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Erin Anderson Date

Trends in recent transmission of tuberculosis in the United States, 2011-2018

By

Erin Anderson

Master of Science in Public Health

Epidemiology

Allison Chamberlain, MS, PhD

Committee Chair

Benjamin Silk, MPH, PhD

Committee Member

Trends in recent transmission of tuberculosis in the United States, 2011-2018

By

Erin Anderson

B.S. in Community Health

University of Maryland, College Park

2016

Faculty Thesis Advisor: Allison Chamberlain, MS, PhD

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Abstract

Trends in recent transmission of tuberculosis in the United States, 2011-2018

By Erin Anderson

Background

Preventing cases of tuberculosis (TB) resulting from recent transmission (RT) is key to eliminating TB in the United States. Monitoring trends in RT over time can aid state and local TB programs in prioritizing TB control activities and developing specific prevention strategies to interrupt TB transmission in their jurisdictions. Using routinely collected data from the National Tuberculosis Surveillance System (NTSS) and molecular surveillance data from CDC's TB Genotyping Information Management System (TBGIMS), we describe geographic trends in RT in the U.S. between 2011 and 2018.

Methods

We analyzed all TB cases reported to NTSS by the 50 U.S. states and the District of Columbia between January 1, 2011 and December 31, 2018 that were eligible to be assessed for RT. Cases estimated to be attributed to RT were identified using a plausible source-case method. We used loglinear regression to evaluate changes in the proportion of genotyped cases estimated to be attributed to RT over time and within geographic area.

Results

Of the 55,868 cases eligible to be assessed for RT, 7,703 (13.8%) were estimated to be attributed to RT. Significant decreasing trends in RT-attributed cases were observed at the national level ($p<0.0001$) as well as in the Midwest ($p<0.005$), Texas ($p<0.01$), and the South ($p<0.05$) from 2011-2018. When comparing the proportions of cases attributed to RT in each sequential two-year time period to the previous two-year time period, we observed a statistically significant reduction in the national proportion of RT-attributed cases in 2017-2018. When stratified by geographic area, statistically significant reductions were observed in Florida (IRR: 0.75; 95% CI: 0.59, 0.95) in 2015-2016 as well as in New York (IRR: 0.79; 95% CI: 0.64, 0.98) and Texas (IRR: 0.85; 95% CI: 0.73, 0.99) in 2017-2018.

Conclusion

Our findings suggest that the national decrease in the proportion of cases attributed to RT from 2011-2018 in the U.S. was not uniformly distributed across geographic areas or two-year time periods. Further research is needed to determine whether decreases in RT among certain subpopulations resulted in an overall decrease in RT.

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MANUSCRIPT

Introduction

Despite a continued decline in cases, tuberculosis (TB) remains a public health concern in the United States. In 2018, there were 9,025 reported cases of TB disease in the U.S. (2.8 cases per 100,000 persons), a 0.7% decline from 2017 (1). In the U.S., four states (California, Florida, New York, and Texas) consistently account for roughly half of reported TB cases, and most TB transmission is thought to occur within the U.S.-born population (1-3). In a systematic review of 21 TB outbreaks in the U.S. from 2009 to 2015 for which the Centers for Disease Control and Prevention (CDC) provided on-site assistance, Mindra et al. found that 79% of the 457 outbreak patients identified were U.S.-born (3).

TB disease can result from reactivation of a previously acquired latent TB infection (LTBI) or from an infection acquired recently (i.e., from recent transmission). Recent transmission (RT) of TB is often defined as transmission that has occurred within the past two years, the time during which an individual is at highest risk for progression from *Mycobacterium tuberculosis* infection to active TB disease (4). TB disease attributed to RT cannot be clinically differentiated from reactivated latent TB infections (5). For this reason, genotyping is commonly used to estimate RT, as cases sharing a common genotype are more likely to be linked in a transmission network (clustered) than cases with differing genotypes (6-11). Clustered cases are often related by RT (9, 11, 12). However, genotyping alone is also insufficient for distinguishing between TB attributed to reactivation and TB attributed to RT; clinical, geographic, and temporal data must be considered collectively (9, 10, 12).

