

Sequencing tuberculosis strain genomes

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(Medical Xpress)—The use of whole genome sequencing to identify different strains of bacteria which cause tuberculosis may unlock the door to improved treatments and more accurate clinical trials, according to a new international study.

A team of researchers, including doctors from the University of St Andrews School of Medicine, has established that the unprecedented accuracy of whole [genome](#) sequencing as a method of identifying individual bacterial strains of TB has important implications for the study and prevention of the [recurrence](#) of TB infection.

TB remains one of the single biggest public health challenges facing mankind. One third of the world's population is thought to have been infected with TB organisms, with new infections occurring in about 1% of the population each year. In 2007, there were an estimated 13.7 million chronic active cases globally, while in 2010, there were an estimated 8.8 million new cases and 1.5 million associated deaths, mostly occurring in developing countries.

More people in the developing world contract tuberculosis because of compromised immunity, largely due to high rates of HIV infection and the corresponding development of AIDS.

Although most forms of TB are treatable with antibiotics, it is not uncommon for TB to recur in patients after treatment. Until now, it was difficult for doctors to establish if a patient with a recurring TB had simply suffered a relapse of the original infection, or an infection with a

new strain. This has important implications for the design of [clinical trials](#) of new TB drugs and makes managing the disease challenging for medics.

The initial and follow-up strains from patients with recurring TB in the REMoxTB clinical trial however, and comparing the results with the standard TB diagnostic test, the research team was able to show that WGS yields a whole new level of diagnostic clarity finding many patients with two strains of the pathogen infecting simultaneously.

Their study, published in *The Lancet Respiratory Medicine* has prompted an editorial from *The Lancet* arguing that the rapid evolution of technology could mean that WGS becomes an affordable gold standard in trials testing new TB regimens.

One of the report's authors - Professor Stephen Gillespie, Sir James Black Professor Medicine and Director of Research at the University of St Andrews School of Medicine, said:

"What surprised us in this study is the frequency with which patients were infected with two different strains of M. [tuberculosis](#).

"As well as being important for future TB clinical trials this result has important implications for the evolution of Multiple Drug Resistant Tuberculosis (MDRTB). With the wider availability of next generation sequencing we hope that follow up studies will reveal more about this devastating disease."

Provided by University of St Andrews

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