



# Establishment of *Mycobacterium tuberculosis* Complex Whole Genome Sequencing Reference Centers, 2015–2019

Whole genome sequencing (WGS) of *Mycobacterium tuberculosis* complex (MTBC) provides detailed genomic information that increases the accuracy of outbreak investigations and can identify drug-resistant strains. Over a four-year period (2015-2019), the Association of Public Health Laboratories (APHL), in collaboration with the US Centers for Disease Control and Prevention (CDC) Division of TB Elimination (DTBE), supported up to six public health laboratories to evaluate and demonstrate the utility of this method by performing WGS on MTBC isolates from their jurisdiction or provided by DTBE.

## PROJECT HIGHLIGHTS

Over the first five contract years of the TB WGS Project (2015-2019):

- Reference centers were set up at the state public health laboratories of California, Iowa, Michigan, New York, Ohio and Virginia, though not all participated every year of the project.
- APHL and CDC provided \$1.49 million in support to the six reference centers.
- A total of 6,712 MTBC isolates were sequenced.
- The project supported the implementation of universal TB sequencing for clinical diagnosis in New York.

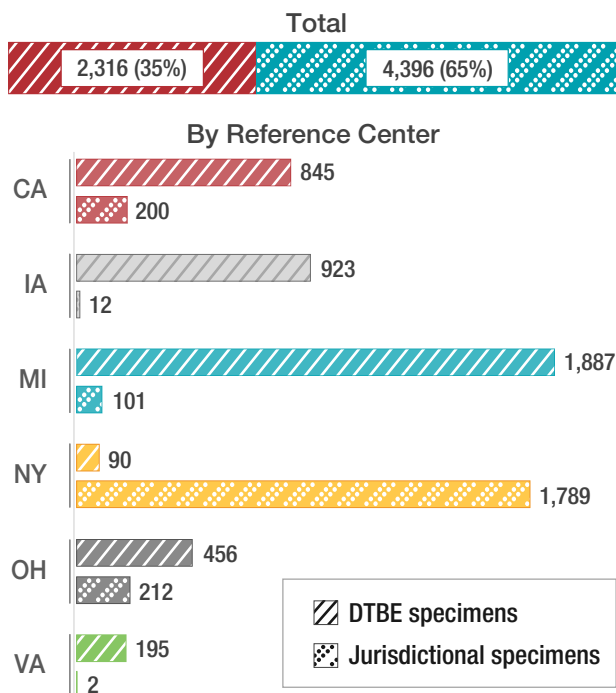
## SUCCESSSES

Major successes included:

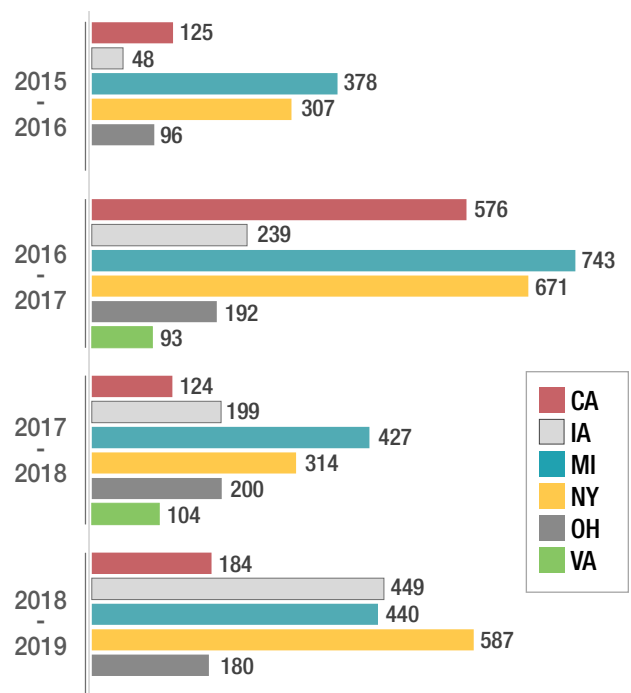
- Increased efficiency
- Decreased turn-around time (TAT)
- Improved protocols
- Better collaboration and idea exchange among participating laboratories

In New York, TAT for WGS results fell from 28 days to 13-15 days over the first six months of their participation in the project (January-June 2016). Also, compared to their first line Drug Susceptibility Testing, WGS resulted in shorter TAT in 36 of 46 cases by an average of 10 days.

Total DTBE and Jurisdictional MTBC Specimens Sequenced, 2015-2019



Total MTBC Specimens Sequenced Each Year, by Reference Center



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