Preventing cases of TB attributable to RT is key to eliminating TB in the United States, as these cases often indicate ongoing transmission and can lead to outbreaks if undetected (12). Furthermore, identifying and monitoring trends in RT over time can help state and local TB programs prioritize TB control activities and develop specific prevention strategies to interrupt TB transmission in their jurisdictions. Using a plausible source-case method developed by France et al., Yuen et al. estimated that 14% of genotyped cases counted between January 1, 2011 and September

30, 2014 in the U.S. were attributed to RT (4, 12). Two-year RT estimates subsequently published in annual surveillance reports by the CDC's Division of TB Elimination (DTBE) showed a decline in the number and proportion of genotyped cases estimated to be attributed to RT from 1,894 cases (13.7%) in 2015-2016 to 1,712 cases (12.6%) in 2017-2018 (1, 13). Additional declines were observed among patients with TB risk factors when comparing the most recent two-year period to the previous two-year period. The proportion of cases attributed to RT among patients with reported injecting drug use (34.0%) and excess alcohol use (28.5%) in 2015-2016 decreased in 2017-2018 to 20.5% and 23.1%, respectively (1, 13). The extent to which declines in specific geographic areas and subpopulations with higher TB burdens impact the overall decline in the number and overall proportion of genotyped cases estimated to be attributed to RT is unclear.

In this study, we used routinely collected data from the National Tuberculosis Surveillance System (NTSS) and molecular surveillance data from CDC's TB Genotyping Information Management System (TB GIMS) to describe trends in recent transmission in the United States by geographic area and two-year time periods between 2011 and 2018.

Methods

Study Population

The study population includes all cases of culture-confirmed TB disease that were reported by TB control programs in the 50 U.S. states and the District of Columbia and counted in NTSS between January 1, 2011 and December 31, 2018 (14). Demographic, clinical, and epidemiologic risk factor data for all confirmed cases of TB disease are recorded using a Report of Verified Case of Tuberculosis (RVCT) form, which is reviewed by a count authority (e.g., state health department) before being counted in NTSS (14). Using TB GIMS, NTSS case reports were linked to conventional genotyping results from the National TB Genotyping Service for >95% of cases using TB GIMS (14). Genotyping results are produced using the combined application of spacer oligonucleotide

typing (spoligotyping) and 24-locus mycobacterial interspersed repetitive unit-variable number tandem repeat (MIRU-VNTR) typing (10, 12).

Geographic Area

We assigned cases to one of four U.S. Census regions based on the state in which the patient resided at the time of diagnosis. Four states with high burdens of TB (California, Florida, New York, and Texas) were excluded from their respective regions and assessed individually. The remaining states were categorized into their respective U.S. Census regions as follows:

i. Midwest: Illinois, Indiana, Iowa, Kansas, Michigan, Minnesota, Missouri, Nebraska, North Dakota, Ohio, South Dakota, Wisconsin;
ii. Northeast: Connecticut, Maine, Massachusetts, New Hampshire, New Jersey, Pennsylvania, Rhode Island, Vermont;
iii. South: Alabama, Arkansas, Delaware, District of Columbia, Georgia, Kentucky, Louisiana, Maryland, Mississippi, North Carolina, Oklahoma, South Carolina, Tennessee, Virginia, West Virginia; and
iv. West: Alaska, Arizona, Colorado, Hawaii, Idaho, Montana, Nevada, New Mexico, Oregon, Utah, Washington, Wyoming.

Cases from U.S. territories and freely associated states were not included in this analysis as the proportions of cases that are culture confirmed and genotyped in these areas are much lower than 95%.

