County, Mississippi. Identification of the locally predominant MS0006 strain allowed for the prompt introduction of aggressive public health measures to interrupt further transmission.

Fig. 1. Patients with tuberculosis in Hinds County diagnosed between 2004 and 2009 included in the study. *Two cases were caused by nontuberculous mycobacteria, and one was missing essential data.

TABLE 1

Socio-demographic, and clinical characteristics of culture positive and culture negative individuals, in Hinds County, Mississippi 2004-2009

Characteristic	No. (%) of subjects		p-value
	Culture (+) n= 117	Culture (-) n=27	
Age*	49.1(15.6)	34.4(26.5)	<0.01
Sex			
Female	24(20.5)	11(40.8)	0.03
Male	93 (79.5)	16 (59.3)	
Race			
Non Black	22(18.8)	7(25.9)	0.4
Black	95(81.2)	20(74.1)	
Country of Origin [§]			
Non US	9(7.7)	2(7.4)	0.96
US	108(92.3)	25(92.6)	
Alcohol [§]			
No	87(74.4)	27(100.0)	<0.01
Yes	29(24.8)	0(0.0)	
Unknown [¥]	1(0.9)	0(0.00)	
Drug Non Inject [§]			
No	92(78.6)	27(100.0)	<0.01
Yes	24(20.5)	0(0.00)	
Unknown [¥]	1(0.9)	0(0.00)	
Homeless			
No	76(64.9)	24(88.9)	0.02
Yes	41(35.1)	3(11.1)	
Unknown			
Jail			
No	114(97.4)	27(100.0)	1
Yes	3(2.6)	0(0.00)	
Sputum Smear			
Negative	45(38.5)	27(100)	<0.01
Positive	72(61.5)	0(0.00)	
HIV Status			
No	80(68.4)	22(81.5)	0.05
Yes	32(27.4)	2(7.4)	
Unknown [¥]	5(4.3)	3(11.1)	
Chest X-ray [§]			
Normal	4(3.4)	2(7.4)	0.32

Characteristic	No. (%) of subjects		p-value
	Culture (+) n= 117	Culture (-) n=27	
Abnormal	112(95.7)	25(92.6)	0.14
Unknown	1(0.9)	0(0.0)	
Abnormality			
Cavitary	34(29.1)	3(11.1)	0.84
MTB ¹	44(37.6)	11(40.7)	
Non-MTB ²	34(29.1)	11(40.7)	
Unknown [¥]	5(4.3)	2(7.4)	
TB Skin Test			1
Negative	23(19.7)	6(22.2)	
Positive	85(72.7)	20(74.1)	
Unknown [¥]	9(7.7)	1(3.7)	
Sputum Smear Conv. [*]			1
Yes	16(13.7)	0(0.00)	
No	94(80.3)	1(3.7)	
Unknown [¥]	7(6.0)	26(96.3)	

Chest x-ray readings performed by board certified radiologists and categorized based upon CDC RVCT form

* Mean and Standard deviation

[§]Fisher Exact Test

[¥]Not included in calculating p-value

¹Non-cavity disease consistent with MTB

²Non-cavity disease not consistent with MTB

TABLE 2

Mycobacterium tuberculosis molecular fingerprinting analysis with strain name, CDC PCR identifier, genotype lineage, sublineage, spoligotyping and MIRU code in Hinds County, Mississippi 2004-2009.

