

# Whole Genome Sequencing (WGS): New Lab Technology Helps Fight an Old Disease

## Why is WGS Useful to Tuberculosis Programs?

By **comparing** the *Mtb* DNA from different patients,



WGS allows health officials to **find** and **investigate** the spread of TB.

This information can help public health officials better respond to TB outbreaks.

## Mapping Related TB Cases

### Conventional Genotyping Methods

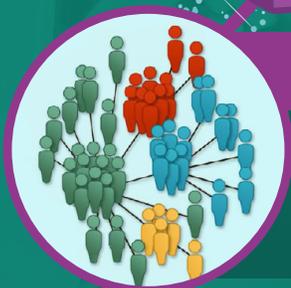
A cluster of TB cases can be indistinguishable by conventional methods.



### WGS Process

### Phylogenetic Map after WGS

A phylogenetic map of TB cases may distinguish between different clusters.



## Key Terms



**Conventional genotyping:** A laboratory-based test that analyzes specific sections of the *Mtb* genome; these distinct patterns can help distinguish different strains of *Mtb*

**Genome:** An organism's total DNA

***Mycobacterium tuberculosis* (Mtb):** The organism that causes TB

**Phylogenetic map:** A diagram of the genetic relationships among *Mtb* cases

**TB genotype cluster:** Two or more patients with matching genotype patterns

**Whole genome sequencing (WGS):** A process that examines the entire DNA of an organism



## WGS is a Significant Scientific Advancement

Conventional genotyping methods examine

**less than 1%**

of the genome.



Whole genome sequencing can examine

**more than 90%**

of the genome.

## CDC Uses WGS to Inform TB Prevention and Response Strategies

CDC's TB Laboratory is a leader in use of WGS for cluster detection to identify potential outbreaks and for surveillance of drug resistance.

CDC funds the National TB Molecular Surveillance Center (NTMSC)

that provides WGS results for *Mtb* samples received from all newly diagnosed patients in the United States. NTMSC is part of the Antibiotic Resistance Laboratory Network.



CDC has supported WGS for **500+** TB clusters in the U.S. since 2012.

The number of TB cases in each of these clusters ranges from **2** to **182**.