Recent Transmission

Using the plausible source-case method (4), DTBE routinely assesses all culture-confirmed TB cases with genotyping results for RT. This method utilizes national molecular surveillance data from TB GIMS and patient characteristics from NTSS to identify cases likely to be attributed to RT. By extension, cases not attributed to RT are also identified. According to this method, a given TB

case is attributed to RT if a plausible source case can be identified in a person who (i) has the same *M. tuberculosis* genotype, (ii) was diagnosed within 2 years prior to the given case, (iii) was 10 years of age or older with a respiratory form of disease (pulmonary or laryngeal), and (iv) resides within a 10-mile radius of the given case (determined using zip code centroids). TB in patients born outside of the U.S. who were diagnosed less than 100 days after U.S. entry are not considered RT-attributable cases, even if a plausible source case is identified. Cases ineligible to be assessed for RT included genotyped cases in patients without a documented city and zip code and cases caused by *M. bovis*. In a systematic evaluation comparing the plausible source-case method to field-validated RT classifications (i.e., the epidemiologic gold standard), the plausible source-case method was shown to have higher accuracy (>90%) than previously published RT estimation methods (4). This method has been systematically incorporated into NTSS, with all genotyped *M. tuberculosis* cases eligible to be assessed for RT and counted since January 1, 2011 designated as either attributed to RT or not attributed to RT.

Statistical Analyses

We used loglinear regression to evaluate changes in the proportion of genotyped cases estimated to be attributed to RT over time and within geographic areas. Cochran-Armitage tests for trend were used to test for overall trends in RT-attributed cases from 2011-2018. Trends were evaluated nationally and for each geographic area. To further identify specific time periods and geographic areas driving these trends, NTSS data were aggregated by two-year time periods (2011-2012, 2013-2014, 2015-2016, 2017-2018) and geographic area to produce strata-specific counts. Two-year time periods were used to account for lower case counts in geographic areas with lower TB burdens and to be consistent with published RT estimates. The log of the total number of genotyped cases eligible to be assessed for RT in each stratum was specified as an offset term to account for differences in counts of genotyped cases eligible to be assessed for RT and to calculate the proportions of genotyped cases attributed to RT. Aggregate counts of cases attributed to RT were

input into a loglinear regression model that included two-year time period, geographic area, two-year time period and geographic area interaction, and the offset term. Estimate statements were used to calculate incidence rate ratios (IRRs) comparing the proportions of RT-attributed cases in each two-year time period to the prior two-year time period, nationally and within each geographic area. Statistical significance was evaluated at an alpha level of 0.05. Analyses were performed using SAS 9.4 (Cary, NC).

Ethics Statement

We analyzed data routinely collected by the CDC for disease surveillance and control purposes. As such, the analysis was considered a non-research public health activity by the CDC and Emory University Institutional Review Boards.

Results

Between January 1, 2011 and December 31, 2018, a total of 76,267 cases of TB were reported to NTSS by the 50 U.S. states and the District of Columbia (Figure 1). During this time period, 55,868 (73.3%) cases were eligible to be assessed for RT. Of these 55,868 cases, 7,703 (13.8%) were estimated to be attributed to RT. Table 1 compares the proportion of TB cases attributed to RT stratified by geographic area and time period. Texas had the highest proportion (20%) of TB cases attributed to RT (n=1,410 cases) (Table 1). The South (15.4%), Florida (15.4%), and New York (15.2%) also had RT-attributed proportions greater than the national average (13.8%) during 2011-2018. California (13.5%) had an RT-attributed proportion similar to the national average, while the Northeast (7.7%), Midwest (10.1%), and West (10.9%) had proportions of cases attributed to RT below that of the national average.

When broken into two-year time periods, the proportion of cases attributed to RT nationally declined from 14.4% in 2011-2012 to 12.6% in 2017-2018. Texas had the highest proportion of TB cases attributed to RT from 2011-2018, ranging from 21.4% in 2011-2012 to 17.4% in 2017-2018.

