Tuberculosis Control Branch Surveillance Definitions for TB Outbreaks

Confirmed outbreak

- ≥4 California culture-positive TB cases[1,2], AND
- Cases occurred within a 3-year period[3], AND
- Definite or probable epidemiologic links[4] AND
- Phylogenetic analysis of WGS data indicates that all isolates from outbreak TB cases are 0-5 SNPs apart

Probable outbreak

- ≥4 California verified[5] TB cases[2], AND
- Cases occurred within a 3-year period[3], AND
- Definite or probable epidemiologic links[4] AND
- Phylogenetic analysis indicates that isolates from TB cases are 0-5 SNPs apart or are unavailable AND
- Does not meet the confirmed outbreak definition

OR

- ≥4 California verified[5] TB cases[2], AND
- Cases occurred within a 3-year period[3], AND
- Possible epidemiologic links[4] AND
- Phylogenetic analysis indicates that isolates from the TB cases are 0-2 SNPs apart or unavailable AND
- Does not meet the confirmed outbreak definition

Suspected outbreak

- ≥3 California verified TB cases[2] AND
- Does not meet the confirmed or probable outbreak definition AND
- Triggered by genotyping surveillance alerts[6]

OR

- ≥3 California verified cases[2] OR patients started on TB treatment due to likely TB disease, AND
- Does not meet the confirmed or probable outbreak definition AND
- Cases occurred within a 3-year period[3], AND
- Any epidemiologic link[4], AND
- Available phylogenetic analysis indicates that isolates from the TB cases are 0-5 SNPs apart

OR

- ≥3 California verified cases[2] OR patients started on TB treatment due to likely TB disease, AND
- Does not meet the confirmed or probable outbreak definition AND
- Cases occurred within a 3-year period[3], AND
- No known epidemiologic links[4], AND
- Available phylogenetic analysis indicates that isolates from the TB cases are 0-2 SNPs apart, AND
- All cases have factors:
    a. Suggesting increased risk of progression to disease (e.g., immunocompromised, children ≤4 years of age) OR
    b. Sharing drug resistant MTB patterns OR
    c. With common demographic characteristics (e.g., age, sex, country of origin)

[1] A single culture-negative pediatric case ≤4 years of age can be included as one of the 4 cases if the case has a definite epidemiologic link to a culture-confirmed case.

[2] One culture-confirmed TB case counted by another U.S. state can be included.

[3] Time interval between cases is calculated using a combination of the following: report date (RVCT Q#1), count date (RVCT Q#2), TB symptom start date (RVCT Q#24), TB treatment start date (RVCT Q#30), or genotyped-specimen collection date

[4] Epidemiologic Link Definitions on the subsequent page

[5] Definition of “verified case" in the CDC 2020 Report of Verified Case of Tuberculosis (RVCT) Instruction Manual, Appendix B, page 69 www.cdc.gov/tb/programs/rvct/InstructionManual.pdf

[6] Alerts such as CDC TB Genotyping Information Management System, CDC large outbreak in the U.S., or genotype surveillance conducted by TBCB

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Epidemiologic Link Definitions

Definite epidemiologic link:

- One of the cases is identified as a contact during one of the case's infectious period

OR

- The two cases were at the same place at the same time during one of the case's infectious period

Probable epidemiologic link:

- The two cases were at the same place around the time of one of the case's infectious period; however, the timing of when the two cases were at the same place, or the timing of the infectious period, was not certain enough to meet the definite epi-link criteria.

OR

- The two cases share a common contact without naming each other as direct contacts

OR

- The two cases are linked on a social network site or in Accurint that provides strong evidence that they had direct contact with each other during one of the case's infectious period

Possible epidemiologic link:

- The two cases reside in the same locally defined neighborhood

OR

- The two cases are linked on a social network site or person-search database (e.g., Accurint) but there is no evidence to suggest that they had direct contact with each other during the case's infectious period

OR

- The two cases have at least one shared friend or associate on a social network site

OR

- The two cases share social or behavioral traits (e.g., injection drug use, homelessness, etc.) that increase the risk of transmission

Tuberculosis Control Branch Surveillance Definitions for TB Outbreaks

BACKGROUND

The California Department of Public Health's TB Control Branch (TBCB) updated its TB outbreak surveillance definitions and epidemiologic link definitions in 2013. These definitions were used from 2013-2021. Resulting outbreak data were used to develop TBCB's first Annual TB Outbreak Surveillance Report and helped describe the burden of recent TB transmission and assess progress towards TB elimination. During this same timeframe, TBCB partnered with CDC and local health departments to increase the use of whole-genome sequencing (WGS) and phylogenetic analysis for TB isolates in California. The primary use of WGS data to date has been to help guide and focus TB outbreak investigations.

In 2017, CDC announced plans to implement universal WGS for TB in the United States starting in spring 2018. The discriminatory power of TB WGS more precisely helps TB control programs identify outbreaks and outbreak cases. For this reason, TBCB recognized that its TB outbreak surveillance definitions needed to be updated to include consideration of WGS results when available. In this new era of genomic epidemiology, this document incorporates phylogenetic analysis of WGS data in TB outbreak surveillance definitions. These updated outbreak surveillance definitions were applied and evaluated to transmission events detected during a testing period in 2019-2020 and were finalized in 2022. TBCB Outbreak Prevention and Control Section began to apply these definitions to outbreak and genotype cluster investigations in 2022.