

**Estimates of Recent Transmission,
2015–2016**

OVERVIEW

Eliminating TB in the United States requires interrupting the TB transmission that is still occurring in some communities. Improved analytic methods can provide estimates of the numbers of TB cases attributed to recent transmission by distinguishing them from cases likely due to reactivation of longstanding, untreated latent TB infection. Distinguishing these cases is an important consideration for state and local TB programs that are designing effective public health interventions.

In this new section of the annual report, CDC is including data from these improved methods¹ for estimating recent TB transmission, which replace the estimates of county-based genotype clustering in previous editions of the annual report that could have overestimated the proportion of cases attributed to recent transmission. These estimates can be used by state and local TB programs to:

- monitor trends in recent transmission,
- use limited public health resources to plan and prioritize TB control activities,
- enhance service delivery by applying sufficient resources,
- identify geographic, demographic, and social disparities in the proportion of cases attributed to recent transmission,
- develop specific prevention strategies and interventions to interrupt transmission, and
- facilitate connections among jurisdictions to share TB control strategies.

Recent transmission is a concerning public health issue regardless of the overall TB incidence in a particular state; even states with a low incidence of TB overall may have counties where transmission is occurring.² Because not only TB incidence but also demographics and molecular epidemiology vary considerably among states and counties, these data should not be compared across jurisdictions.

TERMINOLOGY

Overall recent transmission: Using national surveillance data, a TB case is designated as attributed to recent transmission if a plausible source case¹ can be identified who:

1. has the same *M. tuberculosis* genotype,
2. has an infectious form of TB disease,
3. resides within 10 miles of the TB case,
4. is 10 years of age or older, and
5. was diagnosed within 2 years before the TB case.

Overall recent transmission estimates are mapped as counts to describe the relative numbers of cases attributed to recent TB transmission (Figure 1).

Extensive recent transmission: A TB case is designated as attributed to extensive recent transmission when the criteria above for overall recent transmission are met, and the case belongs to a plausible transmission chain of six or more cases (i.e., the plausible source case and four or more other cases identified within 3 years before the TB case). Extensive recent transmission estimates are presented as a percentage of all genotyped cases to identify areas and populations disproportionately affected by extensive recent transmission among counties with 10 or more genotyped cases (Figure 2).

RECENT TRANSMISSION IN THE UNITED STATES

Nationally, 13.7% of genotyped cases reported during 2015-2016 are attributed to overall recent transmission (Table 65) and 5.0% of genotyped cases are attributed to extensive recent transmission.

Geography

Forty-eight counties (or county equivalents) had >5% of cases attributed to extensive recent transmission (Table 66). In these counties, the median number of genotyped cases was 41, although the number of cases ranged from 10 cases to 986 cases. The median percentage of genotyped cases

occurring in U.S.-born patients (48.4%) was significantly higher in these 48 counties compared with the national proportion of TB cases among U.S.-born persons (31.5%).

Demographic and social characteristics

Cases among U.S.-born persons were more frequently attributed to both overall recent transmission (26.2%) and extensive recent transmission (11.6%) than cases among non-U.S.-born persons (8.1% and 2.1%, respectively) (Table 67). Racial disparities in the proportions of cases attributed to overall and extensive recent transmission were identified among American Indians/Alaska Natives (36.8% and 19.2%, respectively), Native Hawaiian/Other Pacific Islander (25.6% and 12.0%), and non-Hispanic Blacks/African Americans (21.2% and 9.8%).

Greater proportions of cases attributed to overall recent transmission and extensive recent transmission were identified among persons reporting injecting drug use (35.0% and 12.7%, respectively), non-injecting drug use (33.0% and 14.2%), or excess alcohol use (28.8% and 13.2%) within the past year compared with national averages for 2015–2016. Cases also were more frequently attributed to overall and extensive recent transmission among people experiencing homelessness within the past year (36.7% and 21.5%, respectively) and residents of a correctional facility at the time of diagnosis (21.8% and 12.5%).

LIMITATIONS

An important limitation of these methods for estimating recent transmission is that they can only be applied to 13,777 culture-confirmed, genotyped cases in 2015 and 2016. Clinically diagnosed TB cases are excluded from these methods, so pediatric cases are likely underrepresented in the estimates. This limitation is especially relevant for TB cases in young children, which are most likely to be due to recent transmission because of young age.

The proportions of cases attributed to recent transmission are generally higher in areas with

fewer *M. tuberculosis* genotypes. Recent transmission may be overestimated in relatively closed populations and remote areas, such as parts of Alaska, where prevalent genotypes have been predominant for many years. These characteristics make it difficult to distinguish cases attributed to recent transmission from cases due to reactivation of longstanding, untreated latent TB infection.

In general, estimates of recent transmission are limited by the molecular resolution of genotyping. As evidenced by whole-genome sequencing results, genomic diversity may be greater than what is apparent using current genotyping methods among cases reported by areas bordering Mexico. Recent transmission also may be overestimated in some counties with relatively large numbers of common genotypes (Table 24) because plausible source cases and transmission chains are more likely present for these genotypes. Conversely, single locus variants in genotyping results, which are assigned distinct genotypes, would not meet the method's criteria so recent transmission could be underestimated in some cases.

FUTURE APPLICATIONS

The estimates provided here present a description of the U.S. landscape of recent transmission. The estimates should be considered as one type of data to describe TB epidemiology in a particular jurisdiction. Although national surveillance data can only provide aggregated estimates, these methods offer state and local TB control programs new opportunities to track trends in recent transmission and prioritize public health activities and interventions.

REFERENCES

1. France AM, Grant J, Kammerer JS, Navin TR. A field-validated approach using surveillance and genotyping data to estimate tuberculosis attributable to recent transmission in the United States. [Am J Epidemiol](#) 2015; 182: 799-807.
2. Yuen CM, Kammerer JS, Marks K, Navin TR, France AM. Recent Transmission of Tuberculosis - United States, 2011-2014. [PLoS One](#) 2016; 11: e0153728.