Florida, the South, and New York had consistently high proportions of cases attributed to RT. The proportion of cases attributed to RT in Florida went from 16.6% in 2011-2012 and 16.8% in 2013-2014, to 12.6% in 2015-2016, followed by slight increase to 15.3% in 2017-2018. The South experienced a slight decrease in the proportion of cases attributed to RT from 16.5% in 2011-2012 to 14.3% in 2017-2018. The proportion of cases attributed to RT in New York ranged from 15.8% in 2011-2012 to 13.1% in 2017-2018, with a slight increase to 16.5% in 2015-2016. The Northeast had the lowest proportions of cases attributed to RT for each two-year time period (≤9.0%). When looking across two-year time periods, there were notable decreases in the proportion of cases attributed to RT from 2015-2016 to 2017-2018. With the exception of the Northeast and Florida, all geographic areas experienced a decrease in both the count and proportion of RT cases during this time period.

Table 2 provides the results from Cochran-Armitage tests for trend for all cases eligible to be assessed for RT from 2011 to 2018. Significant decreasing trends in RT-attributed cases were observed at the national level ($Z=4.48$, $p<0.0001$), as well as in the Midwest ($Z=3.12$, $p<0.005$), Texas ($Z=2.66$, $p<0.01$), and the South ($Z=2.16$, $p<0.05$). The Northeast was the only geographic area to see an increasing trend in RT-attributed cases. Decreasing trends were observed in New York, Florida, the West, and California, but were not significant at the alpha level of 0.05.

Using loglinear regression, the IRRs comparing the proportions of cases attributed to RT nationally in each sequential two-year time period to the previous two-year time period between 2011-2018 were 0.99 (95% CI: 0.93, 1.06), 0.96 (95% CI: 0.90, 1.03), and 0.91 (95% CI: 0.86, 0.97), respectively (Table 3, Figure 2). The reduction in the national proportion of RT-attributed cases from 2015-2016 to 2017-2018 was statistically significant at the alpha level of 0.05. When stratified by geographic area, statistically significant reductions in the proportions of cases estimated to be attributed to RT were observed in Florida (IRR: 0.75; 95% CI: 0.59, 0.95) from 2013-2014 to 2015-2016 and in New York (IRR: 0.79; 95% CI: 0.64, 0.98) and Texas (IRR: 0.85; 95% CI: 0.73, 0.99) from 2015-2016 to 2017-2018. The Midwest saw consistent declines comparing each two-year time

period to the previous two-year period. New York and Texas experienced increases in the proportions of RT-attributed cases from 2011-2012 to 2013-2014, followed by reductions in 2015-2016 and 2017-2018. Florida experienced a slight increase in the proportions of RT-attributed cases in 2013-2014 (IRR: 1.01; 95% CI: 0.82, 1.25), followed by a significant decrease in 2015-2016 (IRR: 0.75, 95% CI: 0.59, 0.95) and a slight increase in 2017-2018 (IRR 1.21; 95% CI: 0.95, 1.55). The West and California experienced increases in the proportions of cases estimated to be attributed to RT in 2013-2014, followed by decreases in 2015-2016 and 2017-2018.

A statistically significant increase in the proportion of cases attributed to RT was observed in the Northeast from 2011-2012 to 2013-2014 (IRR: 1.34; 95% CI: 1.01, 1.77). Several geographic areas saw increases in RT-attributed proportions that were not statistically significant, including the Northeast in 2017-2018, the South in 2015-2016, the West in 2013-2014, California in 2013-2014, Florida in 2013-2014 and 2017-2018, and New York in 2015-2016.

Discussion

Using NTSS data, we estimated that 13.8% of the 55,868 eligible cases reported between 2011 and 2018 in the 50 U.S. states and the District of Columbia were attributed to RT. During this time period, we found statistically significant decreasing trends in RT for the U.S. overall, the Midwest, South, and Texas, and a statistically significant increasing trend in RT in the Northeast. When divided into two-year time periods, loglinear regression analyses showed a significant decrease in the proportion of cases attributed to RT in the U.S. from 2015-2016 to 2017-2018. Similar decreases were observed in New York and Texas during the same time period, suggesting that decreases in RT-attributed cases in those geographic areas may be driving the overall decline in RT-attributed cases in the U.S. during that time. This finding is not unexpected, as New York and Texas account for nearly a quarter of cases eligible to be assessed for RT, and significant declines in those regions are likely to contribute to the overall decline nationally. The Midwest and the South did not experience statistically significant decreases in proportions of TB cases attributed to RT when

comparing each two-year time period to the prior two-year time period, which could suggest more gradual decreases in RT-attributed cases, or significant year-to-year decreases that may have been obscured by grouping cases into two-year time periods.

