

Importance of Retrospective Analysis Following Large Contact Investigations

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Introduction

In 2017, Indiana reported 100 cases of Tuberculosis (TB), with an incidence rate of 1.5 cases per 100,000 population. Despite a low burden of TB across the state, approximately 40 sputum smear-positive cases are reported annually, requiring contact investigations and potentially leading to ongoing transmission. From 2013-2016, over 6,000 people were identified as contacts to infectious TB cases in Indiana, each potentially having latent TB infection (LTBI) and increasing the reservoir for future TB cases.

In addition to evaluating and monitoring the results of contact investigations for infectious TB cases during their time, the monitoring of genotype results allows for retrospective identification of missed contacts or gaps in previous investigations.

Background

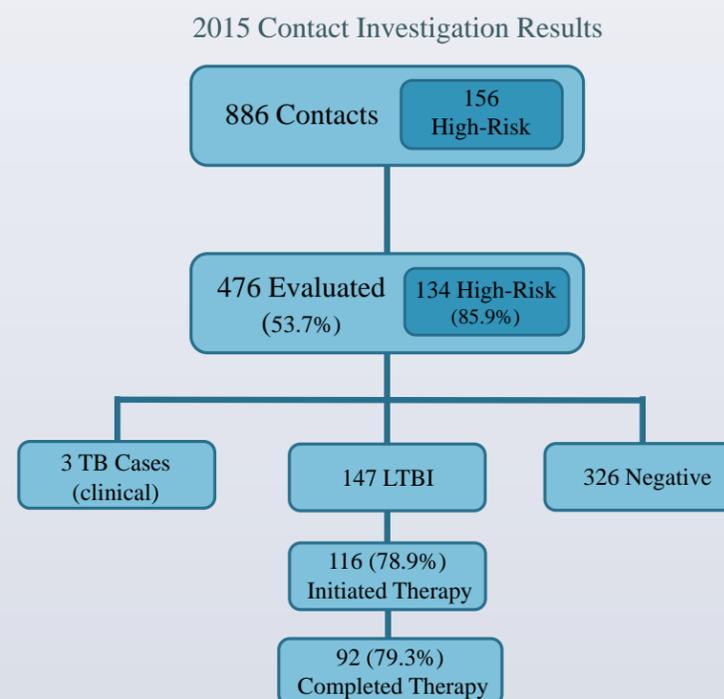
In 2015, a 19-year-old male high school student was diagnosed with pulmonary TB disease. Initial sputum smears showed high bacterial burden at >50 AFB/field and radiologic imaging showed extensive cavitory disease. Sputum cultures were positive for MTB complex, and susceptibility testing showed the strain was pansensitive. Genotyping results identified the strain as genotype G07471, a new strain to Indiana but consistent with other cases in the U.S. with the same country of birth.

Based on symptomology, the infectious period was determined to span 9 months. Initial contact testing included classmates at the high school as well as teammates from a basketball league. Due to a high positivity rate among evaluated contacts, the investigation was expanded to include the entire K-12 school, a church, a university-based basketball practice, and a statewide travel basketball league.

Methods

Results of the 2015 contact investigation and associated LTBI and TB cases were extracted from Indiana's Statewide Investigation, Monitoring and Surveillance System (SWIMSS) along with Excel-based documentation from the investigation. Matching genotype results were found by searching the CDC's TB Genotyping Information Management System (TB GIMS) and combining with the surveillance and investigation data extracted from patients' records in TB SWIMSS.

Results



Post-investigation surveillance through 2017 identified two additional cases of TB disease that are genotypically linked to the 2015 case with genotype G07471. Neither case had been identified as a contact during the initial investigation.

Genotypically Linked Case 1

- 19-year-old male, U.S. born
- Diagnosed in October 2016
- Pulmonary disease with cavitation and positive sputum smears
- Pansensitive and genotype G07471
- Father was a coach in the same basketball league as 2015 case
- No confirmed direct contact with 2015 case

Genotypically Linked Case 2

- 67-year-old male, U.S. born
- Diagnosed in March 2017
- Pulmonary disease with positive sputum smears and history of diabetes
- Pansensitive and genotype G07471
- Son was a known contact to 2015 case, having played on the same basketball team
- Minimal direct contact with 2015 case

Conclusions

Evaluation and treatment outcomes were lower for the 2015 contact investigation than normally seen within Indiana due to several factors. First, the expansion of the investigation to over 800 contacts taxed resources and increased the difficulty of data management. Efforts were further complicated due to the diversity of locations within the investigation and among the contacts, with positive reactors residing in 11 different counties across the state. However, focusing efforts and resources on high-risk contacts was effective in increasing the number of persons evaluated among those with the most exposure. Additionally, increased education and collaboration with healthcare providers led to a strong uptake of LTBI treatment and completion. No cases among identified contacts have occurred in the two years following the investigation.

Although both genotypically linked cases have epi-links to the 2015 case, neither had sufficient contact that would have warranted testing during the original investigation. Ongoing cases in this cluster continue to be expected due to the overall infectiousness of the 2015 case and the virulence of this specific TB strain.

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