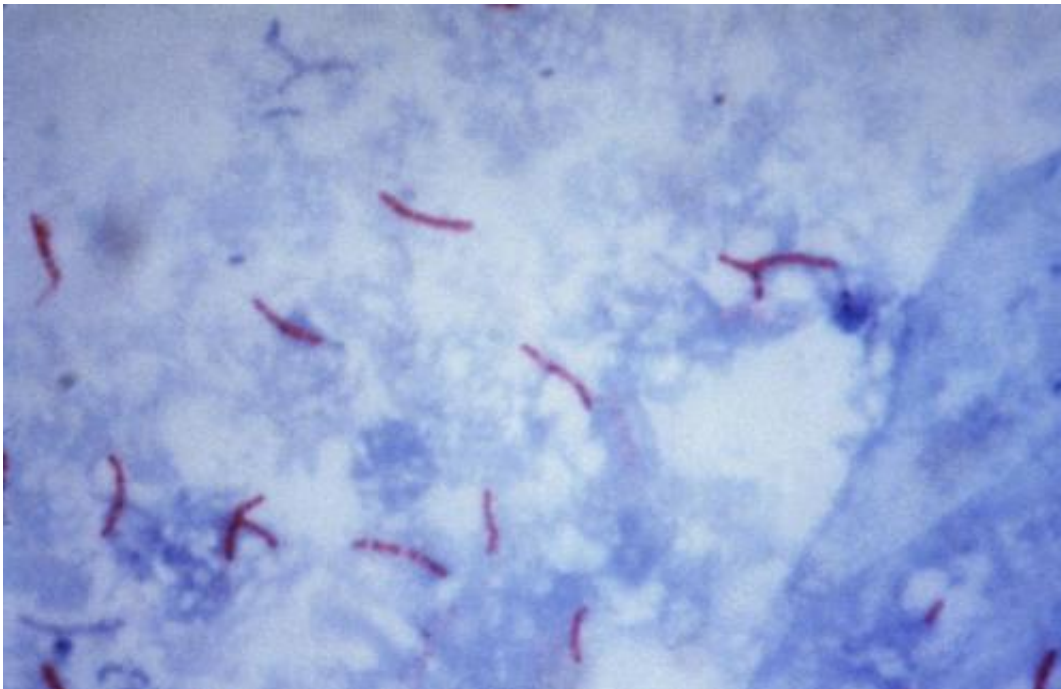


Genome sequencing helps determine end of tuberculosis outbreak

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This photomicrograph reveals *Mycobacterium tuberculosis* bacteria using acid-fast Ziehl-Neelsen stain; Magnified 1000 X. The acid-fast stains depend on the ability of mycobacteria to retain dye when treated with mineral acid or an acid-alcohol solution such as the Ziehl-Neelsen, or the Kinyoun stains that are carbolfuchsin methods specific for *M. tuberculosis*. Credit: public domain

Using genome sequencing, researchers from the University of British Columbia, along with colleagues at the Imperial College in London, now have the ability to determine when a tuberculosis (TB) outbreak is over.

The research is the first of its kind to demonstrate that [genomic analysis](#) can be used to determine when a TB outbreak has ended—valuable knowledge which can assist [public health](#) investigators understand an outbreak's dynamics and guide a real-time public health response. Genomic analysis involves reading the complete genetic instructions of the pathogens causing a [disease](#), and using that data to infer who might have infected whom. By looking for mutations that are shared between the pathogens taken from different people, researchers can see whose pathogens are most closely related to each other, suggesting potential transmission.

"Declaring the end of a TB outbreak is a difficult thing to do," said senior author Jennifer Gardy, assistant professor in UBC's School of Population and Public Health and a senior scientist at the British Columbia Centre for Disease Control. "Because the bacterium that causes TB can lie dormant in someone's lung for months or even years before it causes disease, we had no way of knowing whether a TB case we have just diagnosed was a recent infection - suggesting the outbreak is still going on - or whether the person was infected years ago."

Using mathematical and statistical techniques, the researchers evaluated a TB outbreak that began in May 2008 and were able to determine when each outbreak case was infected. This provided public health officials with a way to determine when disease transmission had stopped and the outbreak had ended. They were able to declare the outbreak over in January 2015, after the data indicated no [disease transmission](#) had occurred since mid-2012.

"By using a series of techniques from the world of mathematics and statistics, we can come up with an estimated time at which each infection occurred," explained Gardy. "This information is incredibly useful to the [public health officials](#) managing an outbreak. Responding to an outbreak requires a lot of effort and resources, and we need to

know when we can step down our response."

"Genomics has been used to monitor infectious disease outbreaks before, but this is the first time it's ever been possible to declare a complicated outbreak of TB over," said Gardy. "It really opens up new doors in the world of TB control."

This study was published in *Microbial Genomics*.

In 2011, Gardy and her colleagues were the first to use the emerging science of genomics to solve a TB outbreak. By reading the complete DNA sequence of the TB bacterium from each patient in an outbreak, her group showed that it was possible to determine who likely infected whom in the [outbreak](#). This new work extends this earlier research by introducing a new method to determine when those infections occurred.

More information: Patrick Tang et al, Declaring a tuberculosis outbreak over with genomic epidemiology, *Microbial Genomics* (2016). [DOI: 10.1099/mgen.0.000060](https://doi.org/10.1099/mgen.0.000060)

Provided by University of British Columbia

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