TB Strain Name	PCR Identification	Genotype Lineage	Sublineage	Spoligotyping octal code	MIRU code	No. (%) of Cases
n=117 (%)						
MS0006	PCR00225	Euro-American	Unknown	777776777760731	224325153334	54 46.2
MS0003	PCR00021	Euro-American	Latin American (LAM)	776137607760771	224226153324	2 1.7
MS0005	PCR00237	Euro-American	Unknown	700076760000011	224325153322	1 0.9
MS0081	PCR05151	Euro-American	Latin American (LAM)	776177607760771	224323153313	2 1.7
MS0013	PCR00015	Euro-American	Unknown	777776777760601	224325153323	3 2.6
MS0018	PCR00028	Euro-American	Unknown	777777777760771	223326153321	1 0.9
MS0019	PCR01347	Euro-American	Unknown	777737777760771	222125153322	10 8.6
MS0020	PCR00027	Euro-American	Unknown	777776777760601	224325153322	1 0.9
MS0021	PCR01423	Euro-American	Unknown	777777777760731	223325153314	1 0.9
MS0023	PCR00036	East Asia	Unknown	000000000003771	223425173563	1 0.9
MS0026	PCR00756	Euro-American	Unknown	760001400000171	224326133224	1 0.9
MS0038	PCR01132	Euro-American	Latin American (LAM)	776137607760771	224226153323	1 0.9
MS0040	PCR00764	Euro-American	Harlem	777777777720771	225313153321	1 0.9
MS0043	PCR00616	Euro-American	Latin American (LAM)	77777607760771	224226143321	4 3.4
MS0044	PCR00552	Euro-American	Unknown	777776770000000	224325153324	1 0.9
MS0053	PCR05597	Euro-American	Unknown	777737777760771	223125153322	1 0.9
MS0072	PCR00079	Euro-American	Unknown	777777777760771	223125153324	1 0.9
MS0077	PCR00744	Euro-American	Unknown	777776777760771	224325153325	1 0.9
MS0078	PCR00698	Euro-American	Unknown	777777777760731	223225153324	1 0.9
MS_Rv/Ra	PCR00029	Euro-American	Unknown	77777477760771	2x2226133321	1 0.9
Non-MS*						28 23.9

* Consisted of various strain types not matched to a strain in Mississippi (See Table 3)

TABLE 3

Molecular fingerprints of the 28 Non-MS strains by name, CDC PCR identifier, spoligotyping and MIRU code, in Hinds County, Mississippi 2004-2009.

TB Strain Name	PCR Identification	Spoligotyping octal code	Miru code
<i>NonMS1</i>	PCR00254	777776777760601	224325143324
<i>Non_MS2</i>	0 *	777776777760771	235325153323
<i>Non_MS3</i>	PCR01488	777777777760771	228225163423
<i>Non_MS4</i>	0 *	77777607760571	224227123211
<i>Non_MS5</i>	0 *	700076777760661	224325153324
<i>Non_MS6</i>	PCR06893	37637777760771	223323153322
<i>Non_MS7</i>	PCR02844	000000007000011	233325153325
<i>Non_MS8</i>	PCR01787	777777777760771	223326143321
<i>Non_MS9</i>	0 *	77777000000011	364225223433
<i>NonMS10</i>	PCR00078	777777777760771	223125153323
<i>NonMS11</i>	PCR07539	777777777760760	223326153321
<i>Non_MS12</i>	PCR04812	776177407760771	224326153323
<i>NonMS13</i>	PCR00262	777777777760771	223425153222
<i>Non_MS14</i>	PCR02967	700036777760771	222325143226
<i>Non_MS15</i>	0 *	777737777760771	22312-153322
<i>Non_MS16</i>	0 *	67777607760771	untypeable
<i>NonMS17</i>	PCR11884	000000000003771	223326171531
<i>Non_MS18</i>	PCR08148	no result [#]	224325153324
<i>Non_MS19</i>	PCR02689	700076777760700	224425143324
<i>Non_MS20</i>	0 *	474377777413771	25232a223332
<i>Non_MS21</i>	PCR00698	777777777760731	223225153324
<i>Non_MS22</i>	0 *	703777740003771	125425173433
<i>Non_MS23</i>	0 *	no result [#]	2233-6153321
<i>Non_MS24</i>	PCR09992	777761777760771	223325152322
<i>Non_MS25</i>	PCR02075	700076777760771	225323143324
<i>Non_MS26</i>	0 *	77777607760071	21432714322-
<i>Non_MS27</i>	PCR02689	700076777760700	224425143324
<i>Non_MS28</i>	PCR05409	777777777760771	223226153331