In 2015, DTBE began using the plausible source case method (4) to categorize all eligible TB cases counted since January 1, 2011 as estimated to be either attributed or not attributed to RT (15). These data have since been used to identify demographic characteristics and social risk factors associated with RT in cases counted between 2011-2014 (12). Since 2016, DTBE has published two-year RT estimates in their annual surveillance report "Reported Tuberculosis in the United States" (1, 13, 16); however, no analyses to date had looked at trends in RT data over time or by region.

The geographic areas used in this analysis vary greatly in their demographics, TB burdens, and TB control capacities, making within-geographic area analyses all the more important, particularly when considering factors associated with increased risk for RT. For example, while the majority of incident TB cases occur in persons born outside of the U.S., nearly two-thirds of cases attributed to RT during 2011-2014 were U.S.-born (12). Therefore, the proportion of cases attributed to RT may differ across geographic areas depending on the underlying distribution of non-U.S.-born cases in that area. Race, ethnicity, and age have also been shown to be associated with TB transmission. In two studies reviewing TB outbreaks in the U.S., researchers found that 265 (67%) of 398 outbreak cases identified from 2002-2008 and 202 (44%) of 457 outbreak cases identified from 2009-2015 occurred among Black/African American patients (2, 3). Additionally, among cases attributed to RT between 2011-2014, being of Hispanic, American Indian/Alaska Native, Black, or Native Hawaiian/Pacific Islander race or ethnicity was positively associated with RT (12). In the same analysis, being 24 years of age or younger was positively associated with RT, whereas being 65 years of age or older was negatively associated with RT (12).

Similarly, large homeless, incarcerated, or substance-using populations in certain geographic areas or during certain time periods could result in higher proportions of RT-attributed cases. In a retrospective cohort analysis of 146 TB genotype clusters identified during 2006-2010, Althomsons

et al. found that clusters in which at least 1 of the 3 first patients reported experiencing homelessness, excess alcohol use, illicit drug use or incarceration had the highest risk for becoming an outbreak (17). Of the nearly 4,000 cases attributed to RT from 2011 to 2014, 37.5% reported experiencing homelessness, 27.1% reported excess alcohol use, and 33.3% reported illicit substance use (12). In the same analysis, these risk factors were independently associated with RT (12). Additionally, when reviewing characteristics of the 457 patients associated with TB outbreaks between 2009-2015, Mindra et al. found that 45% (n=204) experienced homelessness in the year before diagnosis and 83% (n=379) reported excessive alcohol use or illicit substance use (3). Thus, future analyses examining trends in RT among specific subpopulations could aid TB control programs in identifying specific interventions (e.g., improved screening practices, contact investigations) to reduce RT in their jurisdictions.

There are a number of limitations to this analysis. First, the plausible source-case method can only be applied to genotyped cases of TB disease, thus excluding 19,539 culture-negative cases and cases missing genotyping information (4). This is of particular concern for pediatric TB patients who are often unable to provide viable samples, but are most likely to result from RT (16). Second, there are generally higher proportions of cases attributed to RT in areas with less genomic diversity and in areas where common genotypes are prevalent, which could lead to overestimates in certain jurisdictions. Third, in order for a TB case to be attributed to RT, a plausible source case must be identified within 2 years prior to the given case (i.e., cases attributed to RT are dependent on cases meeting the source case requirements during the previous two years). This could result in autocorrelation between model estimates of the proportion of cases attributed to RT and estimates in previous time periods, which is unaccounted for in this analysis. Additionally, categorizing cases into two-year time periods could mask year-to-year changes in RT. In future analyses, this could be assessed by shifting the time window to different single or multi-year categories and performing a series of sensitivity analyses. Finally, our analysis was limited to assessing geographic trends in RT.

