The use of Genotyping in Identifying a Tuberculosis Outbreak, Maine 2016-2017

Emily Tholen*, MPH; Jamie Cotnoir*, MPH
*Maine Center for Disease Control

BACKGROUND: Maine is a low incidence state for active Tuberculosis (TB) cases with around 14 to 23 sporadic cases of TB per year. A confirmed outbreak of TB in Maine is defined as: 1) two or more contacts are found to have of active disease during a contact investigation and at least three of the TB genotypes (any combination of contacts and/or initial case) are identical or 2) two or more patients with active TB disease occur within two years of each other and are not identified during a contact investigation, but are later found to have an epidemiologic link and have identical genotypes. Through the results of genotyping, Maine identified an outbreak of TB in 2017.

METHODS: All patients with infectious active TB disease have a contact investigation, where the Maine Center for Disease Control (Maine CDC) Tuberculosis Control Program and Public Health Nursing staff identify close contacts and evaluate them for TB; all patients with culture positive active TB disease have an isolate sent to the United States Centers for Disease Control (US CDC) for TB genotyping. US CDC maintains the Tuberculosis Genotyping Information Management System (TB GIMS) which reports genotyping results and alerts for clusters of identical TB genotypes, which could be possible outbreaks.

RESULTS: Active TB case patient 2 of 2017 (2_17) identified case patient 21 of 2016 (21_16) and case patient 3 of 2017 (3_17) as close contacts during a routine contact investigation. While initially this seemed like an outbreak, genotyping showed that only patients 21_16 and 3_17 genotypes matched, proving otherwise. Two months later, an isolate from the extrapulmonary TB case 6 of 2017 (6_17) was found to be an identical match to the cluster. The resulting investigation found that patient 21_16 and 6_17 were epidemiologically linked.

CONCLUSIONS: While genotyping initially ruled out an outbreak among a cluster of three patients with active pulmonary TB, it found an additional patient with extrapulmonary TB who would not have been identified as a contact. This confirmed an outbreak of tuberculosis in Maine and allowed the Maine CDC to identify that case 21_16 was likely the source case for both patient 3_17 and 6_17 and expand the contact investigation to test contacts not previously known. Genotyping can be a useful tool in confirming outbreaks and finding additional outbreak-associated cases, especially when case patients may not reveal or remember close contacts.