* PCR identifier was not recorded in CDCIS

[#] Spoligotyping not reported

Socio-demographic, and clinical characteristics of *MS0006* vs. Non-*MS0006* Strain type of 117 patients, in Hinds County, Mississippi 2004 - 2009

TABLE 4

Characteristic	No. (%) of subjects		MS0006 vs. Non-MS0006		p-value
	MS0006 n=53	Non-MS0006 n=64	OR	-95% (0.95 - 1.00)	
Age *	46.13(12.04)	51.61(17.79)	0.98	(0.95 - 1.00)	0.06
Country of Origin					
Non US	0(0.00)	9(14.06)	NA		<0.01
US	53(100.0)	55(85.94)			
Race					
Non Black	5(9.43)	17(26.56)	1.00		0.02
Black	48(90.57)	47(73.44)	3.47	(1.19 - 10.18)	
Sex					
Female	9(16.98)	15(23.44)	1.00	(Reference)	0.4
Male	44(83.02)	49(76.56)	1.50	(0.60 - 3.76)	
Homeless					
No	22(41.51)	54(84.38)	1.00		<0.01
Yes	31(58.49)	10(15.63)	7.61	(3.19 - 17.13)	
Drug Non Inject [§]					
No	34(64.15)	58(90.63)	1		<0.01
Yes	18(33.96)	6(9.38)	5.12	(1.85 - 14.14)	
Unknown [‡]	1(1.89)	0(0.00)			
Jail [§]					
No	50(94.34)	64(100)	NA		0.09
Yes	3(5.66)	0(0.00)			
Alcohol [§]					
No	39(73.58)	48(75.00)	1		1
Yes	13(24.53)	16(25.00)	1	(0.43 - 2.32)	

Characteristic	No. (%) of subjects		MS0006 vs. Non-MS0006		p-value
	MS0006 n= 53	Non-MS0006 n=64	OR	-95% CI	
Unknown [‡]	1(0.00)	0(0.00)			
HIV Status					
No	31(58.49)	49(76.56)	1		0.01
Yes	22(41.51)	10(15.63)	3.48	(1.45 - 8.32)	
Unknown [‡]	0(0.00)	5(7.81)			
Sputum Smear					
Negative	26(49.06)	19(29.69)	1		0.03
Positive	27(50.94)	45(70.31)	0.43	(0.21 - 0.94)	
TB Skin Test					
Negative	14(26.42)	9(14.06)	1		0.03
Positive	30(56.60)	55(85.94)	0.35	(0.16 - 0.91)	
Unknown [‡]	9(16.98)	0(0.00)			
Chest X-ray [§]					
Normal	2(3.77)	2(3.13)	1		0.86
Abnormal	51(96.23)	61(95.31)	0.84	(0.11 - 6.15)	
Unknown	0(0.00)	1(1.56)			
Abnormality					
Cavitary	12(22.64)	22(34.38)	1		0.07
MTB [†]	26(49.06)	18(28.13)	2.65	(1.05 - 6.68)	
Non-MTB ²	13(24.53)	21(32.81)	1.13	(0.42 - 3.04)	
Unknown [‡]	2(3.77)	3(4.69)			
Sputum Smear Conversion [*]					
No	6(13.68)	10(15.63)	1		0.44
Yes	45(94.91)	49(76.56)	1.53	(0.51 - 4.55)	
Unknown [‡]	2(3.77)	5(7.81)			

Chest x-ray readings performed by board certified radiologists and categorized based upon CDC RVCT form.

- * Mean and Standard deviation
- § Fisher Exact Test
- ¶ Not included in calculating p-value and OR
- 1 Non-cavity disease consistent with MTB
- 2 Non-cavity disease not consistent with MTB