Because population demographics can vary by geographic area and over time, further research is needed to identify what subpopulations, if any, are driving this change.

This analysis is the first step in developing an analytic framework to monitor trends in RT over time. Our findings suggest that the overall decrease in the proportion of cases attributed to RT from 2011-2018 in the U.S. was not uniformly distributed across geographic areas or two-year time periods. Though our analysis focused on geographic trends, this framework could be expanded to determine whether decreases in RT among certain subpopulations resulted in an overall decrease in RT in that geographic area or during a specific time period. Additionally, this method could potentially be used to measure the effect of a particular intervention or policy change on RT.

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Tables

Table 1. Counts and Percentages* of Tuberculosis Cases Estimated to be Attributed to Recent Transmission (RT) by Year and Geographic Area, 2011–2018

	Time Period									
	2011–2018		2011–2012		2013–2014		2015–2016		2017–2018	
Geographic Area	No. Eligible^	No. (%) Attributed to RT	No. Eligible	No. (%) Attributed to RT	No. Eligible	No. (%) Attributed to RT	No. Eligible	No. (%) Attributed to RT	No. Eligible	No. (%) Attributed to RT
United States	55,868	7,703 (13.8)	14,555	2,097 (14.4)	13,755	1,969 (14.3)	13,957	1,925 (13.8)	13,601	1,712 (12.6)
Midwest	6,489	658 (10.1)	1,274	201 (12.0)	1,551	161 (10.4)	1,185	155 (9.2)	1,580	141 (8.9)
Northeast	4,964	380 (7.7)	1,677	86 (6.8)	1,262	114 (9.0)	1,681	87 (7.3)	1,243	93 (7.5)
South	10,310	1,590 (15.4)	2,820	465 (16.5)	2,473	374 (15.1)	2,561	400 (15.6)	2,456	351 (14.3)
West	5,434	590 (10.9)	1,408	142 (10.1)	1,347	164 (12.2)	1,337	150 (11.2)	1,342	134 (10.0)
California	12,973	1,757 (13.5)	3,211	436 (13.6)	3,247	460 (14.2)	3,261	448 (13.7)	3,254	413 (12.7)
Florida	3,953	608 (15.4)	1,114	185 (16.6)	963	162 (16.8)	945	119 (12.6)	931	142 (15.3)
New York	4,680	710 (15.2)	1,244	196 (15.8)	1,171	179 (15.3)	1,139	188 (16.5)	1,126	147 (13.1)
Texas	7,065	1,410 (20.0)	1,807	386 (21.4)	1,741	355 (20.4)	1,848	378 (20.5)	1,669	291 (17.4)

*Percentages reflect the proportion of eligible cases estimated to be attributed to RT within region and within time period.
^Eligible cases include culture-confirmed, genotyped cases with complete geographic data that were not caused by *M. bovis*.

Midwest: Illinois, Indiana, Iowa, Kansas, Michigan, Minnesota, Missouri, Nebraska, North Dakota, Ohio, South Dakota, Wisconsin
Northeast: Connecticut, Maine, Massachusetts, New Hampshire, New Jersey, Pennsylvania, Rhode Island, Vermont
South: Alabama, Arkansas, Delaware, District of Columbia, Georgia, Kentucky, Louisiana, Maryland, Mississippi, North Carolina, Oklahoma, South Carolina, Tennessee, Virginia, West Virginia
West: Alaska, Arizona, Colorado, Hawaii, Idaho, Montana, Nevada, New Mexico, Oregon, Utah, Washington, Wyoming

Table 2. Cochran-Armitage Tests for Trend in the Proportion of Cases Attributed to Recent Transmission (RT), by Geographic Area, 2011-2018

Geographic Area	No. Eligible*	Cochran-Armitage Test for Trend 2011–2018	
		Z-score	*p*-value
United States	55,868	**4.48**	**<0.0001**
Midwest	6,489	**3.12**	**0.0018**
Northeast	4,964	-0.82	0.4100
South	10,310	**2.19**	**0.0287**
West	5,434	0.30	0.7627
California	12,973	1.13	0.2570
Florida	3,953	1.70	0.0894
New York	4,680	1.39	0.1633
Texas	7,065	**2.66**	**0.0078**

*Total number of cases eligible to be assessed for RT. Eligible cases include culture-confirmed, genotyped cases with complete geographic data that were not caused by *M. bovis*; ***p<0.05***

Midwest: Illinois, Indiana, Iowa, Kansas, Michigan, Minnesota, Missouri, Nebraska, North Dakota, Ohio, South Dakota, Wisconsin
Northeast: Connecticut, Maine, Massachusetts, New Hampshire, New Jersey, Pennsylvania, Rhode Island, Vermont
South: Alabama, Arkansas, Delaware, District of Columbia, Georgia, Kentucky, Louisiana, Maryland, Mississippi, North Carolina, Oklahoma, South Carolina, Tennessee, Virginia, West Virginia
West: Alaska, Arizona, Colorado, Hawaii, Idaho, Montana, Nevada, New Mexico, Oregon, Utah, Washington, Wyoming

Table 3. Loglinear Regression Results for the Association between Time Period and Proportion of Tuberculosis Cases Attributed to Recent Transmission by Geographic Area, 2011-2018

	Time Period					
	2013–2014 vs. 2011–2012		2015–2016 vs. 2013–2014		2017–2018 vs. 2015–2016	
Geographic Area	IRR	95% CI	IRR	95% CI	IRR	95% CI
United States	0.99	(0.93, 1.06)	0.96	(0.90, 1.03)	**0.91**	**(0.86, 0.97)**
Midwest	0.87	(0.70, 1.07)	0.88	(0.71, 1.11)	0.97	(0.77, 1.22)
Northeast	**1.34**	**(1.01, 1.77)**	0.81	(0.61, 1.07)	1.02	(0.76, 1.37)
South	0.92	(0.80, 1.05)	1.03	(0.90, 1.19)	0.92	(0.79, 1.06)
West	1.20	(0.96, 1.51)	0.92	(0.74, 1.15)	0.89	(0.71, 1.12)
California	1.04	(0.92, 1.19)	0.97	(0.85, 1.10)	0.92	(0.81, 1.06)
Florida	1.01	(0.82, 1.25)	**0.75**	**(0.59, 0.95)**	1.21	(0.95, 1.55)
New York	0.97	(0.79, 1.19)	1.08	(0.88, 1.33)	**0.79**	**(0.64, 0.98)**
Texas	0.95	(0.83, 1.10)	1.00	(0.87, 1.16)	**0.85**	**(0.73, 0.99)**

IRR: incidence rate ratio; CI: confidence interval; ***p<0.05***

Midwest: Illinois, Indiana, Iowa, Kansas, Michigan, Minnesota, Missouri, Nebraska, North Dakota, Ohio, South Dakota, Wisconsin
Northeast: Connecticut, Maine, Massachusetts, New Hampshire, New Jersey, Pennsylvania, Rhode Island, Vermont
South: Alabama, Arkansas, Delaware, District of Columbia, Georgia, Kentucky, Louisiana, Maryland, Mississippi, North Carolina, Oklahoma, South Carolina, Tennessee, Virginia, West Virginia
West: Alaska, Arizona, Colorado, Hawaii, Idaho, Montana, Nevada, New Mexico, Oregon, Utah, Washington, Wyoming

Figures

Figure 1. Inclusion and exclusion criteria for reported cases of tuberculosis (TB) in the United States, 2011-2018

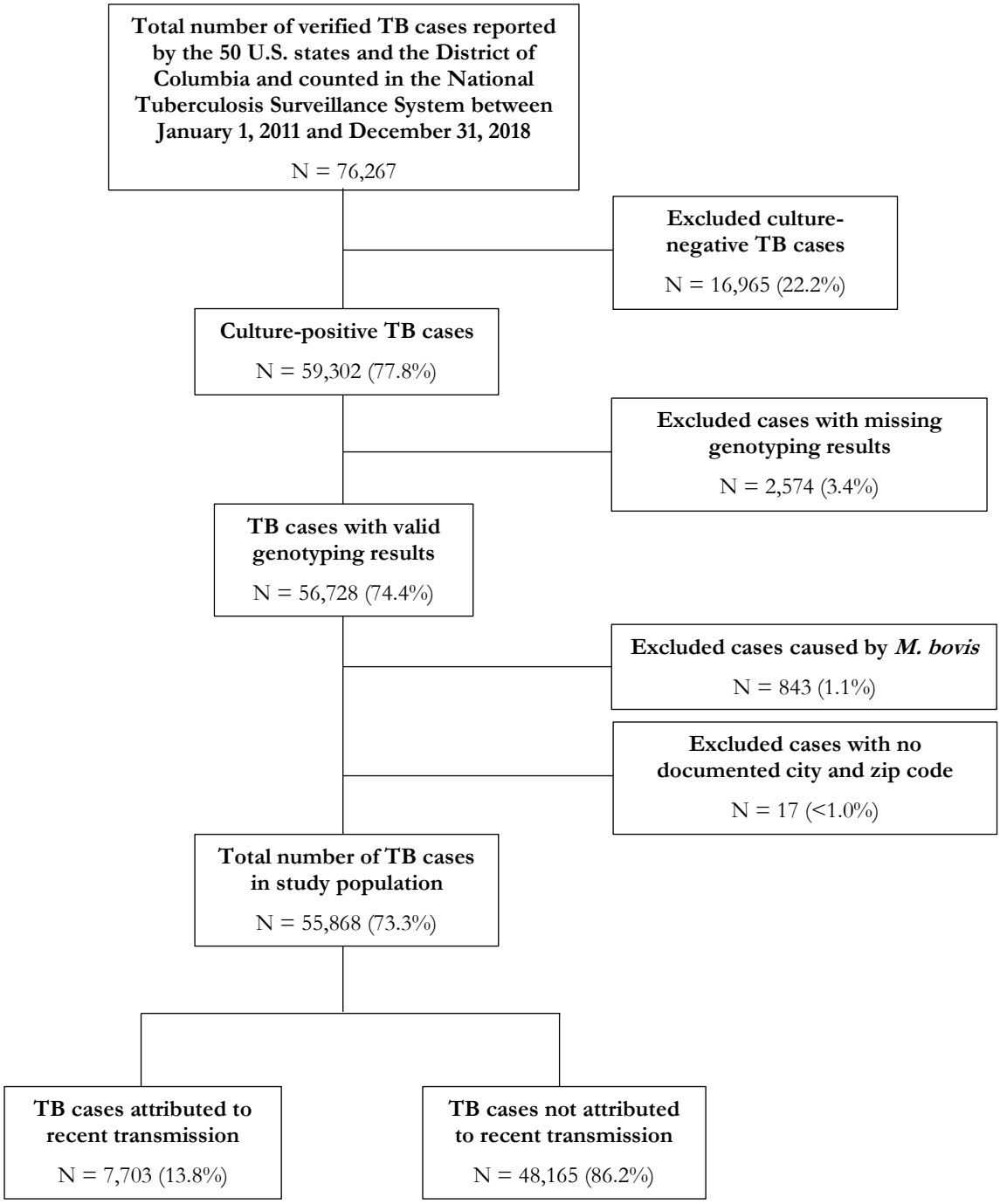

Figure 2. Loglinear Regression Results for the Association between Time Period and Proportion of Tuberculosis Cases Attributed to Recent Transmission by Geographic Area, 2011-2018